PLANT GENOME SEQUENCE AND USES THEREOF

Field of the Invention

The present invention is in the field of plant biochemistry and genetics. More specifically the invention relates to nucleic acid molecules from plant cells, in particular, genomic DNA sequences from *Oryza sativa* (rice) plants and nucleic acid molecules that contain markers, in particular, single nucleotide polymorphism (SNP) and repetitive element markers. In addition, the present invention provides nucleic acid molecules having regulatory elements or encoding proteins or fragments thereof. The invention also relates to proteins and fragments of proteins so encoded and antibodies capable of binding the proteins. The invention also relates to methods of using the nucleic acid molecules, markers, repetitive elements and fragments of repetitive elements, regulatory elements, proteins and fragments of proteins, and antibodies, for example for genome mapping, gene identification and analysis, plant breeding, preparation of constructs for use in plant gene expression, and transgenic plants.

Background of the Invention

I. Rice

Rice is one of three cereals produced annually at worldwide levels of approximately half a billion tons and more than 90% of produced rice is for human consumption (*Goff, S.A. Curr. Opin. Plant Biol. 2*:86-89 (1999), the entirety of which is herein incorporated by reference). Rice, however, is not only a commercially important crop, it is also a model for other cereal crops. The identification in *Oryza sativa* (rice) of proteins, genetic and physical markers, biological agents such as plant promoters, open reading frames, plant gene intron regions, plant gene intron/exon junctions, and regulatory elements, *etc.*,is important in the development of nutritionally enhanced or agriculturally enhanced crops, in particular cereal crops. Such agents are useful

in, for example, marker development, genetic mapping or linkage analysis, marker assisted breeding, physical genome mapping, transgenic crop production, crop monitoring diagnostics, antibody production and gene modification. Such agents can also have pharmaceutical or nutriceutical applications.

Rice can be used as a model for other cereal genomes because it has a genome size smaller than the other major cereals. The size of the rice genome is estimated at 420 to 450 megabase pairs. Sorghum, maize, barley and wheat have larger genomes (1000, 3000, 5000 and 16000 Mpb respectively). The smaller genome size of rice results in a higher gene density relative to the other cereals. Based on estimates of 30,000 genes in a cereal genome, rice will have on average one gene approximately every 15 Kbp. Similarly, maize and wheat have one gene approximately every 100 and 500 kpb, respectively. It has been reported that this higher gene density in rice makes it a target for cereal gene discovery efforts and genomic sequence analysis (*Goff, S.A Curr. Opin. Plant Biol. 2*:86-89 (1999), the entirety of which is herein incorporated by reference). Although the genes in rice are present at a higher relative density than in other cereals, they are predicted to be arranged in a similar general order within the genome (*Goff, S.A Curr. Opin. Plant Biol. 2*:86-89 (1999)). Comparisons of the physical and genetic maps of cereal genomes have lead to reports that colinearity of gene order exists among the various cereal genomes studied.

In addition to the general conservation of gene order among the cereals, studies of a number of individual genes demonstrate that there is also considerable homology among various cereal gene families. This conservation of gene and protein sequence suggests that studies on the functions of genes or proteins from one cereal could lead to the elucidation of the functions of orthologous genes/proteins in other cereals. Non-coding regulatory regions of the genome may also retain similar function between the various cereals. For example, strong constitutive or

tissue-specific promoters from one cereal are likely to retain function when introduced as a portion of a transgene in another species (*Goff, S.A Curr. Opin. Plant Biol. 2*:86-89 (1999).

II. SEQUENCE COMPARISONS

Genome sequence information from rice allows comparisons of rice sequences with other rice sequences as well as with those of other flowering plant genome sequences, particularly other cereal plant species, and also with genome sequences and gene sequences from other organisms, including bacteria, humans, and yeast. Such information provides valuable insights into the translation of plant genetic information into a flowering plant and also reveals genetic differences involved in the differentiation of the plant kingdom. In addition, genome sequencing and mapping provides increased opportunities for identification and isolation of agents associated with plant traits, as well as insight into mechanisms of genome interactions.

Rice sequences can be compared, for example, to sequences that encode promoters or proteins or other sequences. These homologies can be determined by similarity searches (Adams *et al.*, *Science 252*:1651-1656 (1991), the entirety of which is herein incorporated by reference).

A characteristic feature of a DNA sequence is that it can be compared with other DNA sequences. Sequence comparisons can be undertaken by determining the similarity of the test or query sequence with sequences in publicly available or propriety databases ("similarity analysis") or by searching for certain motifs ("intrinsic sequence analysis")(*e.g.*, cis elements)(Coulson, *Trends in Biotechnology*, 12:76-80 (1994); Birren *et al.*, Genome Analysis, 1:543-559 (1997), both of which are herein incorporated by reference in their entirety).

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(http://www.ddbj.nig.ac.jp/); Genebank (http://www-ncbi.nlm.nih.gov/web/Genbank/Index.htlm); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) (http://www.ebi.ac.uk/ebi_docs/embl_db.html). A

number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12*:76-80 (1994); Birren, *et al.*, *Genome Analysis, 1*:543-559 (1997)).

BLASTN takes a nucleotide sequence (the query sequence) and its reverse complement and searches them against a nucleotide sequence database. BLASTN was designed for speed, not maximum sensitivity, and may not find distantly related coding sequences. BLASTX takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database. BLASTX is useful for sensitive analysis of preliminary (single-pass) sequence data and is tolerant of sequencing errors (Gish and States, *Nature Genetics, 3*:266-272 (1993), the entirety of which is herein incorporated by reference).

Given a coding nucleotide sequence and the protein it encodes, it is often preferable to use the protein as the query sequence to search a database because of the greatly increased sensitivity to detect more subtle relationships. This is due to the larger alphabet of proteins (20 amino acids) compared with the alphabet of nucleic acid sequences (4 bases), where it is far easier to obtain a match by chance. In addition, with nucleotide alignments, only a match (positive score) or a mismatch (negative score) is obtained, but with proteins, the presence of conservative amino acid substitutions can be taken into account. Here, a mismatch may yield a positive score if the non-identical residue has physical/chemical properties similar to the one it replaced. Various scoring matrices are used to supply the substitution scores of all possible amino acid pairs. A general purpose scoring system is the BLOSUM62 matrix (Henikoff and Henikoff, *Proteins, 17*:49-61 (1993), the entirety of which is herein incorporated by reference),

which is currently the default choice for BLAST programs. BLOSUM62 is tailored for alignments of moderately diverged sequences and thus may not yield the best results under all conditions. Altschul, *J. Mol. Biol. 36*:290-300 (1993), the entirety of which is herein incorporated by reference, uses a combination of three matrices to cover all contingencies. This may improve sensitivity, but at the expense of slower searches. In practice, a single BLOSUM62 matrix is often used but others (PAM40 and PAM250) may be attempted when additional analysis is necessary. Low PAM matrices are directed at detecting very strong but localized sequence similarities, whereas high PAM matrices are directed at detecting long but weak alignments between very distantly related sequences.

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package available that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol. 25*:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated, and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both the pairwise alignments and the multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: ftp.ebi.ac.uk. Another program is MACAW (Schuler *et al.*, *Proteins, Struct. Func. Genet, 9*:180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows

versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms, and is available by anonymous ftp at: ncbi.nlm.nih.gov (directory/pub/macaw).

Sequence motifs are derived from multiple alignments and can be used to examine individual sequences or an entire database for subtle patterns. With motifs, it is sometimes possible to detect distant relationships that may not be demonstrable based on comparisons of primary sequences alone. Currently, the largest collection of reported sequence motifs is PROSITE (Bairoch and Bucher, *Nucleic Acid Research, 22*:3583-3589 (1994), the entirety of which is herein incorporated by reference). PROSITE may be accessed via either the ExPASy server on the World Wide Web or anonymous ftp site. Many commercial sequence analysis packages also provide search programs that use PROSITE data.

A resource for searching protein motifs is the BLOCKS E-mail server developed by S. Henikoff, *Trends Biochem Sci.*, *18*:267-268 (1993), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Nucleic Acid Research*, *19*:6565-6572 (1991), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Proteins*, *17*:49-61 (1993). BLOCKS searches a protein or nucleotide sequence against a database of protein motifs or "blocks." Blocks are defined as short, ungapped multiple alignments that represent highly conserved protein patterns. The blocks themselves are derived from entries in PROSITE as well as other sources. Either a protein or nucleotide query can be submitted to the BLOCKS server; if a nucleotide sequence is submitted, the sequence is translated in all six reading frames and motifs are sought in these conceptual translations. Once the search is completed, the server will return a ranked list of significant matches, along with an alignment of the query sequence to the matched BLOCKS entries.

Conserved protein domains can be represented by two-dimensional matrices, which measure either the frequency or probability of the occurrences of each amino acid residue and

deletions or insertions in each position of the domain. This type of model, when used to search against protein databases, is sensitive and usually yields more accurate results than simple motif searches. Two popular implementations of this approach are profile searches (such as GCG program ProfileSearch) and Hidden Markov Models (HMMs) (Krough, *et al.*, *J. Mol. Biol.* *235*:1501-1531 (1994); Eddy, *Current Opinion in Structural Biology* *6*:361-365 (1996), both of which are herein incorporated by reference in their entirety). In both cases, a large number of common protein domains have been converted into profiles, as present in the PROSITE library, or HHM models, as in the Pfam protein domain library (Sonnhammer, *et al.*, *Proteins* *28*:405-420 (1997), the entirety of which is herein incorporated by reference). Pfam contains more than 500 HMM models for enzymes, transcription factors, signal transduction molecules, and structural proteins. Protein databases can be queried with these profiles or HMM models, which will identify proteins containing the domain of interest. For example, HMMSW or HMMFS, two programs in a public domain package called HMMER (Sonnhammer, *et al.*, *Proteins* *28*:405-420 (1997)) can be used.

PROSITE and BLOCKS represent collected families of protein motifs. Thus, searching these databases entails submitting a single sequence to determine whether or not that sequence is similar to the members of an established family. Programs working in the opposite direction compare a collection of sequences with individual entries in the protein databases. An example of such a program is the Motif Search Tool, or MoST (Tatusov, *et al.*, *Proc. Natl. Acad. Sci.* *91*:12091-12095 (1994), the entirety of which is herein incorporated by reference). On the basis of an aligned set of input sequences, a weight matrix is calculated by using one of four methods (selected by the user); a weight matrix is simply a representation, position by position in an alignment, of how likely a particular amino acid will appear. The calculated weight matrix is then used to search the databases. To increase sensitivity, newly found sequences are added to

the original data set, the weight matrix is recalculated, and the search is performed again. This procedure continues until no new sequences are found.

III. Contig Assembly

SUB C2

A characteristic feature of a large scale shotgun sequencing project is that the sequence data can be processed and assembled into contiguous sequences (contigs), which represent a reconstruction of the original genome sequence from the cloned fragments. Likewise, individual Bacterial Artificial Chromosome (BAC) clones within a BAC library can be shot gun sequenced and these data can be assembled into contigs within each clone. Programs are available in the public domain that can analyze the sequence output and assemble the sequences into larger sequence regions representing contiguous sequences of the target genome. Examples of such programs can be found at, for example, http://genome.wustl.edu/gsc, http://www.sanger.ac.uk, and http://www.mbt.washington.edu. An example of sequence reading program is Phred (http://www.mbt.washington.edu). Phred reads DNA sequencer trace data, calls bases, assigns quality values to the bases, and writes the base calls and quality values to output files.

SUB C3

The process of assembling DNA sequence fragments generally involves three phases; the overlap phase, the layout phase and the multi-alignment, or consensus, phase. In the overlap phase, each fragment is compared against every other fragment to determine if they share a common subsequence, an indication that they were potentially sampled from overlapping stretches of the original DNA strand. Pairs of fragments are compared in two ways; 1) with both fragments in the same relative orientation, and 2) with one of the fragments having been reverse complemented. In the layout phase, a series of alternate assemblies or layouts of the fragments based on the pairwise overlaps is generated. A layout specifies the relative locations and orientations of the fragments with respect to each other and is typically visualized as an arrangement of overlapping directed lines, one for each fragment. The general criterion for the layout phase is to produce

plausible assemblies of maximum likelihood. In this manner, it can be determined if there is more than one way to put the pieces together and if different solutions appear equally plausible. In such a case, one would return to the lab and obtain additional information to resolve the ambiguity. The multi-alignment, or consensus, phase uses more information than just the pairwise alignments in the layout. The sequences of all the fragments in a layout are simultaneously aligned, giving a final set of contigs representing regions of the target genome. An example of an assembly program is PHRAP, which can be found at http://chimera.biotech.washington.edu/UWGC/tools/phrap.htm.

IV. Gene Mapping and Marker Assisted Introgression of Plant Traits

Genome sequence information from rice provides markers that will assist in the development of improved plants. Marker assisted introgression of traits into plants have been reported. An initial step in that process is the localization of the trait by gene mapping. Gene mapping is the process of determining a gene's position relative to other genes and genetic markers through linkage analysis. The basic principle for linkage mapping is that the closer together two genes are on the chromosome, the more likely they are to be inherited together (Rothwell, *Understanding Genetics. 4th Ed.* Oxford University Press, New York, p. 703 (1988), the entirety of which is herein incorporated by reference). Briefly, a cross is made between two genetically compatible but divergent parents relative to traits under study. Genetic markers are then used to follow the segregation of traits under study in the progeny from the cross (often a backcross, F_2, or recombinant inbred population).

Linkage analysis is based on the level at which markers and genes are co-inherited (Rothwell, *Understanding Genetics. 4th Ed.* Oxford University Press, New York, p. 703 (1988). Statistical tests like chi-square analysis can be used to test the randomness of segregation or linkage (Kochert, *The Rockefeller Foundation International Program on Rice Biotechnology,*

University of Georgia Athens, GA, pp. 1-14 (1989), the entirety of which is herein incorporated by reference). In linkage mapping, the proportion of recombinant individuals out of the total mapping population provides the information for determining the genetic distance between the loci (Young, *Encyclopedia of Agricultural Science, Vol. 3*, pp. 275-282 (1994), the entirety of which is herein incorporated by reference).

Classical mapping studies utilize easily observable, visible traits instead of molecular markers. These visible traits are also known as naked eye polymorphisms. These traits can be morphological like plant height, fruit size, shape and color or physiological like disease response, photoperiod sensitivity or crop maturity. Visible traits are useful and are still in use because they represent actual phenotypes and are easy to score without any specialized lab equipment. By contrast, the other types of genetic markers are arbitrary loci for use in linkage mapping and often not associated to specific plant phenotypes (Young, *Encyclopedia of Agricultural Science,* Vol. 3, pp. 275-282 (1994). Many morphological markers cause such large effects on phenotype that they are undesirable in breeding programs. Many other visible traits have the disadvantage of being developmentally regulated (*i.e.*, expressed only certain stages; or at specific tissue and organs). Oftentimes, visible traits mask the effects of linked minor genes making it nearly impossible to identify desirable linkages for selection (Tanksley *et al., Biotech. 7*:257-264 (1989), the entirety of which is herein incorporated by reference).

Although a number of important agronomic characters are controlled by loci having major effects on phenotype, many economically important traits, such as yield and some forms of disease resistance, are quantitative in nature. This type of phenotypic variation in a trait is typically characterized by continuous, normal distribution of phenotypic values in a particular population (polygenic traits) (Beckmann and Soller, *Oxford Surveys of Plant Molecular Biology, Miffen.* (ed.), Vol. 3, Oxford University Press, UK., pp. 196-250 (1986), the entirety of which is herein

incorporated by reference). Loci contributing to such genetic variation are often termed, minor genes, as opposed to major genes with large effects that follow a Mendelian pattern of inheritance. Polygenic traits are also predicted to follow a Mendelian type of inheritance, however the contribution of each locus is expressed as an increase or decrease in the final trait value.

The advent of DNA markers, such as restriction fragment length polymorphic markers (RFLPs), microsatellite markers, single nucleotide polymorphic markers (SNPs), and random amplified polymorphic markers (RAPDs), allow the resolution of complex, multigenic traits into their individual Mendelian components (Paterson *et al.*, *Nature 335:*721-726 (1988), the entirety of which is herein incorporated by reference). A number of applications of RFLPs and other markers have been suggested for plant breeding. Among the potential applications for RFLPs and other markers in plant breeding include: varietal identification (Soller and Beckmann, *Theor. Appl. Genet. 67:*25-33 (1983); Tanksley *et al.*, *Biotech. 7:*257-264 (1989), both of which are herein incorporated by reference in their entirety); QTL mapping (Edwards *et al.*, *Genetics 116:*113-115 (1987); Nienhuis *et al.*, *Crop Sci. 27:*797-803 (1987); Osborn *et al.*, *Theor. Appl. Genet. 73:*350-356 (1987); Romero-Severson *et al.*, *Use of RFLPs In Analysis Of Quantitative Trait Loci In Maize, In* Helentjaris and Burr (eds.), pp. 97-102 (1989); Young *et al.*, *Genetics 120:*579-585 (1988); Martin *et al.*, *Science 243:*1725-1728 (1989); Sarfatti *et al.*, *Theor. Appl. Genet. 78:*22-26 (1989); Tanksley *et al.*, *Biotech. 7:*257-264 (1989); Barone *et al.*, *Mol. Gen. Genet. 224:*177-182 (1990); Jung *et al.*, *Theor. Appl. Genet. 79:*663-672 (1990); Keim *et al.*, *Genetics 126:*735-742 (1990); Keim *et al.*, *Theor. Appl. Genet. 79:*465-369 (1990); *Paterson et al., Genetics 124:*735-742 (1990); Martin *et al.*, *Proc. Natl. Acad. Sci. USA 88:*2336-2340 (1991); Messeguer *et al.*, *Theor. Appl. Genet. 82:*529-536 (1991); Michelmore *et al.*, *Proc. Natl. Acad. Sci. USA 88:*9828-9832 (1991); Ottaviano *et al.*, *Theor. Appl. Genet. 81:*713-719 (1991); Yu *et al.*, *Theor. Appl. Genet. 81:*471-476 (1991); Diers *et al.*, *Crop Sci. 32:*377-383 (1992);

Diers *et al.*, *Theor. Appl. Genet. 83:*608-612 (1992); *J. Plant Nut. 15:*2127-2136 (1992); Doebley *et al., Proc. Natl. Acad. Sci. USA 87:*9888-9892 (1990), all of which are herein incorporated by reference in their entirety); screening genetic resource strains for useful quantitative trait alleles and introgression of these alleles into commercial varieties (Beckmann and Soller, *Theor. Appl. Genet. 67:*35-43 (1983), the entirety of which is herein incorporated by reference); marker-assisted selection (Tanksley *et al., Biotech. 7:*257-264 (1989)); and map-based cloning (Tanksley *et al., Biotech. 7:*257-264 (1989)). In addition, DNA markers can be used to obtain information about: (1) the number, effect, and chromosomal location of each gene affecting a trait; (2) effects of multiple copies of individual genes (gene dosage); (3) interaction between/among genes controlling a trait (epistasis); (4) whether individual genes affect more than one trait (pleiotropy); and (5) stability of gene function across environments (G x E interactions).

Summary of the Invention

The present invention provides a substantially purified nucleic acid molecule, the nucleic acid molecule capable of specifically hybridizing to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof or fragments of either.

The present invention also provides a substantially purified nucleic acid molecule encoding a rice protein or fragment thereof, wherein the rice protein or fragment thereof is encoded by a nucleic acid sequence selected from the group consisting of 69652 1 through SEQ ID NO: 69652 or complements thereof or fragments of either.

The present invention also provides a substantially purified protein or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof.

The present invention also provides a substantially purified protein or fragment thereof encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof or fragments of either.

The present invention also provides a substantially purified antibody or fragment thereof, the antibody or fragment thereof capable of specifically binding to the protein or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof or fragment of either.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule; which is linked to (B) a structural nucleic acid molecule, wherein the structural nucleic acid molecule is selected from the group consisting of a protein or fragment thereof encoding sequence located within SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof; which is linked to (C) a 3' non-translated sequence that functions in a plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule wherein the promoter nucleic acid molecule is selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof or fragments of either; which is linked to (B) a structural nucleic acid molecule encoding a protein or fragment thereof; which is linked to (C) a 3' non-translated sequence that functions in a plant

cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule; which is linked to (B) a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to a nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof and the transcribed strand is complementary to an endogenous mRNA molecule; which is linked to (C) a 3' non-translated sequence that functions in plant cells to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a transformed plant having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in a plant cell to cause the production of an mRNA molecule wherein the promoter nucleic acid molecule is selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof; which is linked to (B) a transcribed nucleic acid molecule with a transcribed strand and a non-transcribed strand, wherein the transcribed strand is complementary to an endogenous mRNA molecule; which is linked to (C) a 3' non-translated sequence that functions in plant cells to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a computer readable medium having recorded thereon one or more nucleic acid molecules encoding a rice protein or fragment thereof, wherein the rice protein or fragment thereof is encoded by a nucleic acid sequence selected from the

group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof or fragments of either.

The present invention also provides a method of introgressing a trait into a plant comprising using a nucleic acid marker for marker assisted selection of the plant, the nucleic acid marker complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof, and introgressing the trait into a plant.

The present invention also provides a method for screening for a trait comprising interrogating genomic DNA for the presence or absence of a marker molecule that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof; and detecting the presence or absence of the marker.

The present invention also provides a method for determining the likelihood of the presence or absence of a trait in a plant comprising the steps of: (A) obtaining genomic DNA from the plant; (B) detecting a marker nucleic acid molecule; wherein the marker nucleic acid molecule specifically hybridizes with a nucleic acid sequence that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof; (C) determining the level, presence or absence of the marker nucleic acid molecule, wherein the level, presence or absence of the marker nucleic acid molecule is indicative of the likely presence in the plant of the trait.

The present invention also provides a method for determining a genomic polymorphism in a plant that is predictive of a trait comprising the steps: (A) incubating a marker nucleic acid molecule, under conditions permitting nucleic acid hybridization, and a complementary nucleic acid molecule obtained from the plant, the marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or

complements thereof or fragments of either; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism.

The present invention also provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof or fragments of either; and (B) calculating the degree of association between the polymorphism and the plant trait.

The present invention provides a method for isolating a nucleic acid molecule in a non-rice cereal comprising: (A) defining a genomic region of rice by reference to a marker molecule, wherein said marker molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complement thereof or fragment of either; (B) identifying a syntenic genomic region of said non-rice cereal that corresponds to said defined genomic region of rice; and (C) isolating said syntenic genomic region of said non-rice cereal that corresponds to said defined genomic region of rice.

The present invention provides a method for isolating a nucleic acid molecule in a cereal comprising: (A) defining a genomic region of rice by reference to a marker molecule, wherein said marker molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complement thereof or fragment of either; (B) identifying a syntenic genomic region of said cereal that corresponds to said defined genomic region of rice; and (C) isolating said syntenic genomic region of said cereal that corresponds to said defined genomic region of rice.

The present invention provides a method for interrogating a genomic region of a non-rice cereal comprising interrogating genomic DNA for the presence or absence of two marker molecules, wherein said two marker molecules comprise two nucleic acid sequences selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 69652 or complement thereof or fragment of either, and detecting the presence or absence of said two marker molecules.

Detailed Description of the Invention

Agents of the invention:

(a) Nucleic Acid Molecules

Agents of the present invention include nucleic acid molecules and more specifically BACs or nucleic acid fragment molecules thereof.

Agents of the present invention include plant nucleic acid molecules and more specifically include rice, more preferably *Oryza sativa* L (japonica type), and more preferably *Oryza sativa* L (japonica type), *cv.* Nipponbare. A subset of the nucleic acid molecules of the present invention includes nucleic acid molecules that are marker molecules. Another subset of the nucleic molecules of the present invention includes nucleic acid molecules that are promoters and/or regulatory elements. Another subset of the nucleic acid molecules of the present invention includes nucleic acid molecules that encode a gene or fragment thereof. Another subset of the nucleic acid molecules of the present invention encodes proteins or fragments of proteins. In a preferred embodiment the nucleic acid molecules of the present invention are derived from rice, more preferably *Oryza sativa* L (japonica type), and more preferably *Oryza sativa* L (japonica type), *cv.* Nipponbare.

Fragment nucleic acid molecules may encode significant portion(s) of, or indeed most of, these nucleic acid molecules. For example, a fragment nucleic acid molecule can encode a rice protein or fragment thereof. Alternatively, the fragments may comprise smaller oligonucleotides

(having from about 15 to about 400 nucleotide residues, and more preferably, about 15 to about 30 nucleotide residues, or about 50 to about 100 nucleotide residues, or about 100 to about 200 nucleotide residues, or about 200 to about 400 nucleotide residues, or about 275 to about 350 nucleotide residues).

As used herein, an agent, be it a naturally occurring molecule or otherwise may be "substantially purified", if desired, referring to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

The agents of the present invention may also be recombinant. As used herein, the term recombinant means any agent (*e.g.*, DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

It is understood that the agents of the present invention may be labeled with reagents that facilitate detection of the agent (*e.g.*, fluorescent labels (Prober, *et al.*, *Science 238*:336-340 (1987); Albarella *et al.*, EP 144914, chemical labels (Sheldon *et al.*, U.S. Patent 4,582,789; Albarella *et al.*, U.S. Patent 4,563,417, modified bases (Miyoshi *et al.*, EP 119448, all of which are hereby incorporated by reference in their entirety).

It is further understood, that the present invention provides, for example, bacterial, viral, microbial, insect, fungal, algal and plant cells comprising an agent of the present invention.

Nucleic acid molecules or fragment nucleic acid molecules, or BACs or fragments thereof, of the present invention are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel, double-stranded nucleic acid structure. A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, *Molecular Cloning,* A Laboratory Manual, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), and by Haymes *et al., Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985), both of which are herein incorporated by reference in their entirety. Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule, fragment nucleic acid molecule, BAC nucleic acid molecule or fragment BAC nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

Appropriate stringency conditions which promote DNA hybridization are, for example, 6.0 x sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 x SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 x SSC at 50°C to a high stringency of about 0.2 x SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

In a preferred embodiment, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof under moderately stringent conditions, for example at about 2.0 x SSC and about 40°C.

In a particularly preferred embodiment, a nucleic acid of the present invention will specifically hybridize to one or more of the nucleic acid molecules set forth in SEQ ID NO:1 through SEQ ID NO: 69652 or complements thereof under high stringency conditions. In one aspect of the present invention, the nucleic acid molecules of the present invention have one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through to SEQ ID NO: 69652 or complements thereof. In another aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 90% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through to SEQ ID NO: 69652 or complements thereof. In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 95% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through to SEQ ID NO: 69652 or

complements thereof. In a more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 98% sequence identity with one or more of the nucleic acid sequences set forth in SEQ ID NO: 1 through to SEQ ID NO: 69652 or complements thereof. In an even more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention share between 100% and 99% sequence identity with one or more of the sequences set forth in SEQ ID NO: 1 through to SEQ ID NO: 69652 or complements thereof. In a further, even more preferred aspect of the present invention, one or more of the nucleic acid molecules of the present invention exhibit 100% sequence identity with one or more nucleic acid molecules present within the genomic library herein designated BAC#OJ (Monsanto Company, St. Louis, Missouri, United States of America).

(i) Nucleic Acid Molecule Markers

One aspect of the present invention concerns nucleic acid molecules SEQ ID NO:1 through SEQ ID NO: 69652 or complements thereof and other nucleic acid molecules of the present invention, that contain microsatellites, single nucleotide substitutions (SNPs), repetitive elements or parts of repetitive elements or other markers. Microsatellites typically include a 1-6 nucleotide core element that are tandemly repeated from one to many thousands of times. A different "allele" occurs at an SSR locus as a result of changes in the number of times a core element is repeated, altering the length of the repeat region, (Brown *et al., Methods of Genome Analysis in Plants*, (ed.) Jauhar, CRC Press, Inc, Boca Raton, Florida, USA; London, England, UK, pp. 147-159, (1996), the entirety of which is herein incorporated by reference). SSR loci occur throughout plant genomes, and specific repeat motifs occur at different levels of abundance than those found in animals. The relative frequencies of all SSRs with repeat units of 1-6 nucleotides have been surveyed. The most abundant SSR is AAAAAT followed by A_n, AG_n AAT, AAC, AGC, AAG, AATT, AAAT and AC. On average, 1 SSR is found every 21 and 65 kb in

dicots and monocots. Fewer CG nucleotides are found in dicots than in monocots. There is no correlation between abundance of SSRs and nuclear DNA content. The abundance of all tri and tetranucleotide SSR combination jointly have been reported to be equivalent to that of the total di-nucleotide combinations. Mono- di- and tetra-nucleotide repeats are all located in noncoding regions of DNA while 57% of those trinucleotide SSRs containing CG were located within gene coding regions. All repeated trinucleotide SSRs composed entirely of AT are found in noncoding regions, (Brown *et al., Methods of Genome Analysis in Plants, ed.* Jauhar, CRC Press, Inc, Boca Raton, Florida, USA; London, England, UK, pp. 147-159 (1996)).

Microsatellites can be observed in SEQ NO:1 to SEQ NO:69652 or complements thereof by using the BLASTN program to examine sequences for the presence/absence of microsatellites. In this system, raw sequence data is searched through databases, which store SSR markers collected from publications and 692 classes of di-, tri and tetranucleotide repeat markers generated by computer. Microsatellites can also be observed by screening the BAC library of the present invention by colony or plaque hybridization with a labeled probe containing microsatellite markers; isolating positive clones and sequencing the inserts of the positive clones; suitable primers flanking the microsatellite markers.

Single nucleotide polymorphisms (SNPs) are single base changes in genomic DNA sequence. They generally occur at greater frequency than other markers and are spaced with a greater uniformity throughout a genome than other reported forms of polymorphism. The greater frequency and uniformity of SNPs means that there is greater probability that such a polymorphism will be found near or in a genetic locus of interest than would be the case for other polymorphisms. SNPs are located in protein-coding regions and noncoding regions of a genome. Some of these SNPs may result in defective or variant protein expression (*e.g.*, as a result of mutations or defec-

tive splicing). Analysis (genotyping) of characterized SNPs can require only a plus/minus assay rather than a lengthy measurement, permitting easier automation.

SNPs can be characterized using any of a variety of methods. Such methods include the direct or indirect sequencing of the site, the use of restriction enzymes (Botstein *et al.*, *Am. J. Hum. Genet. 32*:314-331 (1980); Konieczny and Ausubel, *Plant J. 4*:403-410 (1993), both of which are herein incorporated by reference in their entirety), enzymatic and chemical mismatch assays (Myers *et al.*, *Nature 313*:495-498 (1985), the entirety of which is herein incorporated by reference), allele-specific PCR (Newton *et al.*, *Nucl. Acids Res. 17*:2503-2516 (1989); Wu *et al.*, *Proc. Natl. Acad. Sci. USA 86*:2757-2760 (1989), both of which are herein incorporated by reference in their entirety), ligase chain reaction (Barany, *Proc. Natl. Acad. Sci. USA 88*:189-193 (1991), the entirety of which is herein incorporated by reference), single-strand conformation polymorphism analysis (Labrune *et al.*, *Am. J. Hum. Genet. 48*: 1115-1120 (1991), the entirety of which is herein incorporated by reference), primer-directed nucleotide incorporation assays (Kuppuswami *et al.*, *Proc. Natl. Acad. Sci. USA 88*:1143-1147 (1991), the entirety of which is herein incorporated by reference), dideoxy fingerprinting (Sarkar *et al.*, *Genomics 13*:441-443 (1992), the entirety of which is herein incorporated by reference), solid-phase ELISA-based oligonucleotide ligation assays (Nikiforov *et al.*, *Nucl. Acids Res. 22*:4167-4175 (1994), the entirety of which is herein incorporated by reference), oligonucleotide fluorescence-quenching assays (Livak *et al.*, *PCR Methods Appl. 4*:357-362 (1995a), the entirety of which is herein incorporated by reference), 5'-nuclease allele-specific hybridization TaqMan™ assay (Livak *et al.*, *Nature Genet. 9*:341-342 (1995), the entirety of which is herein incorporated by reference), template-directed dye-terminator incorporation (TDI) assay (Chen and Kwok, *Nucl. Acids Res. 25*:347-353 (1997), the entirety of which is herein incorporated by reference), allele-specific molecular beacon assay (Tyagi *et al.*, *Nature Biotech. 16*: 49-53 (1998), the entirety of which is

herein incorporated by reference), PinPoint assay (Haff and Smirnov, *Genome Res. 7*: 378-388 (1997), the entirety of which is herein incorporated by reference), and dCAPS analysis (Neff *et al.*, *Plant J. 14*:387-392 (1998), the entirety of which is herein incorporated by reference).

SNPs can be observed by examining sequences of overlapping clones in the BAC library according to the method described by Taillon-Miller *et al. Genome Res. 8*:748-754 (1998), the entirety of which is herein incorporated by reference. SNPs can also be observed by screening the BAC library of the present invention by colony or plaque hybridization with a labeled probe containing SNP markers; isolating positive clones and sequencing the inserts of the positive clones; suitable primers flanking the SNP markers.

Genetic markers of the present invention include "dominant" or "codominant" markers. "Codominant markers" reveal the presence of two or more alleles (two per diploid individual) at a locus. "Dominant markers" reveal the presence of only a single allele per locus. The presence of the dominant marker phenotype (*e.g.*, a band of DNA) is an indication that one allele is present in either the homozygous or heterozygous condition. The absence of the dominant marker phenotype (*e.g.*, absence of a DNA band) is merely evidence that "some other" undefined allele is present. In the case of populations where individuals are predominantly homozygous and loci are predominately dimorphic, dominant and codominant markers can be equally valuable. As populations become more heterozygous and multi-allelic, codominant markers often become more informative of the genotype than dominant markers.

In addition to SSRs and SNPs, repetitive elements can be used as markers. For most eukaryotes, interspersed repeat sequence elements are typically mobile genetic elements (Wright *et al., Genetics 142*:569-578 (1996), the entirety of which is herein incorporated by reference). They are ubiquitous in most living organisms and are present in copy numbers ranging from just a few elements to tens or hundreds or thousands per genome. In the latter case, they can

represent a major fraction of the genome. For example, transposable elements have been estimated to make up greater than 50% of the maize genome (Kidwell, and Lisch *Proc. Natl. Acad. Sci. USA 94*:7704-7711 (1997), the entirety of which is herein incorporated by reference).

Transposable elements are classified in families according to their sequence similarity. Two major classes are distinguished by their differing modes of transposition. Class I elements are retroelements that use reverse transcriptase to transpose by means of an RNA intermediate. They include long terminal repeat retrotransposons and long and short interspersed elements (LINES and SINES, respectively). Class II elements transpose directly from DNA to DNA and include transposons such as the *Activator-Dissociation* (*Ac-Ds*) family in maize, the *P* element in *Drosophila* and the *Tc-1* element in *Caenhorabditis elegans*. Additionally, a category of transposable elements has been discovered whose transpositon mechanism is not yet known. These miniature inverted-repeat transposable elements (*MITEs*) have some properties of both class I and II elements. They are short (100-400 bp in length) and none so far has been found to have any coding potential. They are present in high copy number (3,000-10,000) per genome and have target site preferences for TAA or TA in plants (Kidwell and Lisch, *Proc. Natl. Acad. Sci. USA 94*:7704-7711 (1997)).

Insertion elements are found in two areas of the genome. Some are located in regions distant from gene sequences such as in the heterochromatin or in regions between genes; other repeat elements are found in or near single copy sequences. The insertion of an *Ac-Ds* element into *wx-m9*, an allele of the *waxy* locus in maize is an example of a repetitive element found within a coding region. The effect of this insertion is attenuated by the loss through splicing of the transposable element after transcription (Kidwell and Lisch, *Proc. Natl. Acad. Sci. USA 94*:7704-7711 (1997)).

The genetic variability resulting from transposable elements ranges from changes in the size and arrangement of whole genomes to changes in single nucleotides. They may produce major effects on phenotypic traits or small silent changes detectable only at the DNA sequence level. Transposable elements may also produce variation when they excise, leaving small footprints of their previous presence (Kidwell and Lisch, *Proc. Natl. Acad. Sci. USA 94*:7704-7711 (1997)).

In addition, other markers such as AFLP markers, RFLP markers, RAPD markers, phenotypic markers or isozyme markers can be utilized (Walton, Seed World 22-29,July, 1993); Burow and Blake, *Molecular Dissection of Complex Traits*, 13-29, Eds. Paterson, CRC Press, New York (1988), both of which are herein incorporated by reference in their entirety). DNA markers can be developed from nucleic acid molecules using restriction endonucleases, the PCR and/or DNA sequence information. RFLP markers result from single base changes or insertions/ deletions. These codominant markers are highly abundant in plant genomes, have a medium level of polymorphism and are developed by a combination of restriction endonuclease digestion and Southern blotting hybridization. CAPS are similarly developed from restriction nuclease digestion but only of specific PCR products. These markers are also codominant, have a medium level of polymorphism and are highly abundant in the genome. The CAPS result from single base changes and insertions/deletions. Another marker type, RAPDs, are developed from DNA amplification with random primers and result from single base changes and insertions/deletions in plant genomes. They are dominant markers with a medium level of polymorphisms and are highly abundant. AFLP markers require using the PCR on a subset of restriction fragments from extended adapter primers. These markers are both dominant and codominant, are highly abundant in genomes and exhibit a medium level of polymorphism. SSRs require DNA sequence information. These codominant markers result from repeat length changes, are highly polymor-

phic, and do not exhibit as high a degree of abundance in the genome as CAPS, AFLPs and RAPDs. SNPs also require DNA sequence information. These codominant markers result from single base substitutions. They are highly abundant and exhibit a medium of polymorphism (Rafalski *et al.*, In: *Nonmammalian Genomic Analysis*, ed. Birren and Lai, Academic Press, San Diego, CA, pp. 75-134 (1996), the entirety of which is herein incorporated by reference). Methods to isolate such markers are known in the art.

Long Terminal repeat retrotransposons and *MITEs* have been found to be associated with the genes of many plants where some of the transposable elements contribute regulatory sequences. *MITEs* such as the *Tourist* element in maize and the *Stowaway* element in Sorghum are found frequently in the 5' and 3' noncoding regions of genes and are frequently associated with the regulatory regions of genes of diverse flowering plants (Kidwell and Lisch, *Proc. Natl. Acad. Sci. USA 94*:7704-7711 (1997)). It is understood that one or more of the Long Terminal repeat retrotransposons and/or MITES may be a marker, and even more preferably a marker for a gene.

(ii) Nucleic Acid Molecules Comprising Regulatory Elements

Another class of agents of the present invention are nucleic acid molecules having promoter regions or partial promoter regions within SEQ ID NO: 1 through SEQ ID NO: 69652 or other nucleic acid molecules of the present invention. Such promoter regions are typically found upstream of the trinucleotide ATG sequence at the start site of a protein coding region.

As used herein, a promoter region is a region of a nucleic acid molecule that is capable, when located in *cis* to a nucleic acid sequence that encodes for a protein or fragment thereof to function in a way that directs expression of one or more mRNA molecules that encodes for the protein or fragment thereof.

Promoters of the present invention can include between about 300 bp upstream and about 10 kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region.

Promoters of the present invention can preferably include between about 300 bp upstream and about 5 kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. Promoters of the present invention can more preferably include between about 300 bp upstream and about 2 kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. Promoters of the present invention can include between about 300 bp upstream and about 1 kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. While in many circumstances a 300 bp promoter may be sufficient for expression, additional sequences may act to further regulate expression, for example, in response to biochemical, developmental or environmental signals.

It is also preferred that the promoters of the present invention contain a CAAT and a TATA *cis* element. Moreover, the promoters of the present invention can contain one or more *cis* elements in addition to a CAAT and a TATA box.

By "regulatory element" it is intended a series of nucleotides that determines if, when, and at what level a particular gene is expressed. The regulatory DNA sequences specifically interact with regulatory or other proteins. Many regulatory elements act in *cis* ("*cis* elements") and are believed to affect DNA topology, producing local conformations that selectively allow or restrict access of RNA polymerase to the DNA template or that facilitate selective opening of the double helix at the site of transcriptional initiation. *Cis* elements occur within, but are not limited to promoters, and promoter modulating sequences (inducible elements). *Cis* elements can be identified using known *cis* elements as a target sequence or target motif in the BLAST programs of the present invention.

Promoters of the present invention include homologues of *cis* elements known to effect gene regulation that show homology with the nucleic acid molecules of the present invention. These *cis* elements include, but are not limited to, oxygen responsive *cis* elements (Cowen *et al.*,

*J Biol. Chem. 268(36):*26904-26910 (1993) the entirety of which is herein incorporated by reference), light regulatory elements (Bruce *et al., Plant Cell 2 (11):*1081-1089 (1990); Bruce *et al., EMBO J. 10:*3015-3024 (1991); Rocholl *et al., Plant Sci. 97:*189-198 (1994); Block *et al., Proc. Natl. Acad. Sci. USA 87:*5387-5391 (1990); Giuliano *et al., Proc. Natl. Acad. Sci. USA 85:*7089-7093 (1988); Staiger *et al., Proc. Natl. Acad. Sci. USA 86:*6930-6934 (1989); Izawa *et al., Plant Cell 6:*1277-1287 (1994); Menkens *et al., Trends in Biochemistry 20:*506-510 (1995); Foster *et al., FASEB J. 8:*192-200 (1994); Plesse *et al., Mol Gen Gene 254:*258-266 (1997); Green *et al., EMBO J. 6:*2543-2549 (1987); Kuhlemeier *et al., Ann. Rev Plant Physiol. 38:*221-257 (1987); Villain *et al., J. Biol. Chem. 271:*32593-32598 (1996); Lam *et al., Plant Cell 2:*857-866 (1990); Gilmartin *et al., Plant Cell 2:*369-378 (1990); Datta *et al., Plant Cell 1:*1069-1077 (1989); Castresana *et al., EMBO J.* 7:1929-1936 (1988); Ueda *et al., Plant Cell 1:*217-227 (1989); Terzaghi *et al., Annu. Rev. Plant Physiol. Plant Mol. Biol. 46:*445-474 (1995); Tjaden *et al., Plant Cell 6:*107-118 (1994); Tjaden *et al., Plant Physiol. 108:*1109-1117 (1995); Ngai *et al., Plant J. 12:*1021-1234 (1997), all of which are herein incorporated by reference in their entirety), elements responsive to gibberellin, (Muller *et al., J. Plant Physiol. 145:*606-613 (1995); Croissant *et al., Plant Science 116:*27-35 (1996); Lohmer *et al., EMBO J. 10:*617-624 (1991); Rogers *et al., Plant Cell 4:*1443-1451 (1992); Lanahan *et al., Plant Cell* 4:203-211 (1992); Skriver *et al., Proc. Natl. Acad. Sci. USA 88:*7266-7270 (1991); Gilmartin *et al., Plant Cell 2:*369-378 (1990); Huang *et al., Plant Mol. Biol. 14:*655-668 (1990); Gubler *et al., Plant Cell 7:*1879-1891 (1995), all of which are herein incorporated by reference in their entirety), elements responsive to abscisic acid, (Busk *et al., Plant Cell 9:*2261-2270 (1997); Guiltinan *et al., Science 250:*267-270 (1990); Shen *et al., Plant Cell 7:*295-307 (1995); Shen *et al., Plant Cell 8:*1107-1119 (1996); Seo *et al., Plant Mol. Biol. 27:*1119-1131 (1995); Marcotte *et al., Plant Cell* 1:969-976 (1989); Shen *et al., Plant Cell* 7:295-307 (1995); Iwasaki *et al., Mol Gen Genet*

247:391-398 (1995); Hattori *et al., Genes Dev.* 6:609-618 (1992); Thomas *et al., Plant Cell* 5:1401-1410 (1993), all of which are herein incorporated by reference in their entirety), elements similar to abscisic acid responsive elements, (Ellerstrom *et al., Plant Mol. Biol. 32:*1019-1027 (1996), the entirety of which is herein incorporated by reference), auxin responsive elements (Liu *et al., Plant Cell 6:*645-657 (1994); Liu *et al., Plant Physiol.* 115:397-407 (1997); Kosugi *et al., Plant J.* 7:877-886 (1995); Kosugi *et al., Plant Cell* 9:1607-1619 (1997); Ballas *et al., J. Mol. Biol. 233:*580-596 (1993), all of which are herein incorporated by reference in their entirety), a *cis* element responsive to methyl jasmonate treatment (Beaudoin and Rothstein, *Plant Mol. Biol. 33:*835-846 (1997), the entirety of which is herein incorporated by reference), a *cis* element responsive to abscisic acid and stress response (Straub *et al., Plant Mol. Biol.* 26:617-630 (1994), the entirety of which is herein incorporated by reference), ethylene responsive *cis* elements (Itzhaki *et al., Proc. Natl. Acad. Sci. USA* 91:8925-8929 (1994); Montgomery *et al., Proc. Natl. Acad. Sci. USA 90:*5939-5943 (1993); Sessa *et al., Plant Mol. Biol.* 28:145-153 (1995); Shinshi *et al., Plant Mol. Biol.* 27:923-932 (1995), all of which are herein incorporated by reference in their entirety), salicylic acid *cis* responsive elements, (Strange *et al., Plant J.* 11:1315-1324 (1997); Qin *et al., Plant Cell* 6:863-874 (1994), both of which are herein incorporated by reference in their entirety), a *cis* element that responds to water stress and abscisic acid (Lam *et al., J. Biol. Chem.* 266:17131-17135 (1991); Thomas *et al., Plant Cell* 5:1401-1410 (1993); Pla *et al., Plant Mol Biol* 21:259-266 (1993), all of which are herein incorporated by reference in their entirety), a *cis* element essential for M phase-specific expression (Ito *et al., Plant Cell* 10:331-341 (1998), the entirety of which is herein incorporated by reference), sucrose responsive elements (Huang *et al., Plant Mol. Biol.* 14:655-668 (1990); Hwang *et al., Plant Mol Biol* 36:331-341 (1998); Grierson *et al., Plant J.* 5:815-826 (1994), all of which are herein incorporated by reference in their entirety), heat shock response elements (Pelham *et al., Trends*

Genet. 1:31-35 (1985), the entirety of which is herein incorporated by reference), elements responsive to auxin and/or salicylic acid and also reported for light regulation (Lam *et al., Proc. Natl. Acad. Sci. USA* 86:7890-7897 (1989); Benfey *et al., Science* 250:959-966 (1990), both of which are herein incorporated by reference in their entirety), elements responsive to ethylene and salicylic acid (Ohme-Takagi *et al., Plant Mol. Biol.* 15:941-946 (1990), the entirety of which is herein incorporated by reference), elements responsive to wounding and abiotic stress (Loake *et al., Proc. Natl. Acad. Sci. USA* 89:9230-9234 (1992); Mhiri *et al., Plant Mol. Biol.* 33:257-266 (1997), both of which are herein incorporated by reference in their entirety), antoxidant response elements (Rushmore *et al., J. Biol. Chem.* 266:11632-11639; Dalton *et al., Nucleic Acids Res.* 22:5016-5023 (1994), both of which are herein incorporated by reference in their entirety), Sph elements (Suzuki *et al., Plant Cell 9:*799-807 1997), the entirety of which is herein incorporated reference), Elicitor responsive elements, (Fukuda *et al., Plant Mol. Biol.* 34:81-87 (1997); Rushton *et al., EMBO J.* 15:5690-5700 (1996), both of which are herein incorporated by reference in their entirety), metal responsive elements (Stuart *et al., Nature* 317:828-831 (1985); Westin *et al., EMBO J.* 7:3763-3770 (1988); Thiele *et al., Nucleic Acids Res.* 20:1183-1191 (1992); Faisst *et al., Nucleic Acids Res.* 20:3-26 (1992), all of which are herein incorporated by reference in their entirety), low temperature responsive elements, (Baker *et al., Plant Mol. Biol.* 24:701-713 (1994); Jiang *et al., Plant Mol. Biol.* 30:679-684 (1996); Nordin *et al., Plant Mol. Biol.* 21:641-653 (1993); Zhou *et al., J. Biol. Chem.* 267:23515-23519 (1992), all of which are herein incorporated by reference in their entirety), drought responsive elements, (Yamaguchi *et al., Plant Cell* 6:251-264 (1994); Wang *et al., Plant Mol. Biol.* 28:605-617 (1995); Bray EA, *Trends in Plant Science* 2:48-54 (1997), all of which are herein incorporated by reference in their entirety); enhancer elements for glutenin, (Colot *et al., EMBO J.* 6:3559-3564 (1987); Thomas *et al., Plant Cell* 2:1171-1180 (1990); Kreis *et al., Philos. Trans. R. Soc. Lond.,* B314:355-365

(1986), all of which are herein incorporated by reference in their entirety), light-independent regulatory elements, (Lagrange *et al., Plant Cell* 9:1469-1479 (1997); Villain *et al., J. Biol. Chem.* 271:32593-32598 (1996), both of which are herein incorporated by reference in their entirety), OCS enhancer elements, (Bouchez *et al., EMBO J.* 8:4197-4204 (1989); Foley *et al., Plant J.* 3:669-679 (1993), both of which are herein incorporated by reference in their entirety), ACGT elements, (Foster *et al., FASEB J.* 8:192-200 (1994); Izawa *et al., Plant Cell* 6:1277-1287 (1994); Izawa *et al., J. Mol. Biol.* 230:1131-1144 (1993), all of which are herein incorporated by reference in their entirety), negative *cis* elements in plastid related genes, (Zhou *et al., J. Biol. Chem.* 267:23515-23519 (1992); Lagrange *et al., Mol. Cell Biol.* 13:2614-2622 (1993); Lagrange *et al., Plant Cell* 9:1469-1479 (1997); Zhou *et al., J. Biol. Chem.* 267:23515-23519 (1992), all of which are herein incorporated by reference in their entirety), prolamin box elements, (Forde *et al., Nucleic Acids Res.* 13:7327-7339 (1985); Colot *et al., EMBO J.* 6:3559-3564 (1987); Thomas *et al., Plant Cell* 2:1171-1180 (1990); Thompson *et al., Plant Mol. Biol.* 15:755-764 (1990); Vicente *et al., Proc. Natl. Acad. Sci. USA* 94:7685-7690 (1997), all of which are herein incorporated by reference in their entirety), elements in enhancers from the IgM heavy chain gene (Gillies *et al., Cell* 33:717-728 (1983); Whittier *et al., Nucleic Acids Res.* 15:2515-2535 (1987), both of which are herein incorporated by reference in their entirety).

(iii) Nucleic Acid Molecules Comprising Genes or Fragments Thereof

Nucleic acid molecules of the present invention can comprise one or more genes or fragments thereof. Such genes or fragments thereof include homologues of known genes or protein coding regions in other organisms or genes or fragments thereof that elicit only limited or no matches with known genes or protein coding regions.

Genomic sequences can be screened for the presence of protein homologues or genes utilizing one or a number of different search algorithms have that been developed, one example

of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and under the section titled "Uses of the Agents of the Invention." In addition, unidentified reading frames may be screened for protein coding regions by prediction software such as GenScan, which is located at http://gnomic.standford.edu/GENSCANW.html.

In a preferred embodiment of the present invention, the rice protein or fragment thereof of the present invention is a homologue of another plant protein. In another preferred embodiment of the present invention, the rice protein or fragment thereof is a homologue of a plant protein. In another preferred embodiment of the present invention, the rice protein or fragment thereof of the present invention is a homologue of a cereal protein. In another preferred embodiment of the present invention, the rice protein or fragment thereof of the present invention is a homologue of a fungal protein. In another preferred embodiment of the present invention, the rice protein or fragment thereof of the present invention is a homologue of a mammalian protein. In another preferred embodiment of the present invention, the rice protein or fragment thereof of the present invention is a homologue of a bacterial protein. In another preferred embodiment of the present invention, the rice protein or fragment thereof of the present invention is a homologue of an algal protein.

In a preferred embodiment of the present invention, the rice protein or fragments thereof or nucleic acid molecule or fragment thereof has a BLAST score of more than 200, preferably a BLAST score of more than 300, even more preferably a BLAST score of more than 400 with its homologue.

In another preferred embodiment of the present invention, the nucleic acid molecule encoding the rice protein or fragment thereof and/or nucleic acid molecule or fragment thereof exhibits a % identity with its homologue of between about 25% and about 40%, more preferably

of between about 40 and about 70%, even more preferably of between about 70% and about 90%, and even more preferably between about 90% and 99%. In another preferred embodiment, of the present invention, the nucleic acid molecule encoding the rice protein or fragment thereof exhibits a % identity with its homologue of 100%.

In a preferred embodiment of the present invention, the rice protein or fragment thereof or nucleic acid molecule or fragment thereof exhibits a % coverage of between about 0 % and about 33%, more preferably of between about 34% and about 66%, and even more preferably of between about 67% and about 100%.

Genomic sequences can be screened for the presence of proteins utilizing one or a number of different search algorithms have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background. Nucleic acid molecules of the present invention also include non-rice homologues. Preferred non-rice homologues are selected from the group consisting of alfalfa, *Arabidopsis* barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, maize, pea, peanut, pepper, potato, rye, sorghum, soybean, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, and *Phaseolus*.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1 through SEQ ID NO: 69652 or complements and fragments of either or other nucleic acid molecules of the present invention can be utilized to obtain such homologues.

The degeneracy of the genetic code, which allows different nucleic acid sequences to code for the same protein or peptide, is known in the literature. (U.S. Patent No. 4,757,006, the entirety of which is herein incorporated by reference). As used herein a nucleic acid molecule is

degenerate of another nucleic acid molecule when the nucleic acid molecules encode for the same amino acid sequences but comprise different nucleotide sequences. An aspect of the present invention is that the nucleic acid molecules of the present invention include nucleic acid molecules that are degenerate of those set forth in SEQ ID NO: 1 through to SEQ ID NO: 69652 or complements thereof.

In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a rice protein or fragment thereof in SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof due to the degeneracy in the genetic code in that they encode the same protein but differ in nucleic acid sequence. In another further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a rice homologue or fragment thereof in SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof due to the fact that the different nucleic acid sequence encodes a protein having one or more conservative amino acid residues. In such amino acid sequences, one or more amino acids in the fundamental sequence are substituted with another amino acid(s), the charge and polarity of which are similar to that of the native amino acid, *i.e.*, a conservative amino acid substitution, resulting in a silent change.

Substitutes for an amino acid within the fundamental polypeptide sequence can be selected from other members of the class to which the naturally occurring amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic amino acids, (2) basic amino acids, (3) neutral polar amino acids, and (4) neutral nonpolar amino acids. Representative amino acids within these various groups include, but are not limited to, (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine,

serine, threonine, cysteine, cystine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine.

Conservative amino acid changes within the fundamental polypeptides sequence can be made by substituting one amino acid within one of these groups with another amino acid within the same group.

It is also understood that certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigent-binding regions of antibodies or binding sites on substrate molecules. Because it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence and, of course, its underlying DNA coding sequence and, nevertheless, obtain a protein with like properties.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, *J. Mol. Biol. 157*, 105-132 (1982), herein incorporated by reference in its entirety). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, *J. Mol. Biol. 157*, 105-132 (1982); these are isoleucine (+4.5), valine (+4.2), leucine (+3.8), phenylalanine (+2.8), cysteine/cystine (+2.5), methionine (+1.9), alanine (+1.8), glycine (-0.4), threonine (-0.7), serine (-0.8), tryptophan (-0.9),

tyrosine (-1.3), proline (-1.6), histidine (-3.2), glutamate (-3.5), glutamine (-3.5), aspartate (-3.5), asparagine (-3.5), lysine (-3.9), and arginine (-4.5).

It is known in the art that certain amino acid may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activities, *i.e.*, still obtain a biologically functional equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference in its entirety, states that the greatest local average hydrophilicity of a protein, as govern by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0), lysine (+3.0), aspartate (+3.0±1), glutamate (+3.0±1), serine (+0.3), asparagine (+0.2), glutamine (+0.2), glycine (0), threonine (-0.4), proline (-0.5±1), alanine (-0.5), histidine (-0.5), cysteine (-1.0), methionine (-1.3), valine (-1.5), leucine (-1.8), isoleucine (-1.8), tyrosine (-2.3), phenylalanine (-2.5), and tryptophan (-3.4).

It is known in the art that certain amino acid may be substituted by other amino acids having a similar hydrophilicity value and still result in a protein with similar biological activities, *i.e.*, still obtain a biologically functional equivalent protein. In making such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

(iv) Nucleic Acid Molecules Comprising Introns and/or Intron/Exon Junctions

Nucleic acid molecules of the present invention can comprise an intron and/or one or more intron/exon junction. Sequences of the present invention can be screened for introns and intron/exon junctions utilizing one or a number of different search algorithms that have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and in the section entitled "Uses of the Agents of the Present Invention."

(b) Protein and Peptide Molecules

A class of agents includes one or more of the protein or peptide molecules, including those encoded by nucleic acid molecules disclosed in Table 1, fragments thereof or complements thereof or one or more of the proteins encoded by a nucleic acid molecule or fragment thereof or peptide molecules encoded by other nucleic acid agents of the present invention. Protein and peptide molecules can be identified using known protein or peptide molecules as a target sequence or target motif in the BLAST programs of the present invention. In a preferred embodiment, the protein or peptide molecules of the present invention are derived from rice and more preferably *Oryza sativa* L (japonica type), more preferably *Oryza sativa* L (japonica type), *cv.* Nipponbare.

As used herein, the term "protein molecule" or "peptide molecule" includes any molecule that comprises five or more amino acids. It is well known in the art that proteins or peptides may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term "protein molecule" or "peptide molecule" includes any protein molecule that is

modified by any biological or non-biological process. The terms "amino acid" and "amino acids" refer to all naturally occurring L-amino acids. This definition is meant to include norleucine, ornithine, homocysteine, and homoserine.

One or more of the protein or fragments of peptide molecules may be produced via chemical synthesis, or more preferably, by expression in a suitable bacterial or eukaryotic host. Suitable methods for expression are described by Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual, 2nd Edition,* Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), or similar texts.

A "protein fragment" is a peptide or polypeptide molecule whose amino acid sequence comprises a subset of the amino acid sequence of that protein. A protein or fragment thereof that comprises one or more additional peptide regions not derived from that protein is a "fusion" protein. Such molecules may be derivatized to contain carbohydrate or other moieties (such as keyhole limpet hemocyanin, etc.). Fusion protein or peptide molecules of the present invention are preferably produced via recombinant means.

Another class of agents comprises protein or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof or, fragments or fusions thereof in which conservative, non-essential, or not relevant, amino acid residues have been added, replaced, or deleted. An example of such a homologue is the homologue protein of all non-rice plant species, including but not limited to alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, pea, peanut, pepper, potato, maize, rye, sorghum, soybean, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, peas, lentils, grape, banana, wheat, tea, turf grasses, etc. Particularly preferred non-rice plants to utilize for the isolation of homologues would include alfalfa, barley, cotton, oat, oilseed rape, maize, canola, ornamentals, sugarcane, sugarbeet, tomato, potato, wheat, and

turf grasses. Such a homologue can be obtained by any of a variety of methods. Most preferably, as indicated above, one or more of the disclosed sequences (SEQ ID NO: 1 through SEQ ID NO: 69652 or complements thereof) will be used to define a pair of primers that may be used to isolate the homologue-encoding nucleic acid molecules from any desired species. Such molecules can be expressed to yield homologues by recombinant means. A homologue can also be generated by molecular evolution or DNA shuffling techniques, so that the molecule retains at least one function or structure characteristic of the original protein (*see*, for example, U.S. Patent 5,811238).

(c) Antibodies

One aspect of the present invention concerns antibodies, single-chain antigen binding molecules, or other proteins that specifically bind to one or more of the protein or peptide molecules of the present invention and their homologues, fusions or fragments. Such antibodies may be used to quantitatively or qualitatively detect the protein or peptide molecules of the present invention. As used herein, an antibody or peptide is said to "specifically bind" to a protein or peptide molecule of the present invention if such binding is not competitively inhibited by the presence of non-related molecules. In a preferred embodiment the antibodies of the present invention bind to proteins derived from rice and more preferably bind to proteins or fragments thereof of rice In a preferred embodiment the nucleic acid molecules of the present invention are derived from rice and more preferably *Oryza sativa* L (japonica type), more preferably *Oryza sativa* L (japonica type), *cv.* Nipponbare.

Nucleic acid molecules that encode all or part of the protein of the present invention can be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may

be a "fusion" molecule (*i.e.*, a part of a larger nucleic acid molecule) such that, upon expression, a fusion protein is produced. It is understood that any of the nucleic acid molecules of the present invention may be expressed, via recombinant means, to yield proteins or peptides encoded by these nucleic acid molecules.

The antibodies that specifically bind proteins and protein fragments of the present invention may be polyclonal or monoclonal, and may comprise intact immunoglobulins, or antigen binding portions of immunoglobulins (such as (F(ab'), $F(ab')_2$ fragments), or single-chain immunoglobulins producible, for example, via recombinant means). It is understood that practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of antibodies (see, for example, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1988), the entirety of which is herein incorporated by reference).

Murine monoclonal antibodies are particularly preferred. BALB/c mice are preferred for this purpose, however, equivalent strains may also be used. The animals are preferably immunized with approximately 25 µg of purified protein (or fragment thereof) that has been emulsified in a suitable adjuvant (such as TiterMax adjuvant (Vaxcel, Norcross, GA)). Immunization is preferably conducted at two intramuscular sites, one intraperitoneal site, and one subcutaneous site at the base of the tail. An additional i.v. injection of approximately 25 µg of antigen is preferably given in normal saline three weeks later. After approximately 11 days following the second injection, the mice may be bled and the blood screened for the presence of anti-protein or peptide antibodies. Preferably, a direct binding Enzyme-Linked Immunoassay (ELISA) is employed for this purpose.

More preferably, the mouse having the highest antibody titer is given a third i.v. injection of approximately 25 µg of the same protein or fragment. The splenic leukocytes from this animal

may be recovered 3 days later, and are then permitted to fuse, most preferably, using polyethylene glycol, with cells of a suitable myeloma cell line (such as, for example, the P3X63Ag8.653 myeloma cell line). Hybridoma cells are selected by culturing the cells under "HAT" (hypoxanthine-aminopterin-thymine) selection for about one week. The resulting clones may then be screened for their capacity to produce monoclonal antibodies ("mAbs"), preferably by direct ELISA.

In one embodiment, anti-protein or peptide monoclonal antibodies are isolated using a fusion of a protein, protein fragment, or peptide of the present invention, or conjugate of a protein, protein fragment, or peptide of the present invention, as immunogens. Thus, for example, a group of mice can be immunized using a fusion protein emulsified in Freund's complete adjuvant (*e.g.*, approximately 50 μg of antigen per immunization). At three week intervals, an identical amount of antigen is emulsified in Freund's incomplete adjuvant and used to immunize the animals. Ten days following the third immunization, serum samples are taken and evaluated for the presence of antibody. If antibody titers are too low, a fourth booster can be employed. Polysera capable of binding the protein or peptide can also be obtained using this method.

In a preferred procedure for obtaining monoclonal antibodies, the spleens of the above-described immunized mice are removed, disrupted, and immune splenocytes are isolated over a ficoll gradient. The isolated splenocytes are fused, using polyethylene glycol with BALB/c-derived HGPRT (hypoxanthine guanine phosphoribosyl transferase) deficient P3x63xAg8.653 plasmacytoma cells. The fused cells are plated into 96-well microtiter plates and screened for hybridoma fusion cells by their capacity to grow in culture medium supplemented with hypothanthine, aminopterin and thymidine for approximately 2-3 weeks.

Hybridoma cells that arise from such incubation are preferably screened for their capacity to produce an immunoglobulin that binds to a protein of interest. An indirect ELISA may be used for this purpose. In brief, the supernatants of hybridomas are incubated in microtiter wells that contain immobilized protein. After washing, the titer of bound immunoglobulin can be determined using, for example, a goat anti-mouse antibody conjugated to horseradish peroxidase. After additional washing, the amount of immobilized enzyme is determined (for example through the use of a chromogenic substrate). Such screening is performed as quickly as possible after the identification of the hybridoma in order to ensure that a desired clone is not overgrown by non-secreting neighbors. Desirably, the fusion plates are screened several times since the rates of hybridoma growth vary. In a preferred sub-embodiment, a different antigenic form of immunogen may be used to screen the hybridoma. Thus, for example, the splenocytes may be immunized with one immunogen, but the resulting hybridomas can be screened using a different immunogen. It is understood that any of the protein or peptide molecules of the present invention may be used to raise antibodies.

As discussed below, such antibody molecules or their fragments may be used for diagnostic purposes. Where the antibodies are intended for diagnostic purposes, it may be desirable to derivatize them, for example with a ligand group (such as biotin) or a detectable marker group (such as a fluorescent group, a radioisotope or an enzyme).

The ability to produce antibodies that bind the protein or peptide molecules of the present invention permits the identification of mimetic compounds of those molecules. A "mimetic compound" is a compound that is not that compound, or a fragment of that compound, but which nonetheless exhibits an ability to specifically bind to antibodies directed against that compound.

It is understood that any of the agents of the present invention can be substantially purified and/or be biologically active and/or recombinant.

Exemplary Uses of the Agents of the Invention

Nucleic acid molecules and fragments thereof of the present invention may be employed for genetic mapping studies using linkage analysis (genetic markers). A genetic linkage map shows the relative locations of specific DNA markers along a chromosome. Maps are used for the identification of genes associated with genetic diseases or phenotypic traits, comparative genomics, and as a guide for physical mapping. Through genetic mapping, a fine scale linkage map can be developed using DNA markers, and, then, a genomic DNA library of large-sized fragments can be screened with molecular markers linked to the desired trait. In a preferred embodiment of the present invention, the genomic library screened with the nucleic acid molecules of the present invention is a genomic library of rice.

Mapping marker locations is based on the observation that two markers located near each other on the same chromosome will tend to be passed together from parent to offspring. During gamete production, DNA strands occasionally break and rejoin in different places on the same chromosome or on the homologous chromosome. The closer the markers are to each other, the more tightly linked and the less likely a recombination event will fall between and separate them. Recombination frequency thus provides an estimate of the distance between two markers.

In segregating populations, target genes have been reported to have been placed within an interval of 5-10 cM with a high degree of certainty (Tanksley *et al., Trends in Genetics 11(2):*63-68 (1995), the entirety of which is herein incorporated by reference). The markers defining this interval are used to screen a larger segregating population to identify individuals derived from one or more gametes containing a crossover in the given interval. Such individuals are useful in orienting other markers closer to the target gene. Once identified, these individuals can be analyzed in relation to all molecular markers within the region to identify those closest to the target.

Markers of the present invention can be employed to construct linkage maps and to locate genes with qualitative and quantitative effects. The genetic linkage of additional marker molecules can be established by a genetic mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics, 121*:185-199 (1989), and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics, 121*:185-199 (1989), the entirety of which is herein incorporated by reference and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL,* Whitehead Institute for Biomedical Research, Massachusetts, (1990)). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY, the manual of which is herein incorporated by reference in its entirety). Use of the Qgene software is a particularly preferred approach.

A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an odds ratio (LOD) is then calculated as: LOD = $\log_{10}$ (MLE for the presence of a QTL/MLE given no linked QTL).

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL than in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein, *Genetics, 121*:185-199 (1989), the entirety of which is herein incorporated by reference and further described by Arús and Moreno-González, *Plant Breeding*, Hayward, Bosemark, Romagosa (eds.) Chapman & Hall, London, pp. 314-331 (1993).

Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use of non-parametric methods (Kruglyak and Lander, *Genetics, 139:*1421-1428 (1995), the entirety of which is herein incorporated by reference). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breed*, van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding,* Blackwell, Berlin, 16 (1994). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval, and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics, 136*:1447-1455 (1994) and Zeng, *Genetics, 136*:1457-1468 (1994). Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding,* van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics, 136*:1457-1468 (1994). These models can be extended to multi-environment experiments to analysis genotype-environment interactions (Jansen *et al., Theo. Appl. Genet. 91:*33-37 (1995).

Selection of an appropriate mapping population is important to map construction. The choice of appropriate mapping population depends on the type of marker systems employed (Tanksley *et al., J.P. Gustafson and R. Appels* (eds.), Plenum Press, New York, pp. 157-173 (1988), the entirety of which is herein incorporated by reference). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted

x exotic) and generally yield greatly reduced linkage distances. Wide crosses will usually provide segregating populations with a relatively large array of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

An F_2 population is the first generation of selfing after the hybrid seed is produced. Usually a single F_1 plant is selfed to generate a population segregating for all the genes in Mendelian (1:2:1) fashion. Maximum genetic information is obtained from a completely classified F_2 population using a codominant marker system (Mather, Measurement of Linkage in Heredity: Methuen and Co., (1938), the entirety of which is herein incorporated by reference). In the case of dominant markers, progeny tests (*e.g.*, F_3, BCF_2) are required to identify the heterozygotes, thus making it equivalent to a completely classified F_2 population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of F_2 individuals is often used in map construction where phenotypes do not consistently reflect genotype (*e.g.*, disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations (*e.g.*, F_3 or BCF_2) can be used in map construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations (F_2, F_3), where linkage groups have not been completely disassociated by recombination events (*i.e.*, maximum disequilibrium).

Recombinant inbred lines (RIL) (genetically related lines; usually $>F_5$, developed from continuously selfing F_2 lines towards homozygosity) can be used as a mapping population. Information obtained from dominant markers can be maximized by using RIL because all loci are homozygous or nearly so. Under conditions of tight linkage (*i.e.*, about <10% recombination), dominant and co-dominant markers evaluated in RIL populations provide more information per individual than either marker type in backcross populations (Reiter, *Proc. Natl. Acad. Sci. USA* *89*:1477-1481 (1992)). However, as the distance between markers becomes larger (*i.e.*, loci

become more independent), the information in RIL populations decreases dramatically when compared to codominant markers.

Backcross populations (*e.g.*, generated from a cross between a successful variety (recurrent parent) and another variety (donor parent) carrying a trait not present in the former) can be utilized as a mapping population. A series of backcrosses to the recurrent parent can be made to recover most of its desirable traits. Thus a population is created consisting of individuals nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic regions from the donor parent. Backcross populations can be useful for mapping dominant markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent have contrasting polymorphic marker alleles (Reiter *et al., Proc. Natl. Acad. Sci. USA 89*:1477-1481 (1992)). Information obtained from backcross populations using either codominant or dominant makers is less than that obtained from F_2 populations because one, rather than two, recombinant gametes are sampled per plant. Backcross populations, however, are more informative (at low marker saturation) when compared to RILs as the distance between linked loci increases in RIL populations (*i.e.*, about 0.15% recombination). Increased recombination can be beneficial for resolution of tight linkages, but may be undesirable in the construction of maps with low marker saturation.

Near-isogenic lines (NIL)(created by many backcrosses to produce an array of individuals that are nearly identical in genetic composition except for the trait or genomic region under interrogation) can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci are expected to map to a selected region.

Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore *et al., Proc. Natl. Acad. Sci. USA 88*:9828-9832 (1991)). In BSA, two bulked DNA samples are drawn from a segregating

population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but arbitrary at unlinked regions (*i.e.*, heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

It is understood that one or more of the nucleic acid molecules of the present invention may in one embodiment be used as markers in genetic mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used as markers with rice.

The nucleic acid molecules of the present invention may be used for physical mapping. Physical mapping, in conjunction with linkage analysis, can enable the isolation of genes. Physical mapping has been reported to identify the markers closest in terms of genetic recombination to a gene target for cloning. Once a DNA marker is linked to a gene of interest, the chromosome walking technique can be used to find the genes via overlapping clones. For chromosome walking, random molecular markers or established molecular linkage maps are used to conduct a search to localize the gene adjacent to one or more markers. A chromosome walk (Bukanov *et al.*, *Mol. Microbiol, 11:*509-523 (1994); Birkenbihl *et al.*, *Nucleic Acids Res. 17:*5057-5069 (1989); Wenzel *et al.*, *Nucleic Acids Res. 16:*8323-8336, (1988), all of which are herein incorporated by reference in their entirety) is then initiated from the closest linked marker. Starting from the selected clones, labeled probes specific for the ends of the insert DNA are synthesized and used as probes in hybridizations against a representative library. Clones hybridizing with one of the probes are picked and serve as templates for the synthesis of new probes; by subsequent analysis, contigs are produced.

The degree of overlap of the hybridizing clones used to produce a contig can be determined by comparative restriction analysis. Comparative restriction analysis can be carried

out in different ways all of which exploit the same principle; two clones of a library are very likely to overlap if they contain a limited number of restriction sites for one or more restriction endonucleases located at the same distance from each other. The most frequently used procedures are, fingerprinting (Coulson *et al., Proc. Natl. Acad. Sci. USA* 83:7821-7821, (1986); Knott *et al., Nucleic Acids Res.* 16:2601-2612 (1988); Eiglmeier *et al., Mol. Microbiol.* 7(2):197-206 (1993), all of which are herein incorporated by reference in their entirety), restriction fragment mapping (Smith and Birnstiel, *Nucleic Acids Res.* 3:2387-2398 (1976), the entirety of which is herein incorporated by reference), or the "landmarking" technique (Charlebois *et al., J. Mol. Biol.* 222:509-524 (1991), the entirety of which is herein incorporated by reference).

To generate a physical map of a genome with BACs using the fingerprinting technique, a BAC library containing a number of clones equivalent to 4X-20X haploid genome can be used. (Zhang and Wing, *Plant Mol. Bio.* 35:115-127 (1997)). For example, BAC DNA can be purified with the conventional alkaline lysis procedure as used for plasmid DNA purification, digested with the restriction enzyme used for construction of the BAC libraries and end-labeled with ^{32}P-dATP, digested with Sau3AI and fractionated on a denaturing polyacrylamide gel. The gel is dried to chromatography paper and exposed to X-ray film. Fingerprints are scanned and then converted into database records, according to the positions of each band relative to the bands of the closest molecular-weight marker on a gel. The incoming database of fingerprints are first compared against each other to assemble contigs if overlapped, and then compared against all existing databases to place the incoming BACs and BAC contigs in established contigs if overlapped. The physical length of a contig in kb is estimated according to the number of restriction sites of the enzyme used for the first digestion prior to fragment end labeling.

Restriction analysis of a certain clone can be carried out, for example, according to a method originally described by Smith and Berstiel, *Nucleic Acids Res.* 3:2387-2398 (1976).

First, the number and size of cloned restriction fragments to be mapped are determined by complete digestion and agarose gel electrophoresis. Then, the clone is linearized at a unique restriction site outside of the cloned DNA. Aliquots of the linearized molecules are digested to different extents with the enzyme selected for mapping. These partially cut samples are separated on agarose gels, blotted, and hybridized to a labeled fragment of vector DNA. This probe is derived entirely from one side or the other of the unique site used to linearize the clone.

The results show a ladder of DNA fragments that have the same unique end. By repeating these analyses in pairs with all the neighboring intermediate DNA fragments, the correct order of restriction fragments as well as the orientation of the cloned insert can be deduced. The order of restriction fragments produced by restriction enzymes other than the cloning enzyme can be determined similarly. Fragment data from different enzymes are then combined by a computer program and compared with the alignments of other clones of the library (Kohara *et al., Cell 50:*495-508 (1987), the entirety of which is herein incorporated by reference).

The landmarking technique can be carried out without any labeling and relies on agarose gel analysis. Clones are first digested preferably with a 6 bp specific endonuclease A, if possible with the original clone enzyme. Clones are then digested with a second endonuclease B. Endonuclease B is chosen based on its ability to cut rarely in the genome, for example, on average only once in 30 kbp. Of the fragments generated by digestion of one clone with enzyme A, statistically only a small number (between zero and three fragments) will also be cut by enzyme B. The very specific pattern of those fragments which are produced by double digestion are easily recognized. Any of these fragments which have a restriction site for the rarely cutting endonuclease is called a "landmark" Generally one common landmark is sufficient for defining two overlapping clones.

Alternatively to chromosome walking and the associated comparative restriction analyses methods, chromosome landing also has been reported to be used to locate a gene of interest (Tanksley *et al., Trends in Genetics 11(2):*63-68 (1995), the entirety of which is herein incorporated by reference). For chromosome landing, a DNA marker is isolated at a physical distance from the targeted gene. High resolution linkage analysis is used to identify such a marker that cosegregates with the gene. The marker is isolated at a distance that is less than the average insert size of the genomic library used for clone isolation. The DNA marker is then used to screen the library and isolate (or "land" on) the clone containing the gene without chromosome walking. Genome coverage of a library can also be determined by cross-hybridization of individual large insert clones by screening a BAC library with single copy RFLP markers distributed randomly across the genome by hybridization. To assure accuracy of the physical map, the markers should be single-copy or of single-locus origin, if multiple-copy.

Chromosome landing of large-insert clones using chromosome-specific DNA markers such as STSs microsatellites, RFLPs, or other markers can correlate physical and genetic maps (Zwick *et al., Genetics* 148:1983-1992 (1998), the entirety of which is herein incorporated by reference). These strategies include chromosome landing of BACs containing markers or BAC contigs by BAC-FISH (Fluorescent *In Situ* Hybridization), a technique that involves tagging the DNA marker with an observable label. BAC clones giving positive hybridization signals are individually analyzed by FISH to metaphase chromosome spreads. The location of the labeled probe can be detected after it binds to its complementary DNA strand in an intact chromosome. The FISH of a BAC selected from a BAC contig will directly place the BAC contig to a specific chromosome region and establish a linkage relationships of the BAC contig to another BAC contig.

Markers have been used in physical mapping studies with BAC libraries made from plant genomes. Such mapping studies have been carried out in rice (Kim *et al.*, *Genomics 34*:213-218 (1996); Hang, *Plant Mol. Biol. 35*:129-133 (1997); Zhang and Wing., *Plant Mol. Bio. 35*:115-127 (1997); Chen *et al., Proc. Natl. Acad. Sci. USA 94*:3431-3435 (1997); Wang *et al., Plant J. 7*:525-533 (1995), all of which are herein incorporated by reference in their entirety), sorghum (Zwick *et al., Genetics 148*:1983-1992 (1998); Zhang, *et al., Molecular Breeding 2*:11-24 (1996), both of which are herein incorporated by reference in their entirety) maize, (Chen, *et al., Proc. Natl. Acad. Sci. USA 94*:3431-3435 (1997)), and *Arabidopsis* (Kim, *et al., Genomics 34*:213-218 (1996), the entirety of which is herein incorporated by reference).

Repetitive elements have been used in physical mapping in cereals (Ananiev, *et al., Proc. Natl. Acad. Sci. USA 95*:13073-8 (1998); McLean *et al., Mol Gen Genet 253*:687-694 (1997), both of which are herein incorporated by reference in their entirety).

It is understood that the nucleic acid molecules of the present invention may in one embodiment be used in physical mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used in the physical mapping of rice.

Nucleic acid molecules of the present invention can be used in comparative mapping (physical and genetic) and to isolate molecules from other cereals based on the syntenic relationship between cereals. Comparative mapping within families provides a method to the degree of sequence conservation, gene order, ploidy of species, ancestral relationships and the rates at which individual genomes are evolving. Comparative mapping has been carried out by cross-hybridizing molecular markers across species within a given family.

In a preferred embodiment, the nucleic acid molecules of the present invention can be utilized to isolate corresponding syntenic regions in non-rice plants (Bennetzen and Freeling, *Trends in Genet., 9*(8):259-261 (1993); Ahn *et al., Mol. Gen. Genet., 241*(5-6):483-490 (1993);

Schwarzacher, *Cur. Opin. Genet. & Devel., 4*(6): 868-874 (1994); Kurata *et al.*, *Bio/Technology, 12*:276-278 (1994); Kilian *et al.*, *Nucl. Acids Res., 23(14)*:2729-2733 (1995); Bennett, *Symp. Soc. Exp. Biol., 50*:45-52 (1996); Hu *et al.*, *Genetics, 142(3)*:1021-1031 (1996); Kilian, *Plant Mol. Biol., 35*:187-195 (1997); Bennetzen and Freeling, *Genome Res., 7(4)*:301-306 (1997); Foote *et al.*, *Genetics, 147(2)*:801-807 (1997); Gallego *et al.*, *Genome, 41(3)*:328-336 (1998)). Gale and Devos, *Proc. Natl. Acad. Sci. USA 95*:1971-1974 (1998); Bennetzen *et al.*, *Proc. Natl. Acad. Sci. USA, 95*:1975-1978 (1998); Messing and Llaca, *Proc. Natl. Acad. Sci. USA 95*:2017-2020 (1998); McCouch, *Proc. Natl. Acad. Sci. USA, 95*:1983-1985 (1998); Goff, *Curr. Opin. Plant Biol. 2*:85-89 (1999); Bailey *et al.*, *Theor. Appl. Genet., 98*:281-284 (1999); Zhang *et al.*, *Proc. Natl. Acad. Sci. USA, 91*:8675-8679 (1994); Yano and Sasaki, *Plant Mol. Biol., 35*:145-153 (1997); Leister *et al.*, *Proc. Natl. Acad. Sci. USA, 95*:370-375 (1998); Lin *et al.*, *Phytopathology 86(11)*:1156-1159 (1996); Havukkala, *Curr. Opin. Genet. Dev., 96*:711-713 (1996); and Lee, *The Society for Experimental Biology*, pp. 31-38 (1996), all of which are herein incorporated by reference in their entirety). Synteny between rice and barley has recently been reported in the genomic region carrying malting quality Quantitative Trait Loci (QTL) (*Kleinhofs et al., Genome 41*:373-380 (1998), the entirety of which is herein incorporated by reference). Likewise, mapping of the liguless region of sorghum, a region containing a developmental control gene, was facilitated using molecular markers from a syntenic region of the rice genome (Christou *et al., Genetics 148:*1983-1992 (1998), the entirety of which is herein incorporated by reference).

In a particularly preferred embodiment, the nucleic acid molecules of the present invention that define a genomic region in rice plants associated with a desirable phenotype are utilized to obtain corresponding syntenic regions in non-rice plants. A region can be defined either physically or genetically. In an even more preferred embodiment, the nucleic acid molecules of the present invention that define a genomic region in rice plants associated with a

desirable phenotype are utilized to obtain corresponding syntenic regions in rice plants. A region can be defined either physically or genetically.

One or more of the nucleic acids molecules may be used to define a physical genomic region. For example, two nucleic acid molecules of the present invention can act to define a physical genomic region that lies between them. Moreover, for example, a physical genomic region may be defined by a distance relative to a nucleic acid molecule. In a preferred embodiment of the present invention, the defined physical genomic region is less than about 1,000 kb, more preferably less than about 500 kb, even more preferably less than about 100 kb or less than about 50 kb.

One or more of the nucleic acids molecules may be used to define a genomic region by its genetic distance from one or more nucleic acid molecules. In a preferred embodiment of the present invention, the genomic region is defined by its linkage to a nucleic acid molecule of the present invention. In such a preferred embodiment, the genomic region that is defined by one or more nucleic acid molecules of the present invention is located within about 50 centimorgans, more preferably within about 20 centimorgans, even more preferably with about 10, about 5 or about 2 centimorgans of the trait or marker at issue.

In another particularly preferred embodiment, two or more nucleic acid molecules of the present invention derived from rice plants that flank a genomic region of interest in rice plants are used to isolate the syntenic region in another cereal, more preferably maize, sorghum, barley, or wheat. Regions of interest in rice include, without limitation, those regions that are associated with a commercially desirable phenotype in rice. In another particularly preferred embodiment the desirable phenotype in rice is the result of a quantitative trait locus (QTL) present in the region.

One exemplary approach to isolate syntenic genomic regions is as follows. Nucleic acid molecules derived from rice of the present invention can be used to select large insert clones from a total genomic DNA library of a related species such as maize, sorghum, barley, or wheat. Any appropriate method to screen the genomic library with a nucleic acid molecule of the present invention may be used to select the required clones (*See, for example,* Birren *et al., Detecting Genes: A Laboratory Manual,* Cold Spring Harbor, New York, NY (1998). For example, direct hybridization of a nucleic acid molecule of the present invention to mapping filters comprising the genomic DNA of the syntenic species can be used to select large insert clones from a total genomic DNA library of a related species. The selected clones can then be used to physically map the region in the target species. An advantage of this method for comparative mapping is that no mapping population or linkage map of the target species is needed and the clones may also be used in other closely related species. By comparing the results obtained by genetic mapping in model plants, with those from other species, similarities of genomic structure among plants species can be established. Cross-hybridization of RFLP markers have been reported and conserved gene order has been established in many studies. Such macroscopic synteny is utilized for the estimation of correspondence of loci among these crops. These loci include not only Mendelian genes but also Quantitative Trait Loci (QTL) (Mohan *et al., Molecular Breeding* 3:87-103 (1997), the entirety of which is herein incorporated by reference). Other methods to isolate syntenic nucleic acid molecules may be used.

It is understood that markers of the present invention may be used in comparative mapping. In a preferred embodiment the markers of present invention may be used in the comparative mapping of cereals, more preferably maize, barley, sorgham, and wheat.

It is understood that markers of the present invention may be used to isolate nucleic acid molecules from other cereals based on the syntenic relationship between such cereals. In a

preferred embodiment the cereal is selected from the group of maize, sorgham, barley, and wheat.

The nucleic acid molecules of the present invention can be used to identify polymorphisms. In one embodiment, one or more of the nucleic acid molecules or a BAC nucleic acid molecule (or a sub-fragment of either) may be employed as a marker nucleic acid molecule to identify such polymorphism(s). Alternatively, such polymorphisms can be detected through the use of a marker nucleic acid molecule or a marker protein that is genetically linked to (*i.e.*, a polynucleotide that co-segregates with) such polymorphism(s). In a preferred embodiment, the plant is selected from the group consisting of cereals, and more preferably rice, maize, barley, sorgham, and wheat.

In an alternative embodiment, such polymorphisms can be detected through the use of a marker nucleic acid molecule that is physically linked to such polymorphism(s). For this purpose, marker nucleic acid molecules comprising a nucleotide sequence of a polynucleotide located within 1 mb of the polymorphism(s), and more preferably within 100 kb of the polymorphism(s), and most preferably within 10 kb of the polymorphism(s) can be employed.

The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem. 55*:831-854 (1986)). A "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species. The variant sequence and the "original" sequence co-exist in the species' population. In some instances, such co-existence is in stable or quasi-stable equilibrium.

A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the original sequence (*i.e.*, the original "allele") whereas other members may have the variant sequence (*i.e.*, the variant "allele"). In the

simplest case, only one variant sequence may exist, and the polymorphism is thus said to be di-allelic. In other cases, the species' population may contain multiple alleles, and the polymorphism is termed tri-allelic, etc. A single gene may have multiple different unrelated polymorphisms. For example, it may have a di-allelic polymorphism at one site, and a multi-allelic polymorphism at another site.

The variation that defines the polymorphism may range from a single nucleotide variation to the insertion or deletion of extended regions within a gene. In some cases, the DNA sequence variations are in regions of the genome that are characterized by short tandem repeats (STRs) that include tandem di- or tri-nucleotide repeated motifs of nucleotides. Polymorphisms characterized by such tandem repeats are referred to as "variable number tandem repeat" ("VNTR") polymorphisms. VNTRs have been used in identity analysis (Weber, U.S. Patent 5,075,217; Armour *et al.*, *FEBS Lett. 307*:113-115 (1992); Jones *et al.*, *Eur. J. Haematol. 39*:144-147 (1987); Horn *et al.*, PCT Application WO91/14003; Jeffreys, European Patent Application 370,719; Jeffreys, U.S. Patent 5,175,082; Jeffreys *et al.*, *Amer. J. Hum. Genet. 39*:11-24 (1986); Jeffreys *et al.*, *Nature 316*:76-79 (1985); Gray *et al.*, *Proc. R. Acad. Soc. Lond. 243*:241-253 (1991); Moore *et al.*, *Genomics 10*:654-660 (1991); Jeffreys *et al.*, *Anim. Genet. 18*:1-15 (1987); Hillel *et al.*, *Anim. Genet. 20*:145-155 (1989); Hillel *et al.*, *Genet. 124*:783-789 (1990), all of which are herein incorporated by reference in their entirety).

The detection of polymorphic sites in a sample of DNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

The most preferred method of achieving such amplification employs the polymerase chain reaction ("PCR") (Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol. 51*:263-273 (1986); Erlich *et al.*, European Patent Appln. 50,424; European Patent Appln. 84,796, European Patent Application 258,017, European Patent Appln. 237,362; Mullis, European Patent Appln. 201,184; Mullis, *et al.*, U.S. Patent No. 4,683,202; Erlich., U.S. Patent No. 4,582,788; and Saiki *et al.*, U.S. Patent No. 4,683,194, all of which are herein incorporated by reference), using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

In lieu of PCR, alternative methods, such as the "Ligase Chain Reaction" ("LCR") may be used (Barany, *Proc. Natl. Acad. Sci. USA 88*:189-193 (1991), the entirety of which is herein incorporated by reference). LCR uses two pairs of oligonucleotide probes to exponentially amplify a specific target. The sequences of each pair of oligonucleotides is selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependent ligase. As with PCR, the resulting products thus serve as a template in subsequent cycles and an exponential amplification of the desired sequence is obtained.

LCR can be performed with oligonucleotides having the proximal and distal sequences of the same strand of a polymorphic site. In one embodiment, either oligonucleotide will be designed to include the actual polymorphic site of the polymorphism. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide that is complementary to the polymorphic site present on the oligonucleotide. Alternatively, the oligonucleotides may be selected such that they do not include the polymorphic site (see, Segev, PCT Application WO 90/01069, the entirety of which is herein incorporated by reference).

The "Oligonucleotide Ligation Assay" ("OLA") may alternatively be employed (Landegren *et al.*, *Science 241*:1077-1080 (1988), the entirety of which is herein incorporated by reference). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. OLA, like LCR, is particularly suited for the detection of point mutations. Unlike LCR, however, OLA results in "linear" rather than exponential amplification of the target sequence.

Nickerson *et al.* have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson *et al.*, *Proc. Natl. Acad. Sci. USA 87*:8923-8927 (1990), the entirety of which is herein incorporated by reference). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA. In addition to requiring multiple, and separate, processing steps, one problem associated with such combinations is that they inherit all of the problems associated with PCR and OLA.

Schemes based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, are also known (Wu *et al.*, *Genomics 4*:560 (1989), the entirety of which is herein incorporated by reference), and may be readily adapted to the purposes of the present invention.

Other known nucleic acid amplification procedures, such as allele-specific oligomers, branched DNA technology, transcription-based amplification systems, or isothermal amplification methods may also be used to amplify and analyze such polymorphisms (Malek *et al.*, U.S. Patent 5,130,238; Davey *et al.*, European Patent Application 329,822; Schuster *et al.*, U.S. Patent 5,169,766; Miller *et al.*, PCT Application WO 89/06700; Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA 86*:1173-1177 (1989); Gingeras *et al.*, PCT Application WO 88/10315; Walker *et*

al., *Proc. Natl. Acad. Sci. USA 89*:392-396 (1992), all of which are herein incorporated by reference in their entirety).

The identification of a polymorphism can be determined in a variety of ways. By correlating the presence or absence of it in an plant with the presence or absence of a phenotype, it is possible to predict the phenotype of that plant. If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (*e.g.*, a VNTR polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms" ("RFLPs"). RFLPs have been widely used in human and plant genetic analyses (Glassberg, UK Patent Application 2135774; Skolnick *et al.*, *Cytogen. Cell Genet. 32*:58-67 (1982); Botstein *et al.*, *Ann. J. Hum. Genet. 32*:314-331 (1980); Fischer *et al.* PCT Application WO90/13668; Uhlen, PCT Application WO90/11369).

Polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) analysis. The SSCP technique is a method capable of identifying most sequence variations in a single strand of DNA, typically between 150 and 250 nucleotides in length (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996); Orita *et al., Genomics 5:*874-879 (1989), both of which are herein incorporated by reference in their entirety). Under denaturing conditions a single strand of DNA will adopt a conformation that is uniquely dependent on its sequence conformation. This conformation usually will be different, even if only a single base is changed. Most conformations have been reported to alter the physical configuration or size sufficiently to be detectable by electrophoresis. A number of protocols have been described for SSCP including, but not limited to Lee *et al.*,

*Anal. Biochem. 205:*289-293 (1992); Suzuki *et al., Anal. Biochem. 192:*82-84 (1991); Lo *et al., Nucleic Acids Research 20:*1005-1009 (1992); Sarkar *et al., Genomics 13:*441-443 (1992), all of which are herein incorporated by reference in their entirety). It is understood that one or more of the nucleic acids of the present invention, may be utilized as markers or probes to detect polymorphisms by SSCP analysis.

Polymorphisms may also be found using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA. Vos *et al.*, *Nucleic Acids Res. 23*:4407-4414 (1995), the entirety of which is herein incorporated by reference. This method allows for the specific co-amplification of high numbers of restriction fragments, which can be visualized by PCR without knowledge of the nucleic acid sequence.

AFLP employs basically three steps. Initially, a sample of genomic DNA is cut with restriction enzymes and oligonucleotide adapters are ligated to the restriction fragments of the DNA. The restriction fragments are then amplified using PCR by using the adapter and restriction sequence as target sites for primer annealing. The selective amplification is achieved by the use of primers that extend into the restriction fragments, amplifying only those fragments in which the primer extensions match the nucleotide flanking the restriction sites. These amplified fragments are then visualized on a denaturing polyacrylamide gel.

AFLP analysis has been performed on *Salix* (Beismann *et al., Mol. Ecol. 6*:989-993 (1997), the entirety of which is herein incorporated by reference); *Acinetobacter* (Janssen *et al., Int. J. Syst. Bacteriol 47*:1179-1187 (1997), the entirety of which is herein incorporated by reference), *Aeromonas popoffi* (Huys *et al., Int. J. Syst. Bacteriol. 47*:1165-1171 (1997), the entirety of which is herein incorporated by reference), rice (McCouch *et al., Plant Mol. Biol. 35*:89-99 (1997); Nandi *et al., Mol. Gen. Genet. 255*:1-8 (1997); Cho *et al., Genome 39*:373-378

(1996), all of which are herein incorporated by reference in their entirety), barley (*Hordeum vulgare*) (Simons *et al.*, *Genomics 44*:61-70 (1997); Waugh *et al.*, *Mol. Gen. Genet. 255*:311-321 (1997); Qi *et al.*, *Mol. Gen. Genet. 254*:330-336 (1997); Becker *et al.*, *Mol. Gen. Genet. 249*:65-73 (1995), all of which are herein incorporated by reference in their entirety), potato (Van der Voort *et al.*, *Mol. Gen. Genet. 255*:438-447 (1997); Meksem *et al.*, *Mol. Gen. Genet. 249*:74-81 (1995), both of which are herein incorporated by reference in their entirety), *Phytophthora infestans* (Van der Lee *et al.*, *Fungal Genet. Biol. 21*:278-291 (1997), the entirety of which is herein incorporated by reference), *Bacillus anthracis* (Keim *et al.*, *J. Bacteriol. 179*:818-824 (1997)), *Astragalus cremnophylax* (Travis *et al.*, *Mol. Ecol. 5*:735-745 (1996), the entirety of which is herein incorporated by reference), *Arabidopsis* (Cnops *et al.*, *Mol. Gen. Genet. 253*:32-41 (1996), the entirety of which is herein incorporated by reference), *Escherichia coli* (Lin *et al.*, *Nucleic Acids Res. 24*:3649-3650 (1996), the entirety of which is herein incorporated by reference), *Aeromonas* (Huys *et al.*, *Int. J. Syst. Bacteriol. 46*:572-580 (1996), the entirety of which is herein incorporated by reference), nematode (Folkertsma *et al.*, *Mol. Plant Microbe Interact. 9*:47-54 (1996), the entirety of which is herein incorporated by reference), tomato (Thomas *et al.*, *Plant J. 8*:785-794 (1995), the entirety of which is herein incorporated by reference), and human (Latorra *et al.*, *PCR Methods Appl. 3*:351-358 (1994) the entirety of which is herein incorporated by reference). AFLP analysis has also been used for fingerprinting mRNA (Money *et al.*, *Nucleic Acids Res. 24*:2616-2617 (1996); Bachem, *et al.*, *Plant J. 9*:745-753 (1996), both of which are herein incorporated by reference in their entirety). It is understood that one or more of the nucleic acid molecules of the present invention, may be utilized as markers or probes to detect polymorphisms by AFLP analysis for fingerprinting mRNA.

Polymorphisms may also be found using random amplified polymorphic DNA (RAPD) (Williams *et al.*, *Nucl. Acids Res. 18*:6531-6535 (1990), the entirety of which is herein

incorporated by reference) and cleavable amplified polymorphic sequences (CAPS) (Lyamichev *et al.*, *Science 260*:778-783 (1993), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention, may be utilized as markers or probes to detect polymorphisms by RAPD or CAPS analysis.

Nucleic acid molecules of the present invention can be used to monitor expression. A microarray-based method for high-throughput monitoring of plant gene expression may be utilized to measure gene-specific hybridization targets. This 'chip'-based approach involves using microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding plant genes (Schena *et al.*, *Science 270*:467-470 (1995); Shalon, Ph.D. Thesis. Stanford University (1996), both of which are herein incorporated by reference in their entirety). Every nucleotide in a large sequence can be queried at the same time. Hybridization can be used to efficiently analyze nucleotide sequences.

Several microarray methods have been described. One method compares the sequences to be analyzed by hybridization to a set of oligonucleotides or cDNA molecules representing all possible subsequences (Bains and Smith, *J. Theor. Biol.* 135:303 (1989), the entirety of which is herein incorporated by reference). A second method hybridizes the sample to an array of oligonucleotide or cDNA probes. An array consisting of oligonucleotides or cDNA molecules complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount, and detect differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be screened with protein molecules or fragments thereof to determine nucleic acid molecules that specifically bind protein molecules or fragments thereof.

Additionally, microarrays of BACs may be prepared to sufficiently cover 3X of an entire genome. Such microarrays can be used in a variety of genomics experiments including gene

mapping, DNA fingerprinting and promoter identification. Microarrays of genomic DNA can also be used for parallel analysis of genomes at single gene resolution (Lemieux *et al., Molecular Breeding* 277-289 (1988), the entirety of which is herein incorporated by reference). It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a genomic microarray based method. In a preferred embodiment of the present invention, one or more of the rice nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a genomic microarray based method. For example, Genomic Mismatch Scanning (GMS), a hybridization-based method of linkage analysis that allows rapid identification of regions of identity-by-descent between two related individuals, can be carried out with microarrays. GMS is reported to have been used to identify genetically common chromosomal segments based on the ability of these DNA sequences to form extensive regions of mismatch-free heteroduplexes. A series of enzymatic steps, coupled with filter binding, is used to selectively remove heteroduplexes that contain mismatches (*i.e.*, chromosomal regions that do not share identity-by descent.). Fragments of chromosomal DNA representing inherited regions are hybridized to a microarray of ordered genomic clones and positive hybridization signals pinpoint regions of identity-by-descent at high resolution (Lemieux *et al., Molecular Breeding* 277-289 (1988)).

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to locate regions of identity-by-descent between related individuals. In a preferred embodiment of the present invention, one or more of the rice nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to locate regions of identity-by-

descent between related individuals. The GMS microarray approach can also be used as a tool to map mutigenic traits. For example, in yeast, the entire genomic sequence is known and it has been reported that the genes responsible for growth at elevated temperature, a trait required for the pathogenicity of certain yeast strains, may be determined using GMS (Lemieux *et al.*, *Molecular Breeding* 277-289 (1988)). By analyzing the inheritance of large numbers of tetrads derived from crosses of pathogenic and wild type strains, all the genes responsible for a yeast strain's ability to grow at 42°C, for example, could be identified.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to map multigenic traits. In a preferred embodiment of the present invention, one or more of the rice nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to map multigenic traits.

Plant repeat elements may be used with GMS microarraying to identify species specific chromosomes in another species background. For example, the maize genome contains moderately repetitive DNA sequences (ZLRS) representing about 2500 copies per haploid genome; these sequences are present in the genus *Zea* and absent in other graminaceous species. Ananiev *et al.*, *Proc. Natl. Acad. Sci. USA 94*:3526-3529 (1997), the entirety of which is herein incorporated by reference, have reported unusual plants with individual maize chromosomes added to a complete oat genome generated by embryo rescue from oat (*Avena sativa*) x *Zea mays* crosses. By using highly repetitive maize-specific sequences as probes, Ananiev *et al.*, *Proc. Natl. Acad. Sci. USA 94*:3526-3529 (1997) were able to selectively isolate cosmid clones containing maize genomic DNA.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method using repeat elements to selectively isolate clones containing species specific DNA. In a preferred embodiment of the present invention, one or more of the rice nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to selectively isolate clones containing species specific DNA. A particularly preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes that are homologues of known genes or nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that are homologues of known genes and nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that elicit only limited or no matches to known genes.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a microarray based method.

In a preferred embodiment of the present invention, one or more of the nucleic acid molecules or protein molecules or fragments thereof or other agents of the present invention may be utilized in a microarray based method.

Nucleic acid molecules of the present invention may be used in site directed mutagenesis. Site-directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a

technique that allows one or more of the amino acids encoded by a nucleic acid molecule to be altered (*e.g.*, a threonine to be replaced by a methionine). Three basic methods for site-directed mutagenesis are often employed. These are cassette mutagenesis (Wells *et al.*, *Gene 34*:315-23 (1985), the entirety of which is herein incorporated by reference), primer extension (Gilliam *et al.*, *Gene 12*:129-137 (1980); Zoller and Smith, *Methods Enzymol. 100*:468-500 (1983); and Dalbadie-McFarland *et al., Proc. Natl. Acad. Sci. USA 79*:6409-6413 (1982), all of which are herein incorporated by reference in their entirety) and methods based upon PCR (Scharf *et al., Science 233*:1076-1078 (1986); Higuchi *et al., Nucleic Acids Res. 16*:7351-7367 (1988), both of which are herein incorporated by reference in their entirety). Site-directed mutagenesis approaches are also described in European Patent 0 385 962, European Patent 0 359 472, and PCT Patent Application WO 93/07278, all of which are herein incorporated by reference in their entirety.

Site-directed mutagenesis strategies have been applied to plants for both *in vitro* as well as *in vivo* site-directed mutagenesis (Lanz *et al., J. Biol. Chem.* 266:9971-6 (1991); Kovgan and Zhdanov, *Biotekhnologiya 5*:148-154, No. 207160n, Chemical Abstracts 110:225 (1989); Ge *et al., Proc. Natl. Acad. Sci. USA 86*:4037-4041 (1989); Zhu *et al., J. Biol. Chem. 271*:18494-18498 (1996), Chu *et al., Biochemistry 33*:6150-6157 (1994); Small *et al., EMBO J. 11*:1291-1296 (1992); Cho *et al., Mol. Biotechnol. 8*:13-16 (1997), Kita *et al., J. Biol. Chem. 271*:26529-26535 (1996); Jin *et al., Mol. Microbiol. 7*:555-562 (1993); Hatfield and Vierstra, *J. Biol. Chem. 267*:14799-14803 (1992); Zhao *et al., Biochemistry 31*:5093-5099 (1992), all of which are herein incorporated by reference in their entirety).

Any of the nucleic acid molecules of the present invention may either be modified by site-directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification. It is understood that mutants with more than one altered

nucleotide can be constructed using techniques that practitioners skilled in the art are familiar with such as isolating restriction fragments and ligating such fragments into an expression vector (*see*, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989)). In a preferred embodiment of the present invention, one or more of the rice nucleic acid molecules or fragments thereof of the present invention may be modified by site-directed mutagenesis.

Nucleic acid molecules of the present invention may be used in transformation. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of being inserted into any organism. In a preferred embodiment of the present invention the exogenous genetic material can include rice genetic material. A particularly preferred embodiment is exogenous genetic material that comprises a nucleic acid molecule of the present invention. Such genetic material may be transferred into either monocotyledons and dicotyledons including but not limited to the plants, maize and *Arabidopsis thaliana* and rice (See specifically, Chistou, *Particle Bombardment for Genetic Engineering of Plants,* pp. 63-69 (maize), pp50-60 (rice), Biotechnology Intelligence Unit, Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference and generally Chistou, *Particle Bombardment for Genetic Engineering of Plants,* Biotechnology Intelligence Unit, Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference).

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the present invention may be overexpressed in a

transformed cell or transformed plant. Such overexpression may be the result of transient or stable transfer of the exogenous material.

Exogenous genetic material may be transferred into a plant cell by the use of a DNA vector or construct designed for such a purpose. Preferred exogenous genetic material comprise a nucleic acid molecule of the present invention. Vectors have been engineered for transformation of large DNA inserts into plant genomes. Vectors have been designed to replicate in both *E. coli* and *A. tumefaciens* and have all of the features required for transferring large inserts of DNA into plant chromosomes (Choi and Wing, http://genome.clemson.edu/protocols2-nj.html July, 1998). ApBACwich system has been developed to achieve site-directed integration of DNA into the genome. A 150 kb cotton BAC DNA is reported to have been transferred into a specific *lox* site in tobacco by biolistic bombardment and *Cre-lox* site specific recombination.

A construct or vector may include a plant promoter to express the protein or protein fragment of choice. A number of promoters which are active in plant cells have been described in the literature. These include the nopaline synthase (NOS) promoter (Ebert *et al.*, *Proc. Natl. Acad. Sci. USA 84*:5745-5749 (1987), the entirety of which is herein incorporated by reference), the octopine synthase (OCS) promoter (which are carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*), the caulimovirus promoters such as the cauliflower mosaic virus (CaMV) 19S promoter (Lawton *et al.*, *Plant Mol. Biol. 9*:315-324 (1987), the entirety of which is herein incorporated by reference) and the CaMV 35S promoter (Odell *et al.*, *Nature 313*:810-812 (1985), the entirety of which is herein incorporated by reference), the figwort mosaic virus 35S-promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate carboxylase (ssRUBISCO), the Adh promoter (Walker *et al.*, *Proc. Natl. Acad. Sci. USA 84*:6624-6628 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase promoter (Yang *et al.*, *Proc. Natl. Acad. Sci. USA 87*:4144-4148 (1990), the entirety of

which is herein incorporated by reference), the R gene complex promoter (Chandler *et al.*, *The Plant Cell 1*:1175-1183 (1989), the entirety of which is herein incorporated by reference), and the chlorophyll a/b binding protein gene promoter, etc. These promoters have been used to create DNA constructs which have been expressed in plants; *see*, *e.g.*, PCT publication WO 84/02913, herein incorporated by reference in its entirety.

Promoters which are known or are found to cause transcription of DNA in plant cells can be used in the present invention. Such promoters may be obtained from a variety of sources such as plants and plant viruses. It is preferred that the particular promoter selected should be capable of causing sufficient expression to result in the production of an effective amount of protein to cause the desired phenotype. In addition to promoters which are known to cause transcription of DNA in plant cells, other promoters may be identified for use in the current invention by screening a plant cDNA library for genes which are selectively or preferably expressed in the target tissues or cells.

For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. For this purpose, one may choose from a number of promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea (Edwards *et al.*, *Proc. Natl. Acad. Sci. USA 87*:3459-3463 (1990), herein incorporated by reference in its entirety), the chloroplast fructose-1,6-biphosphatase (FBPase) promoter from wheat (Lloyd *et al.*, *Mol. Gen. Genet. 225*:209-216 (1991), herein incorporated by reference in its entirety), the nuclear photosynthetic ST-LS1 promoter from potato (Stockhaus *et al.*, *EMBO J.. 8*:2445-2451 (1989), herein incorporated by reference in its entirety), the phenylalanine ammonia-lyase (PAL) promoter and the chalcone synthase (CHS) promoter from *Arabidopsis*

thaliana. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, cab6, from pine (Yamamoto *et al.*, *Plant Cell Physiol. 35*:773-778 (1994), herein incorporated by reference in its entirety), the promoter for the Cab-1 gene from wheat (Fejes *et al.*, *Plant Mol. Biol. 15*:921-932 (1990), herein incorporated by reference in its entirety), the promoter for the CAB-1 gene from spinach (Lubberstedt *et al.*, *Plant Physiol. 104*:997-1006 (1994), herein incorporated by reference in its entirety), the promoter for the cab1R gene from rice (Luan *et al.*, *Plant Cell. 4*:971-981 (1992), the entirety of which is herein incorporated by reference), the pyruvate, orthophosphate dikinase (PPDK) promoter from maize (Matsuoka *et al.*, *Proc. Natl. Acad. Sci. USA 90*:9586-9590 (1993), herein incorporated by reference in its entirety), the promoter for the tobacco Lhcb1*2 gene (Cerdan *et al.*, *Plant Mol. Biol. 33*:245-255. (1997), herein incorporated by reference in its entirety), the *Arabidopsis thaliana* SUC2 sucrose-H+ symporter promoter (Truernit *et al.*, *Planta. 196*:564-570 (1995), herein incorporated by reference in its entirety), and the promoter for the thylacoid membrane proteins from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other promoters for the chlorophyll a/b-binding proteins may also be utilized in the present invention, such as the promoters for LhcB gene and PsbP gene from white mustard (*Sinapis alba*; Kretsch *et al.*, *Plant Mol. Biol. 28*:219-229 (1995), the entirety of which is herein incorporated by reference).

For the purpose of expression in sink tissues of the plant, such as the tuber of the potato plant, the fruit of tomato, or the seed of maize, wheat, rice, and barley, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. A number of promoters for genes with tuber-specific or -enhanced expression are known, including the class I patatin promoter (Bevan *et al.*, *EMBO J.. 8*:1899-1906 (1986); Jefferson *et al.*, *Plant Mol. Biol. 14*995-1006 (1990), both of which are herein incorporated by

reference in its entirety), the promoter for the potato tuber ADPGPP genes, both the large and small subunits, the sucrose synthase promoter (Salanoubat and Belliard, *Gene. 60*:47-56 (1987), Salanoubat and Belliard, *Gene. 84*:181-185 (1989), both of which are incorporated by reference in their entirety), the promoter for the major tuber proteins including the 22 kd protein complexes and proteinase inhibitors (Hannapel, *Plant Physiol. 101*:703-704 (1993), herein incorporated by reference in its entirety), the promoter for the granule bound starch synthase gene (GBSS) (Visser *et al.*, *Plant Mol. Biol. 17*:691-699 (1991), herein incorporated by reference in its entirety), and other class I and II patatins promoters (Koster-Topfer *et al.*, *Mol. Gen. Genet. 219*:390-396 (1989); Mignery *et al.*, *Gene. 62*:27-44 (1988), both of which are herein incorporated by reference in their entirety).

Other promoters can also be used to express a fructose 1,6 bisphosphate aldolase gene in specific tissues, such as seeds or fruits. The promoter for β-conglycinin (Chen *et al.*, *Dev. Genet. 10*:112-122 (1989), herein incorporated by reference in its entirety) or other seed-specific promoters such as the napin and phaseolin promoters, can be used. The zeins are a group of storage proteins found in maize endosperm. Genomic clones for zein genes have been isolated (Pedersen *et al.*, *Cell 29*:1015-1026 (1982), herein incorporated by reference in its entirety), and the promoters from these clones, including the 15 kD, 16 kD, 19 kD, 22 kD, 27 kD, and gamma genes, could also be used. Other promoters known to function, for example, in maize, include the promoters for the following genes: *waxy, Brittle, Shrunken 2*, Branching enzymes I and II, starch synthases, debranching enzymes, oleosins, glutelins, and sucrose synthases. A particularly preferred promoter for maize endosperm expression is the promoter for the glutelin gene from rice, more particularly the Osgt-1 promoter (Zheng *et al.*, *Mol. Cell Biol. 13*:5829-5842 (1993), herein incorporated by reference in its entirety). Examples of promoters suitable for expression in wheat include those promoters for the ADPglucose pyrophosphorylase (ADPGPP) subunits,

the granule bound and other starch synthases, the branching and debranching enzymes, the embryogenesis-abundant proteins, the gliadins, and the glutenins. Examples of such promoters in rice include those promoters for the ADPGPP subunits, the granule bound and other starch synthases, the branching enzymes, the debranching enzymes, sucrose synthases, and the glutelins. A particularly preferred promoter is the promoter for rice glutelin, Osgt-1. Examples of such promoters for barley include those for the ADPGPP subunits, the granule bound and other starch synthases, the branching enzymes, the debranching enzymes, sucrose synthases, the hordeins, the embryo globulins, and the aleurone specific proteins.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac *et al.*, *Plant Mol. Biol. 25*:587-596 (1994), the entirety of which is herein incorporated by reference). Expression in root tissue could also be accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have been identified (Lam *et al.*, *Proc. Natl. Acad. Sci. USA 86*:7890-7894 (1989), herein incorporated by reference in its entirety). Other root cell specific promoters include those reported by Conkling *et al.* (Conkling *et al.*, *Plant Physiol. 93*:1203-1211 (1990), the entirety of which is herein incorporated by reference).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619, 5,391,725, 5,428,147, 5,447,858, 5,608,144, 5,608,144, 5,614,399, 5,633,441, 5,633,435, and 4,633,436, all of which are herein incorporated in their entirety. In addition, a tissue specific enhancer may be used (Fromm *et al.*, *The Plant Cell 1*:977-984 (1989), the entirety of which is herein incorporated by reference).

Constructs or vectors may also include, with the coding region of interest, a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the nos 3' sequence

(Ingelbrecht *et al.*, *The Plant Cell 1*:671-680 (1989); Bevan *et al.*, *Nucleic Acids Res. 11*:369-385 (1983), both of which are herein incorporated by reference in their entirety), or the like.

A vector or construct may also include regulatory elements. Examples of such include the Adh intron 1 (Callis *et al.*, *Genes and Develop. 1*:1183-1200 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase intron (Vasil *et al.*, *Plant Physiol.* 91:1575-1579 (1989), the entirety of which is herein incorporated by reference) and the TMV omega element (Gallie *et al.*, *The Plant Cell 1*:301-311 (1989), the entirety of which is herein incorporated by reference). These and other regulatory elements may be included when appropriate.

A vector or construct may also include a selectable marker. Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to, a neo gene (Potrykus *et al.*, *Mol. Gen. Genet. 199*:183-188 (1985), the entirety of which is herein incorporated by reference) which codes for kanamycin resistance and can be selected for using kanamycin, G418, etc.; a bar gene which codes for bialaphos resistance; a mutant EPSP synthase gene (Hinchee *et al.*, *Bio/Technology 6*:915-922 (1988), the entirety of which is herein incorporated by reference) which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil (Stalker *et al.*, *J. Biol. Chem. 263*:6310-6314 (1988), the entirety of which is herein incorporated by reference); a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204 (Sept. 11, 1985), the entirety of which is herein incorporated by reference); and a methotrexate resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem. 263*:12500-12508 (1988), the entirety of which is herein incorporated by reference).

A vector or construct may also include a transit peptide. Incorporation of a suitable chloroplast transit peptide may also be employed (European Patent Application Publication

Number 0218571, the entirety of which is herein incorporated by reference). Translational enhancers may also be incorporated as part of the vector DNA. DNA constructs could contain one or more 5' non-translated leader sequences which may serve to enhance expression of the gene products from the resulting mRNA transcripts. Such sequences may be derived from the promoter selected to express the gene or can be specifically modified to increase translation of the mRNA. Such regions may also be obtained from viral RNAs, from suitable eukaryotic genes, or from a synthetic gene sequence. For a review of optimizing expression of transgenes, see Koziel *et al., Plant Mol. Biol. 32*:393-405 (1996), the entirety of which is herein incorporated by reference.

A vector or construct may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include a β-glucuronidase or uidA gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, *Plant Mol. Biol, Rep. 5:*387-405 (1987); Jefferson *et al., EMBO J.. 6:*3901-3907 (1987), both of which are herein incorporated by reference in their entirety); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues ((Dellaporta *et al.*, Stadler Symposium *11*:263-282 (1988), the entirety of which is herein incorporated by reference); a β-lactamase gene (Sutcliffe *et al., Proc. Natl. Acad. Sci. USA 75*:3737-3741 (1978), the entirety of which is herein incorporated by reference), a gene which encodes an enzyme for which various chromogenic substrates are known (*e.g.*, PADAC, a chromogenic cephalosporin); a luciferase gene (Ow *et al., Science 234*:856-859 (1986), the entirety of which is herein incorporated by reference) a xylE gene (Zukowsky *et al., Proc. Natl. Acad. Sci. USA 80*:1101-1105 (1983), the entirety of which is herein incorporated by reference) which encodes a catechol diozygenase that can convert chromogenic catechols; an α-amylase gene (Ikatu *et al., Bio/Technol. 8*:241-242 (1990), the entirety of which is herein incorporated by

reference); a tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol. 129*:2703-2714 (1983), the entirety of which is herein incorporated by reference) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α-galactosidase, which will turn a chromogenic α-galactose substrate.

Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible proteins detectable, *e.g.*, by ELISA, small active enzymes detectable in extracellular solution (*e.g.*, α-amylase, β-lactamase, phosphinothricin transferase), or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

Methods and compositions for transforming a bacteria and other microorganisms are known in the art (see for example Sambrook *et al., Molecular Cloning: A Laboratory Manual*, Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1989), the entirety of which is herein incorporated by reference).

There are many methods for introducing transforming nucleic acid molecules into plant cells. Suitable methods are believed to include virtually any method by which nucleic acid molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of nucleic acid molecules such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc. (Pottykus, *Ann. Rev. Plant Physiol. Plant Mol. Biol. 42*:205-225 (1991); Vasil, *Plant Mol. Biol. 25*:925-937 (1994), both of

which are herein incorporated by reference in their entirety). For example, electroporation has been used to transform maize protoplasts (Fromm *et al.*, *Nature 312*:791-793 (1986), the entirety of which is herein incorporated by reference).

Technology for introduction of DNA into cells is well known to those of skill in the art. Four general methods for delivering a gene into cells have been described: (1) chemical methods (Graham and van der Eb, *Virology, 54*:536-539 (1973), the entirety of which is herein incorporated by reference); (2) physical methods such as microinjection (Capecchi, *Cell 22*:479-488 (1980), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun., 107*:584-587 (1982); Fromm *et al., Proc. Natl. Acad. Sci. USA*, 82:5824-5828 (1985); U.S. Patent No. 5,384,253; and the gene gun (Johnston and Tang, *Methods Cell Biol. 43*:353-365 (1994), all of which are herein incorporated by reference in their entirety; (3) viral vectors (Clapp, *Clin. Perinatol., 20*:155-168 (1993); Lu *et al., J. Exp. Med., 178*:2089-2096 (1993); Eglitis and Anderson, *Biotechniques, 6*:608-614 (1988), all of which are herein incorporated by reference in their entirety); and (4) receptor-mediated mechanisms (Curiel *et al., Hum. Gen. Ther., 3*:147-154 (1992); Wagner *et al., Proc. Natl. Acad. Sci. USA, 89*:6099-6103 (1992), all of are herein incorporated by reference in their entirety).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid molecules to plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou, eds., *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994), the entirety of which is herein incorporated by reference). Non-biological particles (microprojectiles) that may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum, and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly, and stably transforming monocotyledons, is that neither the isolation of protoplasts (Cristou *et al.*, *Plant Physiol. 87*:671-674 (1988), the entirety of which is herein incorporated by reference) nor the susceptibility of *Agrobacterium* infection is required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics-particle delivery system, which can be used to propel particles coated with DNA through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with corn cells cultured in suspension. Gordon-Kamm *et al.*, describes the basic procedure for coating tungsten particles with DNA (Gordon-Kamm *et al.*, *Plant Cell 2*:603-618 (1990), the entirety of which is herein incorporated by reference). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the present invention is the helium acceleration PDS-1000/He gun which is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California)(Sanford *et al.*, *Technique 3*:3-16 (1991), the entirety of which is herein incorporated by reference).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the macroprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein one may obtain up to 1000 or more foci of cells transiently expressing a marker gene. The

number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from one to ten and average one to three.

In bombardment transformation, one may optimize the prebombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable transformants. Both the physical and biological parameters for bombardment are important in this technology. Physical factors are those that involve manipulating the DNA/microprojectile precipitate or those that affect the flight and velocity of either the macro- or microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment, and also the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al. Proc. Natl. Acad. Sci. USA 87*:8526-8530 (1990); Svab and Maliga *Proc. Natl. Acad. Sci. USA 90:*913-917 (1993)); Staub, J. M. and Maliga, P. *EMBO J. 12:*601-606 (1993), U.S. Patents 5, 451,513 and 5,545,818, all of which are herein incorporated by reference in their entirety).

Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue distance, and helium pressure. One may also minimize the trauma reduction factors by modifying conditions which influence the physiological state of the recipient cells and which

may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration and the subculture stage or cell cycle of the recipient cells may be adjusted for optimum transformation. The execution of other routine adjustments will be known to those of skill in the art in light of the present disclosure.

Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example the methods described (Fraley *et al., Biotechnology 3*:629-635 (1985); Rogers *et al., Meth. In Enzymol, 153*:253-277 (1987), both of which are herein incorporated by reference in their entirety. Further, the integration of the Ti-DNA is a relatively precise process resulting in few rearrangements. The region of DNA to be transferred is defined by the border sequences, and intervening DNA is usually inserted into the plant genome as described (Spielmann *et al., Mol. Gen. Genet., 205*:34 (1986), the entirety of which is herein incorporated by reference).

Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al., In: Plant DNA Infectious Agents*, T. Hohn and J. Schell, eds., Springer-Verlag, New York, pp. 179-203 (1985), the entirety of which is herein incorporated by reference). Moreover, recent technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The vectors described have convenient multi-linker regions flanked by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes and are suitable for present purposes (Rogers *et al., Meth. In Enzymol., 153*:253-277 (1987), the entirety of which is herein incorporated by reference). In

addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for the added structural gene; *i.e.*, a transgenic plant that contains two added genes, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) an independent segregant transgenic plant that contains a single added gene, germinating some of the seed produced and analyzing the resulting plants produced for the gene of interest.

It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes. Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these treatments. See for example (Potrykus *et al., Mol. Gen. Genet., 205*:193-200 (1986); Lorz *et al., Mol. Gen. Genet., 199*:178, (1985); Fromm *et al., Nature, 319*:791,(1986); Uchimiya *et al., Mol. Gen. Genet.*:204:204, (1986); Callis *et al., Genes and Development, 1183*,(1987); Marcotte *et al., Nature, 335*:454, (1988), all of which the entirety is herein incorporated by reference).

Application of these systems to different plant strains depends upon the ability to regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration

of cereals from protoplasts are described (Fujimura *et al.*, *Plant Tissue Culture Letters, 2*:74,(1985); Toriyama *et al., Theor Appl. Genet. 205*:34. (1986); Yamada *et al., Plant Cell Rep., 4*:85, (1986); Abdullah *et al., Biotechnology, 4*:1087, (1986), all of which the entirety is herein incorporated by reference).

To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology, 6*:397,(1988), the entirety of which is herein incorporated by reference). In addition, "particle gun" or high-velocity microprojectile technology can be utilized (Vasil *et al., Bio/Technology 10*:667, (1992), the entirety of which is herein incorporated by reference).

Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al., Nature, 328*:70, (1987); Klein *et al., Proc. Natl. Acad. Sci. USA*, 85:8502-8505, (1988); McCabe *et al., Biotechnology, 6*:923, (1988), all of which the entirety is herein incorporated by reference). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

Other methods of cell transformation can also be used and include but are not limited to introduction of DNA into plants by direct DNA transfer into pollen (Hess *et al., Intern Rev. Cytol., 107*:367, (1987); Luo *et al., Plant Mol. Biol. Reporter, 6*:165, (1988), all of which the entirety is herein incorporated by reference), by direct injection of DNA into reproductive organs of a plant (Pena *et al.*, Nature, 325:274, (1987), the entirety of which is herein incorporated by reference), or by direct injection of DNA into the cells of immature embryos followed by the rehydration of dessicated embryos (Neuhaus *et al., Theor. Appl. Genet., 75*:30, (1987), the entirety of which is herein incorporated by reference).

The regeneration, development, and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, *In: Methods for Plant Molecular Biology*, (Eds.), Academic Press, Inc., San Diego, CA, (1988), the entirety of which is herein incorporated by reference). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants, as discussed before. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens*, and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863, U.S. Patent No. 5,159,135, U.S. Patent No. 5,518,908, all of which the entirety is herein incorporated by reference); rice (U.S. Patent No. 5,569,834, U.S. Patent No. 5,416,011, McCabe *et al.*, *Biotechnology 6*:923, (1988), Christou *et al.*, *Plant Physiol.*, *87*:671-674 (1988), all of which the entirety is herein incorporated by reference); *Brassica* (U.S. Patent No. 5,463,174, the entirety of

which is herein incorporated by reference); peanut (Cheng *et al., Plant Cell Rep. 15*:653-657 (1996), McKently *et al., Plant Cell Rep. 14*:699-703 (1995), all of which the entirety is herein incorporated by reference); papaya (Yang *et al.*, (1996), the entirety of which is herein incorporated by reference); pea (Grant *et al., Plant Cell Rep. 15*:254-258, (1995), the entirety of which is herein incorporated by reference).

Transformation of monocotyledons using electroporation, particle bombardment, and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier *et al., Proc. Natl. Acad. Sci. USA 84*:5345, (1987), the entirety of which is herein incorporated by reference); barley (Wan and Lemaux, *Plant Physiol 104*:37, (1994), the entirety of which is herein incorporated by reference); maize (Rhodes *et al., Science 240*:204, (1988), Gordon-Kamm *et al., Plant Cell, 2*:603, (1990), Fromm *et al., Bio/Technology 8*:833, (1990), Koziel *et al., Bio/Technology 11*:194, (1993), Armstrong *et al., Crop Science 35*:550-557, (1995), all of which the entirety is herein incorporated by reference); oat (Somers *et al., Bio/Technology, 10*:1589, (1992), the entirety of which is herein incorporated by reference); orchardgrass (Horn *et al., Plant Cell Rep. 7*:469, (1988), the entirety of which is herein incorporated by reference); rice (Toriyama *et al., Theor Appl. Genet. 205*:34, (1986); Park *et al., Plant Mol. Biol.,32*:1135-1148, (1996); Abedinia *et al., Aust. J. Plant Physiol.24*:133-141, (1997); Zhang and Wu, *Theor. Appl. Genet. 76*:835, (1988); Zhang *et al., Plant Cell Rep. 7*:379, (1988); Battraw and Hall, *Plant Sci. 86*:191-202, (1992); Christou *et al., Bio/Technology 9*:957, (1991), all of which the entirety is herein incorporated by reference); sugarcane (Bower and Birch, *Plant J.* 2:409, (1992), the entirety of which is herein incorporated by reference); tall fescue (Wang *et al.*, Bio/Technology 10:691, (1992), the entirety of which is herein incorporated by reference), and wheat (Vasil *et al.*, Bio/Technology 10:667, (1992), the entirety of which is

herein incorporated by reference; U.S. Patent No. 5,631,152, the entirety of which is herein incorporated by reference.

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte, *et al., Nature, 335*:454-457 (1988); Marcotte, *et al., Plant Cell, 1*:523-532 (1989); McCarty, *et al., Cell 66*:895-905 (1991); Hattori, *et al., Genes Dev. 6*:609-618 (1992); Goff, *et al., EMBO J.. 9*:2517-2522 (1990), all of which are herein incorporated by reference in their entirety). Transient expression systems may be used to functionally dissect gene constructs (*See generally*, Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995)).

Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters enhancers etc. Further any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a manner that allows for over expression of the protein or fragment thereof encoded by the nucleic acid molecule.

Nucleic acid molecules of the present invention may be used in cosuppression. Cosuppression is the reduction in expression levels, usually at the level of RNA, of a particular endogenous gene or gene family by the expression of a homologous sense construct that is capable of transcribing mRNA of the same strandedness as the transcript of the endogenous gene (Napoli *et al., Plant Cell 2*:279-289 (1990); van der Krol *et al., Plant Cell 2*:291-299 (1990), both of which are herein incorporated by reference in their entirety). Cosuppression may result from stable transformation with a single copy nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Prolls and Meyer, *Plant J. 2*:465-475 (1992), the entirety of which is herein incorporated by reference) or with multiple copies of a nucleic acid

molecule that is homologous to a nucleic acid sequence found with the cell (Mittlesten *et al., Mol. Gen. Genet. 244*: 325-330 (1994), the entirety of which is herein incorporated by reference). Genes, even though different, linked to homologous promoters may result in the cosuppression of the linked genes (Vaucheret, *C.R. Acad. Sci. III 316*: 1471-1483 (1993), the entirety of which is herein incorporated by reference).

This technique has, for example been applied to generate white flowers from red petunia and tomatoes that do not ripen on the vine. Up to 50% of petunia transformants that contained a sense copy of the chalcone synthase (CHS) gene produced white flowers or floral sectors; this was as a result of the post-transcriptional loss of mRNA encoding CHS (Flavell, *Proc. Natl. Acad. Sci. USA 91*:3490-3496 (1994)), the entirety of which is herein incorporated by reference). Cosuppression may require the coordinate transcription of the transgene and the endogenous gene, and can be reset by a developmental control mechanism (Jorgensen, *Trends Biotechnol, 8*:340344 (1990); Meins and Kunz, In: *Gene Inactivation and Homologous Recombination in Plants* (Paszkowski, J., ed.), pp. 335-348. Kluwer Academic, Netherlands (1994), both of which are herein incorporated by reference in their entirety).

It is understood that one or more of the nucleic acids of the present invention comprising SEQ ID NO:1 or complement thereof through SEQ ID NO: 69652 or complement thereof or fragment thereof or other nucleic acid molecules of the present invention, may be introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the co-suppression of an endogenous protein.

Nucleic acid molecules of the present invention may be used to reduce gene function. Antisense approaches are a way of preventing or reducing gene function by targeting the genetic material (Mol *et al., FEBS Lett. 268*:427-430 (1990), the entirety of which is herein incorporated by reference). The objective of the antisense approach is to use a sequence complementary to the

target gene to block its expression and create a mutant cell line or organism in which the level of a single chosen protein is selectively reduced or abolished. Antisense techniques have several advantages over other 'reverse genetic' approaches. The site of inactivation and its developmental effect can be manipulated by the choice of promoter for antisense genes or by the timing of external application or microinjection. Antisense can manipulate its specificity by selecting either unique regions of the target gene or regions where it shares homology to other related genes (Hiatt *et al., In Genetic Engineering,* Setlow (ed.), Vol. 11, New York: Plenum 49-63 (1989), the entirety of which is herein incorporated by reference).

The principle of regulation by antisense RNA is that RNA that is complementary to the target mRNA is introduced into cells, resulting in specific RNA:RNA duplexes being formed by base pairing between the antisense substrate and the target mRNA (Green *et al.*, *Annu. Rev. Biochem. 55*:569-597 (1986), the entirety of which is herein incorporated by reference). Under one embodiment, the process involves the introduction and expression of an antisense gene sequence. Such a sequence is one in which part or all of the normal gene sequences are placed under a promoter in inverted orientation so that the 'wrong' or complementary strand is transcribed into a noncoding antisense RNA that hybridizes with the target mRNA and interferes with its expression (Takayama and Inouye, *Crit. Rev. Biochem. Mol. Biol. 25*:155-184 (1990), the entirety of which is herein incorporated by reference). An antisense vector is constructed by standard procedures and introduced into cells by transformation, transfection, electroporation, microinjection, or by infection, etc. The type of transformation and choice of vector will determine whether expression is transient or stable. The promoter used for the antisense gene may influence the level, timing, tissue, specificity, or inducibility of the antisense inhibition.

It is understood that protein synthesis activity in a plant cell may be reduced or depressed by growing a transformed plant cell containing a nucleic acid molecule of the present invention.

Antibodies have been expressed in plants (Hiatt *et al., Nature 342:*76-78 (1989); Conrad and Fielder, *Plant Mol. Biol. 26:*1023-1030 (1994), both of which are herein incorporated by reference in their entirety). Cytoplasmic expression of a scFv (single-chain Fv antibodies) has been reported to delay infection by artichoke mottled crinkle virus. Transgenic plants that express antibodies directed against endogenous proteins may exhibit a physiological effect (Philips *et al., EMBO J.. 16:*4489-4496 (1997); Marion-Poll, *Trends in Plant Science 2:*447-448 (1997), both of which are herein incorporated by reference in their entirety). For example, expressed anti-abscisic antibodies reportedly result in a general perturbation of seed development (Philips *et al., EMBO J.. 16:*4489-4496 (1997)).

Nucleic acid molecules of the present invention may be used as antibodies. Antibodies that are catalytic may also be expressed in plants (abzymes). The principle behind abzymes is that since antibodies may be raised against many molecules, this recognition ability can be directed toward generating antibodies that bind transition states to force a chemical reaction forward (Persidas, *Nature Biotechnology 15*:1313-1315 (1997); Baca *et al., Ann. Rev. Biophys. Biomol. Struct. 26*:461-493 (1997), both of which are herein incorporated by reference in their entirety). The catalytic abilities of abzymes may be enhanced by site directed mutagenesis. Examples of abzymes are, for example, set forth in U.S. Patent No: 5,658,753; U.S. Patent No. 5,632,990; U.S. Patent No. 5,631,137; U.S. Patent 5,602,015; U.S. Patent No. 5,559,538; U.S. Patent No. 5,576,174; U.S. Patent No. 5,500,358; U.S. Patent 5,318,897; U.S. Patent No. 5,298,409; U.S. Patent No. 5,258,289 and U.S. Patent No. 5,194,585, all of which are herein incorporated in their entirety.

It is understood that any of the antibodies of the present invention may be expressed in plants and that such expression can result in a physiological effect. It is also understood that any of the expressed antibodies may be catalytic.

In addition to the above discussed procedures, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (*e.g.*, DNA molecules, plasmids, etc.), generation

of recombinant organisms and the screening and isolating of clones, (see for example, Sambrook *et al., Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989); Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995); Birren *et al., Genome Analysis: Analyzing DNA,* 1, Cold Spring Harbor, New York (1998), both of which are herein incorporated by reference in their entirety).

The nucleotide sequence provided in SEQ ID NO:1, through SEQ ID NO: 69652 or fragment thereof, or complement thereof, or a nucleotide sequence at least 90% identical, preferably 95%, identical even more preferably 99% or 100% identical to the sequence provided in SEQ ID NO:1 through SEQ ID NO: 69652 or fragment thereof, or complement thereof, can be "provided" in a variety of mediums to facilitate use fragment thereof. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences.

In a preferred embodiment, 20, preferably 50, more preferably 100, even more preferably 1,000, 2,000, 3,000, or 4,000 of the nucleic acid sequences of the present invention can be provided in a variety of mediums.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium, and magnetic tape: optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate media comprising the nucleotide sequence information of the present invention. A variety of data storage structures are

available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data processor structuring formats (*e.g.*, text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing one or more of nucleotide sequences of the present invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990)) and BLAZE (Brutlag *et al., Comp. Chem. 17:*203-207 (1993), the entirety of which is herein incorporated by reference) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the sequences of the present invention and are useful in producing commercially important proteins such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification, and DNA replication, restriction, modification, recombination, and repair.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the present invention. As used

herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the present invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above, and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments sequence of the present invention. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990)) can be used to identify open frames within the nucleic acid molecules of the present invention. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Example 1

BACs are stable, non-chimeric cloning systems having genomic fragment inserts (100-300 kb) and their DNA can be prepared for most types of experiments including DNA sequencing. BAC vector, pBeloBAC11, is derived from the endogenous *E. coli* F-factor plasmid, which contains genes for strict copy number control and unidirectional origin of DNA replication. Additionally, pBeloBAC11 has three unique restriction enzyme sites (*Hind* III, *Bam* HI and *Sph* I) located within the *LacZ* gene which can be used as cloning sites for megabase-size plant DNA. Indigo, another BAC vector contains *Hind* III and *Eco* RI cloning sites. This vector also contains a random mutation in the *LacZ* gene that allows for darker blue colonies.

As an alternative, the P1-derived artificial chromosome (PAC) can be used as a large DNA fragment cloning vector (Ioannou, *et al.*, *Nature Genet. 6*:84-89 (1994); Suzuki, *et al.*, *Gene 199*:133-137 (1997), both of which are herein incorporated by reference in their entirety). The PAC vector has most of the features of the BAC system, but also contains some of the elements of the bacteriophage P1 cloning system.

BAC libraries are generated by ligating size-selected restriction digested DNA with pBeloBAC11 followed by electroporation into *E. coli.* BAC library construction and characterization is extremely efficient when compared to YAC (yeast artificial chromosome) library construction and analysis, particularly because of the chimerism associated with YACs and difficulties associated with extracting YAC DNA.

There are general methods for preparing megabase-size DNA from plants. For example, the protoplast method yields megabase-size DNA of high quality with minimal breakage. The process involves preparing young leaves which are manually feathered with a razor-blade before being incubated for four to five hours with cell-wall-degrading enzymes. The second method developed by Zhange *et al.*, *Plant J.* 7:175-184 (1995), the entirety of which is herein incorporated by reference, is a universal nuclei method that works well for several divergent plant taxa. Fresh or frozen tissue is homogenized with a blender or mortar and pestle. Nuclei are

then isolated and embedded. DNA prepared by the nucleic method is often more concentrated and is reported to contain lower amounts of chloroplast DNA than the protoplast method.

Once protoplasts or nuclei are produced, they are embedded in an agarose matrix as plugs or microbeads. The agarose provides a support matrix to prevent shearing of the DNA while allowing enzymes and buffers to diffuse into the DNA. The DNA is purified and manipulated in the agarose and is stable for more than one year at 4°C.

Once high molecular weight DNA has been prepared, it is fragmented to the desired size range. In general, DNA fragmentation utilizes two general approaches, 1) physical shearing and 2) partial digestion with a restriction enzyme that cuts relatively frequently within the genome. Since physical shearing is not dependent upon the frequency and distribution of particular restriction enzymes sites, this method should yield the most random distribution of DNA fragments. However, the ends of the sheared DNA fragments must be repaired and cloned directly or restriction enzyme sites added by the addition of synthetic linkers. Because of the subsequent steps required to clone DNA fragmented by shearing, most protocols fragment DNA by partial restriction enzyme digestion. The advantage of partial restriction enzyme digestion is that no further enzymatic modification of the ends of the restriction fragments are necessary. Four common techniques that can be used to achieve reproducible partial digestion of megabase-size DNA are 1) varying the concentration of the restriction enzyme, 2) varying the time of incubation with the restriction enzyme 3) varying the concentration of an enzyme cofactor (*e.g.*, Mg^{2+}) and 4) varying the ratio of endonuclease to methylase.

There are three cloning sites in pBeloBAC11, but only *Hind* III and *Bam* HI produce 5' overhangs for easy vector dephosphorylation. These two restriction enzymes are primarily used to construct BAC libraries. The optimal partial digestion conditions for megabase-size DNA are determined by wide and narrow window digestions. To optimize the optimum amount of *Hind* III, 1, 2, 3, 10, and 5- units of enzyme are each added to 50 ml aliquots of microbeads and incubated at 37 °C for 20 minutes.

After partial digestion of megabase-size DNA, the DNA is run on a pulsed-field gel, and DNA in a size range of 100-500 kb is excised from the gel. This DNA is ligated to the BAC vector or subjected to a second size selection on a pulsed field gel under different running conditions. Studies have previously reported that two rounds of size selection can eliminate small DNA fragments co-migrating with the selected range in the first pulse-field fractionation. Such a strategy results in an increase in insert sizes and a more uniform insert size distribution. A practical approach to performing size selections is to first test for the number of clones/microliter of ligation and insert size from the first size selected material. If the numbers are good (500 to 2000 white colony/microliter of ligation) and the size range is also good (50 to 300 kb) then a second size selection is practical. When performing a second size selection one expects a 80 to 95% decrease in the number of recombinant clones per transformation.

Twenty to two hundred nanograms of the size-selected DNA is ligated to dephosphorylated BAC vector (molar ratio of 10 to 1 in BAC vector excess). Most BAC libraries use a molar ratio of 5 to 15 : 1 (size selected DNA:BAC vector).

Transformation is carried out by electroporation and the transformation efficiency for BACs is about 40 to 1,500 transformants from one microliter of ligation product or 20 to 1000 transformants/ng DNA.

Several tests can be carried out to determine the quality of a BAC library. Three basic tests to evaluate the quality include: the genome coverage of a BAC library-average insert size, average number of clones hybridizing with single copy probes and chloroplast DNA content.

The determination of the average insert size of the library is assessed in two ways. First, during library construction every ligation is tested to determine the average insert size by assaying 20-50 BAC clones per ligation. DNA is isolated from recombinant clones using a standard mini preparation protocol, digested with *Not* I to free the insert from the BAC vector and then sized using pulsed field gel electrophoresis (Maule, *Molecular Biotechnology* 9:107-126 (1998), the entirety of which is herein incorporated by reference).

To determine the genome coverage of the library, it is screened with single copy RFLP markers distributed randomly across the genome by hybridization. Microtiter plates containing BAC clones are spotted onto Hybond membranes. Bacteria from 48 or 72 plates are spotted twice onto one membrane resulting in 18,000 to 27,648 unique clones on each membrane in either a 4X4 or 5X5 orientation. Since each clone is present twice, false positives are easily eliminated and true positives are easily recognized and identified.

Finally, the chloroplast DNA content in the BAC library is estimated by hybridizing three chloroplast genes spaced evenly across the chloroplast genome to the library on high density hybridization filters.

There are strategies for isolating rare sequences within the genome. For example, higher plant genomes can range in size from 100 Mb/1C (*Arabidopsis*) to 15,966 Mb/C (*Triticum aestivum*), (Arumuganathan and Earle, *Plant Mol Bio Rep.*9:208-219 (1991), the entirety of which is herein incorporated by reference). The number of clones required to achieve a given probability that any DNA sequence will be represented in a genomic library is N = (ln(1-P))/(ln(1-L/G)) where N is the number of clones required, P is the probability desired to get the target sequence, L is the length of the average clone insert in base pairs and G is the haploid genome length in base pairs (Clarke *et al.*, *Cell* 9:91-100 (1976) the entirety of which is herein incorporated by reference).

The rice BAC library of the present invention is constructed in the pBeloBAC11 or similar vector. Inserts are generated by partial *Eco* RI or other enzymatic digestion of DNA. The 25X library provides 4-5X coverage sequence from BAC clones across genome.

Example 2

Two basic methods can be used for DNA sequencing, the chain termination method of Sanger *et al., Proc. Natl. Acad. Sci. USA 74:*5463-5467 (1977), the entirety of which is herein incorporated by reference and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci. USA 74:*560-564 (1977), the entirety of which is herein incorporated by

reference. Automation and advances in technology such as the replacement of radioisotopes with fluorescence-based sequencing have reduced the effort required to sequence DNA (Craxton, *Methods, 2:*20-26 (1991); Ju *et al., Proc. Natl. Acad. Sci. USA 92:*4347-4351 (1995); Tabor and Richardson, *Proc. Natl. Acad. Sci. USA 92:*6339-6343 (1995), all of which are herein incorporated by reference in their entirety). Automated sequencers are available from, for example, Pharmacia Biotech, Inc., Piscataway, New Jersey (Pharmacia ALF), LI-COR, Inc., Lincoln, Nebraska (LI-COR 4,000) and Millipore, Bedford, Massachusetts (Millipore BaseStation).

In addition, advances in capillary gel electrophoresis have also reduced the effort required to sequence DNA and such advances provide a rapid high resolution approach for sequencing DNA samples (Swerdlow and Gesteland, *Nucleic Acids Res. 18:*1415-1419 (1990); Smith, *Nature 349:*812-813 (1991); Luckey *et al., Methods Enzymol. 218:*154-172 (1993); Lu *et al., J. Chromatog. A. 680:*497-501 (1994); Carson *et al., Anal. Chem. 65:*3219-3226 (1993); Huang *et al., Anal. Chem. 64:*2149-2154 (1992); Kheterpal *et al., Electrophoresis 17:*1852-1859 (1996); Quesada and Zhang, *Electrophoresis 17:*1841-1851 (1996); Baba, *Yakugaku Zasshi 117:*265-281 (1997), all of which are herein incorporated by reference in their entirety).

A number of sequencing techniques are known in the art, including fluorescence-based sequencing methodologies. These methods have the detection, automation and instrumentation capability necessary for the analysis of large volumes of sequence data. Currently, the 377 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) allows the most rapid electrophoresis and data collection. With these types of automated systems, fluorescent dye-labeled sequence reaction products are detected and data entered directly into the computer, producing a chromatogram that is subsequently viewed, stored, and analyzed using the corresponding software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al., Genome Analysis: Analyzing DNA*,1, Cold Spring Harbor, New York (1999), the entirety of which is herein incorporated by reference).

PHRED is used to call the bases from the sequence trace files (http://www.mbt.washington.edu). Phred uses Fourier methods to examine the four base traces in the region surrounding each point in the data set in order to predict a series of evenly spaced predicted locations. That is, it determines where the peaks would be centered if there were no compressions, dropouts, or other factors shifting the peaks from their "true" locations. Next, PHRED examines each trace to find the centers of the actual, or observed peaks and the areas of these peaks relative to their neighbors. The peaks are detected independently along each of the four traces so many peaks overlap. A dynamic programming algorithm is used to match the observed peaks detected in the second step with the predicted peak locations found in the first step.

After the base calling is completed, contaminating sequences (E. coli, BAC vector sequences > 50 bases and sub-cloning vector are removed and constraints are made for the assembler. Contigs are assembled using CAP3 (Huang, *et al., Genomics 46*: 37-45 (1997) the entirety of which is herein incorporated by reference).

Example 3

This example illustrates the identification of combigenes within the rice genomic contig library as assembled in Example 2. The genes and partial genes embedded in such contigs are identified through a series of informatic analyses. The tools to define genes fall into two categories: homology-based and predictive-based methods. Homology-based searches (*e.g.*, GAP2, BLASTX supplemented by NAP and TBLASTX) detect conserved sequences during comparisons of DNA sequences or hypothetically translated protein sequences to public and/or proprietary DNA and protein databases. Existence of an *Oryza sativa* gene is inferred if significant sequence similarity extends over the majority of the target gene. Since homology-based methods may overlook genes unique to *Oryza sativa*, for which homologous nucleic acid molecules have not yet been identified in databases, gene prediction programs are also used. Predictive methods employed in the definition of the *Oryza sativa* genes included the use of the GenScan gene predictive software program which is available from Stanford University (*e.g.* at

the web site http://gnomic/stanford.edu/GENSCANW.html). GenScan, in general terms, infers the presence and extent of a gene through a search for "gene-like" grammar.

The homology-based methods used to define the *Oryza sativa* gene set included GAP2, BLASTX supplemented by NAP and TBLASTX. For a description of BLASTX and TBLASTX *see* Coulson, *Trends in Biotechnology* 12:76-80 (1994) and Birren *et al., Genome Analysis,* 1:543-559 (1997). GAP2 and NAP are part of the Analysis and Annotation Tool (AAT) for Finding Genes in Genomic Sequences which was developed by Xiaoqiu Huang at Michigan Tech University and is available at the web site http://genome.cs.mtu.edu/ . The AAT package includes two sets of programs, one set DPS/NAP (referred to as "NAP") for comparing the query sequence with a protein database, and the other set DDS/GAP2 (referred to as "GAP2") for comparing the query sequence with a cDNA database. Each set contains a fast database search program and a rigorous alignment program. The database search program quickly identifies regions of the query sequence that are similar to a database sequence. Then the alignment program constructs an optimal alignment for each region and the database sequence. The alignment program also reports the coordinates of exons in the query sequence. *See* Huang, *et al., Genomics 46*: 37-45 (1997). The GAP2 program computes an optimal global alignment of a genomic sequence and a cDNA sequence without penalizing terminal gaps. A long gap in the cDNA sequence is given a constant penalty. The DNA-DNA alignment by GAP2 adjusts penalties to accommodate introns. The GAP2 program makes use of splice site consensuses in alignment computation. GAP2 delivers the alignment in linear space, so long sequences can be aligned. *See* Huang, *Computer Applications in the Biosciences 10* 227-235 (1994). The GAP2 program aligned the *Oryza sativa* contigs with a library of *Oryza sativa* 25,384 cDNAs.

The NAP program computes a global alignment of a DNA sequence and a protein sequence without penalizing terminal gaps. NAP handles frameshifts and long introns in the DNA sequence. The program delivers the alignment in linear space, so long sequences can be aligned. It makes use of splice site consensuses in alignment computation. Both strands of the DNA sequence are compared with the protein sequence and one of the two alignments with the

larger score is reported. *See* Huang, and Zhang, "*Computer Applications in the Biosciences* 12(6), 497-506 (1996).

NAP takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database (*e.g.* the non-redundant protein (*i.e.*, nr-aa) database maintained by the National Center for Biotechnology Information as part of GenBank and available at the web site: http://www.ncbi.nlm.nih.gov).

The first homology-based search for genes in the *Oryza sativa* contigs is effected using the GAP2 program and the *Oryza sativa* library of clustered *Oryza sativa* cDNA. The *Oryza sativa* clusters are mapped onto an assembly of *Oryza sativa* contigs represented by SEQ ID NO. 1 through SEQ ID NO. 69652 using the GAP2 program. GAP2 standards for selecting a DNA-DNA match were $\geq$ 82% sequence identity with the following parameters:

gap extension penalty = 1

match score = 2

gap open penalty = 6

gap length for constant penalty = 20

mismatch penalty = -2

minimum exon length = 21

When a particular *Oryza sativa* cDNA aligns to more than one *Oryza sativa* contig, the alignment with the highest identity is selected and alignments with lower levels of identity are filtered out as surreptitious alignments. *Oryza sativa* cDNA sequences aligning to *Oryza sativa* contigs with exceptionally low complexity were filtered out when the basis for alignment included a high number of cDNAs with poly A tails aligning to genomic regions with extended repeats of A or T.

The second homology-based method used for gene discovery is BLASTX hits extended with the NAP software package. BLASTX is run with the *Oryza sativa* genomic contigs represented by SEQ ID NO. 1 through SEQ ID NO. 69652 as queries against the GenBank non-

redundant protein data library identified as "nr-aa". NAP is used to better align the amino acid sequences as compared to the genomic sequence. NAP extends the match in regions where BLASTX has identified high-scoring-pairs (HSPs), predicts introns, and then links the exons into a single ORF prediction. Experience suggests that NAP tends to mis-predict the first exon. The NAP parameters are:

gap extension penalty = 1

gap open penalty = 15

gap length for constant penalty = 25

min exon length (in aa) = 7

homology > 30%

The NAP alignment score and GenBank reference number for best match are reported for each contig for which there is a NAP hit.

In the final homology-based method, TBLASTX, is used with cDNA information from three plant sequencing projects: 12,217 sequences from *Triticum aestivum,* 101,574 sequences from *Glycine max,* 113,242 sequences from *Zea mays* and 56,754 sequences from *Arabidopsis thaliana.* Conservative standards for inclusion of TBLASTX hits into the gene set are utilized. These standards are a minimal E value of 1E-20, and for terminal exons, a minimal match of 200 bp within the 1000 most 5' and 3' ends of an *Oryza sativa* contig.

The GenScan program is "trained" with *Arabidopsis thaliana* characteristics. Though better than the "off-the-shelf" version, the GenScan trained to identify *Oryza sativa* genes proved more proficient at predicting exons than predicting full-length genes. Predicting full-length genes is compromised by point mutations in the unfinished contigs, as well as by the short length of the contigs relative to the typical length of a gene. Due to the errors found in the full-length gene predictions by GenScan, inclusion of GenScan-predicted genes is limited to those genes and exons whose probabilities are above a conservative probability threshold. The GenScan parameters are:

weighted mean GenScan P value > 0.4

mean GenScan T value > 0

mean GenScan Coding score > 50

length > 200 bp

minimum TBLASTX E value < 1E-20

The weighted mean GenScan P value is a probability for correctly predicting ORFs or partial ORFs and is defined as the $(1/\Sigma\, l_i)(\Sigma\, l_i\, P_i)$, where "l" is the length of a exon and "P" is the probability or correctness for the exon.

The gene predictions from these programs are stored in a database and then combigenes are derived from these predictions. A combigene is a cluster of putative genes which satisfy the following criteria: 1) all genes making up a single combigene are located on the same strand of a contig 2) individual genes have at least 100 bp overlap with each other 3) if an individal gene is predicted by NAP it has at least 30% sequence identity to its hit 4) if an individual gene is predicted by GAP2 it has at least 85% sequence identity to its hit 5) if an individual gene is predicted by Genscan the weighted average of the probabilities calculated for all of its exons is not less than 0.4. The gene boundaries of a Genscan-predicted gene are determined while taking into account only exons. Since TBLASTX-predicted genes are standless the combigene which is made up of such genes can be assigned a strand only if there is a gene in the cluster that was predicted by a strand-defining gene-predicting program.

Seq. No.	1	Seq. ID	OJ990503_31.9819.C2
Gene No.	1	Strand	-
Start	397	End	1864
Name	OJ990503_31.9819.C2.o1.gs	Method	GENSCAN
Start	397	End	1238
GI	none	Score	.93
Exons	397..591, 879..1238		

Seq. No.	1	Seq. ID	OJ990503_31.9819.C2
Gene No.	1	Strand	-
Start	397	End	1864
Name	OJ990503_31.9819.C2.o1.tm	Method	TBLASTX:Maize
Start	1017	End	1864
GI	none	Score	150
Exons	1017..1250, 1018..1245, 1020..1247, 1243..1296, 1249..1296, 1377..1418, 1382..1420, 1532..1600, 1534..1596, 1706..1735, 1745..1864		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	2	Strand	+
Start	174	End	602
Name	OJ990503_31.9819.C3.o1.gs	Method	GENSCAN
Start	174	End	602
GI	none	Score	.71
Exons	174..282, 433..602		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	3	Strand	+
Start	3700	End	6180
Name	OJ990503_31.9819.C3.o3.gs	Method	GENSCAN
Start	3700	End	6180
GI	none	Score	.6
Exons	3700..3774, 5421..5727, 6146..6180		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	4	Strand	-
Start	723	End	3656
Name	OJ990503_31.9819.C3.o1.tm	Method	TBLASTX:Maize
Start	644	End	2562
GI	none	Score	71
Exons	644..814, 750..842, 763..849, 867..1037, 1057..1089, 1144..1263, 1165..1263, 1378..1434, 1480..1554, 1700..1816, 1713..1820, 2404..2562		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	4	Strand	-
Start	723	End	3656
Name	OJ990503_31.9819.C3.o2.gs	Method	GENSCAN
Start	723	End	2799
GI	none	Score	.88
Exons	723..1047, 1139..1294, 1376..1551, 1655..1832, 2393..2799		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	4	Strand	-
Start	723	End	3656
Name	OJ990503_31.9819.C3.o1.np	Method	AAT/NAP
Start	729	End	3656

GI	6598934	Score	514
Exons	729..1090, 1139..1300, 1376..1598, 1703..1832, 2396..2562, 2653..2694, 3537..3656		
GI Descrip.	(AC018721) unknown protein [Arabidopsis thaliana]		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	4	Strand	-
Start	723	End	3656
Name	OJ990503_31.9819.C3.o1.tc	Method	TBLASTX:Cress
Start	750	End	1281
GI	none	Score	82
Exons	750..845, 867..1064, 1141..1281		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	4	Strand	-
Start	723	End	3656
Name	OJ990503_31.9819.C3.o1.ts	Method	TBLASTX:Soybean
Start	750	End	1242
GI	none	Score	115
Exons	750..980, 754..885, 1138..1242		

Seq. No.	2	Seq. ID	OJ990503_31.9819.C3
Gene No.	4	Strand	-
Start	723	End	3656
Name	OJ990503_31.9819.C3.o2.ts	Method	TBLASTX:Soybean
Start	1715	End	2565
GI	none	Score	181
Exons	1715..1783, 2407..2565		

Seq. No.	3	Seq. ID	OJ990503_31.9819.C4
Gene No.	5	Strand	+
Start	801	End	4477
Name	OJ990503_31.9819.C4.o1.gs	Method	GENSCAN
Start	801	End	2147
GI	none	Score	.84
Exons	801..859, 971..1208, 1627..1696, 1745..1881, 2058..2147		

Seq. No.	3	Seq. ID	OJ990503_31.9819.C4
Gene No.	5	Strand	+
Start	801	End	4477
Name	OJ990503_31.9819.C4.o1.np	Method	AAT/NAP
Start	806	End	4477
GI	4580462	Score	116
Exons	806..859, 971..1132, 1313..1430, 1521..1577, 4437..4477		
GI Descrip.	(AC006081) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	3	Seq. ID	OJ990503_31.9819.C4
Gene No.	6	Strand	-
Start	2754	End	5683
Name	OJ990503_31.9819.C4.o2.tm	Method	TBLASTX:Maize
Start	2609	End	3650
GI	none	Score	59
Exons	2609..2677, 2626..2673, 2757..2867, 2767..2850, 2945..3043, 3146..3298, 3199..3291, 3267..3335, 3544..3645, 3546..3650		

Seq. No.	3	Seq. ID	OJ990503_31.9819.C4
Gene No.	6	Strand	-

Start	2754	End	5683
Name	OJ990503_31.9819.C4.o2.np	Method	AAT/NAP
Start	2754	End	5564
GI	5903036	Score	529
Exons	2754..2848, 3154..3288, 3543..3647, 3789..3858, 4064..4100, 5422..5564		
GI Descrip.	(AC008016) F6D8.5 [Arabidopsis thaliana]		

Seq. No.	3	Seq. ID	OJ990503_31.9819.C4
Gene No.	6	Strand	-
Start	2754	End	5683
Name	OJ990503_31.9819.C4.o1.tm	Method	TBLASTX:Maize
Start	3799	End	5683
GI	none	Score	83
Exons	3799..3858, 3800..3862, 4059..4103, 4061..4102, 5418..5546, 5422..5538, 5426..5566, 5645..5683		

Seq. No.	4	Seq. ID	OJ990503_31.9819.C5
Gene No.	7	Strand	-
Start	3996	End	6251
Name	OJ990503_31.9819.C5.o2.gs	Method	GENSCAN
Start	3996	End	6251
GI	none	Score	.77
Exons	3996..4145, 4616..4699, 4787..4827, 4919..5013, 5088..5183, 5254..5342, 5421..5680, 6182..6251		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	8	Strand	+
Start	1271	End	2159
Name	OJ990503_31.9819.C6.o1.gs	Method	GENSCAN
Start	1271	End	2159
GI	none	Score	.7
Exons	1271..1336, 2133..2159		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	9	Strand	+
Start	2940	End	6958
Name	OJ990503_31.9819.C6.o1.np	Method	AAT/NAP
Start	2931	End	6958
GI	2760839	Score	1450
Exons	2931..4275, 6290..6958		
GI Descrip.	(AC003105) putative receptor-like protein kinase [Arabidopsis thaliana]		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	9	Strand	+
Start	2940	End	6958
Name	OJ990503_31.9819.C6.o2.gs	Method	GENSCAN
Start	2940	End	5279
GI	none	Score	.6
Exons	2940..4275, 4433..4571, 5168..5279		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	9	Strand	+
Start	2940	End	6958
Name	OJ990503_31.9819.C6.o3.gs	Method	GENSCAN
Start	6316	End	6927

GI	none	Score	.97
Exons	6316..6927		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	10	Strand	+
Start	7841	End	8245
Name	OJ990503_31.9819.C6.o4.gs	Method	GENSCAN
Start	7841	End	8245
GI	none	Score	1
Exons	7841..8245		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	11	Strand	-
Start	8971	End	10455
Name	OJ990503_31.9819.C6.o1.gp	Method	AAT/GAP
Start	8853	End	9318
GI	none	Score	470
Exons	8853..9102, 9258..9318		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	11	Strand	-
Start	8971	End	10455
Name	OJ990503_31.9819.C6.o2.np	Method	AAT/NAP
Start	8918	End	9840
GI	431154	Score	481
Exons	8918..9102, 9258..9377, 9496..9840		
GI Descrip.	(D21813) ORF [Lilium longiflorum]		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	11	Strand	-
Start	8971	End	10455
Name	OJ990503_31.9819.C6.o5.gs	Method	GENSCAN
Start	8971	End	10131
GI	none	Score	1
Exons	8971..9102, 9258..9377, 9496..9911, 10086..10131		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	11	Strand	-
Start	8971	End	10455
Name	OJ990503_31.9819.C6.o2.gp	Method	AAT/GAP
Start	9634	End	10455
GI	29536_1.R1084	Score	1256
Exons	9634..9911, 10086..10455		
GI Descrip.	'3513744 3.0e-22 (AF080118) contains similarity to Medicago truncatula MtN3 (GB:Y08726) [Arabidopsis thaliana]'		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o3.tm	Method	TBLASTX:Maize
Start	3012	End	4112
GI	none	Score	273
Exons	3012..3329, 3270..3398, 3351..3653, 3978..4112, 3978..4103		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534

Name	OJ990503_31.9819.C6.o2.tc	Method	TBLASTX:Cress
Start	3132	End	6783
GI	none	Score	235
Exons	3132..3461, 3189..3398, 3498..3569, 3585..3602, 3983..4276, 3996..4277, 6274..6507, 6507..6650, 6508..6645, 6628..6783		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o3.ts	Method	TBLASTX:Soybean
Start	3132	End	3578
GI	none	Score	315
Exons	3132..3578, 3374..3577		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o1.tw	Method	TBLASTX:Wheat
Start	3996	End	4202
GI	none	Score	201
Exons	3996..4202, 3996..4073, 4037..4195		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o1.ts	Method	TBLASTX:Soybean
Start	4008	End	6783
GI	none	Score	334
Exons	4008..4277, 4008..4076, 4037..4276, 6274..6645, 6513..6644, 6633..6683, 6637..6717, 6742..6783, 6750..6782		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o1.tm	Method	TBLASTX:Maize
Start	4115	End	6777
GI	none	Score	217
Exons	4115..4276, 4116..4277, 6274..6513, 6288..6545, 6507..6776, 6508..6777		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o2.tm	Method	TBLASTX:Maize
Start	9255	End	9918
GI	none	Score	125
Exons	9255..9377, 9267..9377, 9286..9378, 9487..9582, 9497..9817, 9646..9918, 9781..9840		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o1.tc	Method	TBLASTX:Cress
Start	9273	End	9918
GI	none	Score	53
Exons	9273..9374, 9297..9374, 9482..9583, 9496..9582, 9649..9918, 9668..9817, 9769..9891		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o2.ts	Method	TBLASTX:Soybean
Start	9646	End	9939
GI	none	Score	95
Exons	9646..9939, 9689..9811, 9781..9858, 9878..9919		

Seq. No.	5	Seq. ID	OJ990503_31.9819.C6
Gene No.	12	Strand	-
Start	10835	End	11534
Name	OJ990503_31.9819.C6.o6.gs	Method	GENSCAN
Start	10835	End	11534
GI	none	Score	.64
Exons	10835..10981, 11376..11534		

Seq. No.	6	Seq. ID	OJ990503_31.9819.C7
Gene No.	13	Strand	+
Start	389	End	756
Name	OJ990503_31.9819.C7.o1.gs	Method	GENSCAN
Start	389	End	756
GI	none	Score	.8
Exons	389..479, 494..756		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	14	Strand	+
Start	1108	End	5012
Name	OJ990503_31.9819.C8.o1.np	Method	AAT/NAP
Start	1108	End	5012
GI	6539553	Score	6645
Exons	1108..5012		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	15	Strand	+
Start	7773	End	9928
Name	OJ990503_31.9819.C8.o2.np	Method	AAT/NAP
Start	7773	End	9928
GI	4469013	Score	607
Exons	7773..7951, 9171..9622, 9686..9928		
GI Descrip.	(AL035602) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	16	Strand	+
Start	18361	End	18564
Name	OJ990503_31.9819.C8.o3.gs	Method	GENSCAN
Start	18361	End	18564
GI	none	Score	.56
Exons	18361..18564		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	17	Strand	+
Start	19072	End	23048

Name	OJ990503_31.9819.C8.o4.np	Method	AAT/NAP
Start	19072	End	23036
GI	6735379	Score	1196
Exons	19072..19159, 19786..20280, 20329..20610, 21227..21424, 21531..21719, 21801..22134, 22214..22418, 22675..22766, 22887..23036		
GI Descrip.	(AL137082) putative protein [Arabidopsis thaliana]		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	17	Strand	+
Start	19072	End	23048
Name	OJ990503_31.9819.C8.o4.gs	Method	GENSCAN
Start	19718	End	23048
GI	none	Score	.57
Exons	19718..20610, 20642..20749, 21227..21428, 21535..21719, 21771..22134, 22214..22418, 22675..22781, 22887..23048		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	18	Strand	-
Start	13656	End	13739
Name	OJ990503_31.9819.C8.o3.np	Method	AAT/NAP
Start	13656	End	13739
GI	5852084	Score	70
Exons	13656..13739		
GI Descrip.	(AL117264) zwh0007.1 [Oryza sativa]		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o4.tw	Method	TBLASTX:Wheat
Start	1102	End	1488
GI	none	Score	347
Exons	1102..1488, 1113..1487		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o6.tm	Method	TBLASTX:Maize
Start	1237	End	1533
GI	none	Score	343
Exons	1237..1533, 1245..1532		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o4.tm	Method	TBLASTX:Maize
Start	2050	End	2372
GI	none	Score	264
Exons	2050..2304, 2057..2371, 2077..2370, 2205..2372		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o7.ts	Method	TBLASTX:Soybean
Start	2399	End	2785
GI	none	Score	88
Exons	2399..2554, 2537..2785		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o5.tw	Method	TBLASTX:Wheat
Start	2504	End	2842
GI	none	Score	274
Exons	2504..2842, 2575..2715, 2636..2821, 2739..2822		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o9.tm	Method	TBLASTX:Maize
Start	2573	End	3007
GI	none	Score	297
Exons	2573..3007, 2782..2982		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o3.ts	Method	TBLASTX:Soybean
Start	2795	End	3193
GI	none	Score	193
Exons	2795..3019, 2803..2973, 3020..3193, 3028..3066, 3109..3168		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o1.tw	Method	TBLASTX:Wheat
Start	2843	End	3598
GI	none	Score	625
Exons	2843..3307, 2851..3330, 3351..3581, 3359..3598, 3381..3578, 3439..3597		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o4.ts	Method	TBLASTX:Soybean
Start	3518	End	3980
GI	5509260	Score	69
Exons	3518..3625, 3669..3980, 3734..3829, 3902..3961		
GI Descrip.	-		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o2.tc	Method	TBLASTX:Cress
Start	3663	End	3869
GI	none	Score	196
Exons	3663..3869		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o7.tm	Method	TBLASTX:Maize
Start	3665	End	4115
GI	none	Score	330

Exons	3665..3832, 3669..4115, 3786..3968, 3902..4012		
Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o3.tw	Method	TBLASTX:Wheat
Start	3666	End	4196
GI	none	Score	292
Exons	3666..3995, 3798..3971, 3990..4196, 4064..4186		
Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o2.ts	Method	TBLASTX:Soybean
Start	4049	End	4394
GI	none	Score	314
Exons	4049..4249, 4050..4394		
Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o8.tm	Method	TBLASTX:Maize
Start	4205	End	4544
GI	none	Score	310
Exons	4205..4543, 4206..4544		
Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o2.tw	Method	TBLASTX:Wheat
Start	4400	End	4876
GI	none	Score	101
Exons	4400..4471, 4401..4475, 4490..4876, 4491..4838, 4492..4875		
Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o6.ts	Method	TBLASTX:Soybean
Start	4407	End	4748
GI	none	Score	92
Exons	4407..4526, 4433..4513, 4539..4748, 4544..4669, 4551..4727		
Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o10.tm	Method	TBLASTX:Maize
Start	7745	End	8116
GI	none	Score	185
Exons	7745..7942, 7746..7940, 8036..8116, 8036..8116		
Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	9180	End	9937
GI	none	Score	56
Exons	9180..9230, 9181..9237, 9182..9238, 9234..9452, 9236..9775,		

9236..9400, 9243..9404, 9250..9414, 9455..9760, 9487..9768, 9764..9937, 9769..9936

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o5.ts	Method	TBLASTX:Soybean
Start	9536	End	9937
GI	none	Score	109
Exons	9536..9622, 9539..9622, 9638..9709, 9748..9930, 9749..9937		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o5.tm	Method	TBLASTX:Maize
Start	21237	End	21852
GI	none	Score	247
Exons	21237..21437, 21239..21430, 21535..21630, 21536..21628, 21571..21645, 21633..21725, 21634..21720, 21651..21722, 21780..21851, 21799..21852		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o1.ts	Method	TBLASTX:Soybean
Start	21312	End	22297
GI	none	Score	115
Exons	21312..21437, 21798..22103, 21799..22137, 21928..22092, 22214..22297		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o1.tc	Method	TBLASTX:Cress
Start	21765	End	22319
GI	none	Score	350
Exons	21765..22124, 21772..22137, 21925..22089, 22214..22318, 22224..22319		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o2.tm	Method	TBLASTX:Maize
Start	21853	End	23033
GI	none	Score	397
Exons	21853..22137, 21857..22132, 21858..22136, 21928..22101, 22212..22433, 22214..22420, 22673..22783, 22674..22784, 22674..22784, 22678..22785, 22886..23032, 22887..23033		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o5.gs	Method	GENSCAN
Start	24837	End	28524
GI	none	Score	.62
Exons	24837..25260, 26277..26319, 26413..26610, 26700..26805, 27345..27454, 27996..28125, 28396..28524		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o1.gp	Method	AAT/GAP
Start	25873	End	26330
GI	454496	Score	691
Exons	25873..26178, 26277..26330		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o3.tm	Method	TBLASTX:Maize
Start	26256	End	28429
GI	none	Score	83
Exons	26256..26321, 26267..26326, 26410..26592, 26414..26593, 26415..26594, 26701..26805, 26702..26806, 27103..27174, 27104..27172, 27105..27179, 27339..27455, 27342..27455, 27346..27456, 28206..28292, 28218..28271, 28385..28429, 28396..28428		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o5.np	Method	AAT/NAP
Start	26356	End	27452
GI	2827667	Score	420
Exons	26356..26610, 26700..26805, 27103..27171, 27345..27452		
GI Descrip.	(AL021637) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o6.np	Method	AAT/NAP
Start	27976	End	28645
GI	2827666	Score	327
Exons	27976..28165, 28219..28310, 28396..28524, 28577..28645		
GI Descrip.	(AL021637) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o11.tm	Method	TBLASTX:Maize
Start	27989	End	28146
GI	none	Score	193
Exons	27989..28144, 27989..28138, 27997..28146, 27997..28143		

Seq. No.	7	Seq. ID	OJ990503_31.9819.C8
Gene No.	19	Strand	-
Start	24837	End	28645
Name	OJ990503_31.9819.C8.o2.gp	Method	AAT/GAP
Start	28015	End	28645
GI	14778_1.R1084	Score	638
Exons	28015..28146, 28221..28310, 28396..28524, 28626..28645		
GI Descrip.	'2827666/emb|CAA16620.1| 9.0e-37 (AL021637) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	20	Strand	+
Start	3351	End	5026
Name	OJ990503_31.9819.C9.o2.gs	Method	GENSCAN
Start	3351	End	5026
GI	none	Score	.77
Exons	3351..3441, 3848..3909, 4145..4213, 4355..5026		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	20	Strand	+
Start	3351	End	5026
Name	OJ990503_31.9819.C9.o2.gp	Method	AAT/GAP
Start	4165	End	4700
GI	none	Score	722
Exons	4165..4213, 4325..4700		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	21	Strand	+
Start	5406	End	7097
Name	OJ990503_31.9819.C9.o3.np	Method	AAT/NAP
Start	5406	End	7097
GI	3281853	Score	117
Exons	5406..5440, 6613..6741, 6815..6923, 7070..7097		
GI Descrip.	(AL031004) putative protein [Arabidopsis thaliana]		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	22	Strand	-
Start	294	End	4848
Name	OJ990503_31.9819.C9.o1.np	Method	AAT/NAP
Start	294	End	2586
GI	2827666	Score	318
Exons	294..423, 976..1132, 2394..2586		
GI Descrip.	(AL021637) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	22	Strand	-
Start	294	End	4848
Name	OJ990503_31.9819.C9.o1.gp	Method	AAT/GAP
Start	298	End	1468
GI	14778_1.R1084	Score	953
Exons	298..423, 976..1113, 1207..1468		
GI Descrip.	'2827666/emb|CAA16620.1| 9.0e-37 (AL021637) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	22	Strand	-
Start	294	End	4848
Name	OJ990503_31.9819.C9.o1.gs	Method	GENSCAN
Start	298	End	1440
GI	none	Score	.66
Exons	298..423, 976..1440		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	22	Strand	-
Start	294	End	4848
Name	OJ990503_31.9819.C9.o1.tc	Method	TBLASTX:Cress
Start	304	End	1134

GI	none	Score	71
Exons	304..426, 305..379, 316..423, 955..1134, 971..1111		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	22	Strand	-
Start	294	End	4848
Name	OJ990503_31.9819.C9.o2.np	Method	AAT/NAP
Start	1297	End	4848
GI	228937	Score	227
Exons	1297..1485, 4314..4848		
GI Descrip.	Hyp-rich glycoprotein [Zea mays]		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	23	Strand	
Start	6609	End	6922
Name	OJ990503_31.9819.C9.o1.tm	Method	TBLASTX:Maize
Start	6609	End	6922
GI	none	Score	202
Exons	6609..6743, 6611..6742, 6794..6919, 6799..6915, 6815..6922		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	23	Strand	
Start	6609	End	6922
Name	OJ990503_31.9819.C9.o1.tw	Method	TBLASTX:Wheat
Start	6610	End	6919
GI	none	Score	208
Exons	6610..6741, 6611..6742, 6611..6742, 6619..6753, 6794..6919, 6816..6914		

Seq. No.	8	Seq. ID	OJ990503_31.9819.C9
Gene No.	23	Strand	
Start	6609	End	6922
Name	OJ990503_31.9819.C9.o2.tc	Method	TBLASTX:Cress
Start	6611	End	6841
GI	none	Score	166
Exons	6611..6742, 6612..6686, 6613..6741, 6817..6837, 6818..6841		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	24	Strand	+
Start	1	End	2981
Name	OJ990503_31.9819.C10.o1.np	Method	AAT/NAP
Start	1	End	2027
GI	3281853	Score	437
Exons	1..37, 136..294, 415..501, 679..943, 1815..2027		
GI Descrip.	(AL031004) putative protein [Arabidopsis thaliana]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	24	Strand	+
Start	1	End	2981
Name	OJ990503_31.9819.C10.o1.gs	Method	GENSCAN
Start	136	End	2981
GI	none	Score	.69
Exons	136..294, 415..501, 757..770, 869..943, 1815..1950, 2917..2981		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	24	Strand	+
Start	1	End	2981

Name	OJ990503_31.9819.C10.o1.gp	Method	AAT/GAP
Start	1152	End	1664
GI	none	Score	997
Exons	1152..1664		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	25	Strand	+
Start	3881	End	5888
Name	OJ990503_31.9819.C10.o2.gs	Method	GENSCAN
Start	3881	End	5885
GI	none	Score	.68
Exons	3881..4231, 4268..4466, 4723..4897, 5100..5170, 5257..5885		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	25	Strand	+
Start	3881	End	5888
Name	OJ990503_31.9819.C10.o2.np	Method	AAT/NAP
Start	3908	End	5888
GI	4454051	Score	1371
Exons	3908..4231, 4346..4466, 4723..4897, 5100..5170, 5257..5888		
GI Descrip.	(AL035394) putative polygalacturonase [Arabidopsis thaliana]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	26	Strand	+
Start	6151	End	6470
Name	OJ990503_31.9819.C10.o3.gp	Method	AAT/GAP
Start	6151	End	6470
GI	none	Score	606
Exons	6151..6470		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	27	Strand	-
Start	1814	End	2077
Name	OJ990503_31.9819.C10.o2.gp	Method	AAT/GAP
Start	1814	End	2077
GI	none	Score	330
Exons	1814..2077		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o6.ts	Method	TBLASTX:Soybean
Start	114	End	1949
GI	none	Score	217
Exons	114..293, 137..292, 138..293, 139..303, 413..499, 414..503, 424..504, 659..766, 672..770, 675..770, 866..943, 1812..1940, 1814..1948, 1815..1949		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o3.tw	Method	TBLASTX:Wheat
Start	121	End	283
GI	none	Score	225
Exons	121..282, 137..283, 138..281, 139..282, 140..283		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10

Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o6.tm	Method	TBLASTX:Maize
Start	137	End	2044
GI	none	Score	234
Exons	137..292, 138..305, 412..504, 414..503, 659..772, 672..770, 680..772, 864..944, 866..943, 867..944, 898..945, 1812..1952, 1812..1943, 1814..1951, 1949..2044, 1950..2015		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o4.tw	Method	TBLASTX:Wheat
Start	899	End	1964
GI	none	Score	79
Exons	899..943, 901..948, 904..945, 1817..1963, 1818..1964		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o5.tm	Method	TBLASTX:Maize
Start	4003	End	4897
GI	none	Score	64
Exons	4003..4053, 4004..4054, 4133..4231, 4133..4231, 4138..4233, 4343..4474, 4345..4467, 4457..4495, 4709..4897, 4710..4895		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o7.tc	Method	TBLASTX:Cress
Start	4021	End	4859
GI	none	Score	42
Exons	4021..4053, 4022..4054, 4130..4231, 4135..4224, 4336..4467, 4342..4464, 4343..4474, 4703..4858, 4710..4859		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o2.ts	Method	TBLASTX:Soybean
Start	4346	End	5855
GI	none	Score	190
Exons	4346..4474, 4357..4467, 4379..4474, 4709..4897, 4710..4895, 5092..5169, 5094..5177, 5240..5773, 5241..5768, 5787..5855, 5789..5854		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o1.tm	Method	TBLASTX:Maize
Start	5251	End	5892
GI	none	Score	175
Exons	5251..5601, 5255..5881, 5256..5882, 5262..5891, 5647..5892		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o5.tc	Method	TBLASTX:Cress

Start	5255	End	5717
GI	none	Score	160
Exons	5255..5365, 5256..5405, 5408..5716, 5409..5717		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o5.tw	Method	TBLASTX:Wheat
Start	5504	End	5717
GI	none	Score	191
Exons	5504..5716, 5505..5717		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o2.tw	Method	TBLASTX:Wheat
Start	5724	End	5882
GI	none	Score	227
Exons	5724..5882, 5735..5881		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o10.np	Method	AAT/NAP
Start	6339	End	32393
GI	93144	Score	171
Exons	6339..6405, 8717..8886, 9274..9447, 12875..13481, 13724..13870, 17352..18012, 19570..19661, 20359..20575, 24239..24366, 32263..32393		
GI Descrip.	hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhuser or Becker) gi|334068 (M57505) ORF2 [Pseudorabies virus]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o3.gs	Method	GENSCAN
Start	6475	End	9507
GI	none	Score	.4
Exons	6475..6612, 7105..9507		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o2.tc	Method	TBLASTX:Cress
Start	6988	End	7527
GI	none	Score	108
Exons	6988..7149, 6997..7149, 7141..7248, 7165..7527, 7265..7483		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o11.tm	Method	TBLASTX:Maize
Start	6997	End	7251
GI	none	Score	96
Exons	6997..7170, 6998..7153, 7162..7251		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o7.ts	Method	TBLASTX:Soybean
Start	6997	End	7308
GI	none	Score	64
Exons	6997..7149, 6998..7147, 7168..7293, 7201..7308		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o3.np	Method	AAT/NAP
Start	7000	End	8502
GI	5262157	Score	1280
Exons	7000..8502		
GI Descrip.	(AL080237) putative protein (fragment) [Arabidopsis thaliana]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o2.tm	Method	TBLASTX:Maize
Start	7252	End	9180
GI	none	Score	125
Exons	7252..8133, 7541..7834, 7798..8148, 7832..8065, 8035..8334, 8182..8340, 8218..8655, 8287..8646, 8357..8515, 8401..9054, 8641..8730, 8653..9036, 8725..8973, 8764..9180, 9034..9153, 9055..9144		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o4.ts	Method	TBLASTX:Soybean
Start	7312	End	7839
GI	none	Score	60
Exons	7312..7836, 7316..7459, 7520..7837, 7636..7839		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o6.tc	Method	TBLASTX:Cress
Start	7531	End	9138
GI	none	Score	143
Exons	7531..7656, 7633..8220, 8053..8235, 8203..8334, 8203..8325, 8287..8736, 8566..8742, 8704..8835, 8716..9138		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o1.tw	Method	TBLASTX:Wheat
Start	7694	End	9090
GI	none	Score	165
Exons	7694..8152, 7699..8154, 8137..8325, 8290..8688, 8315..8641, 8575..8784, 8698..9090, 8764..8952, 8948..9076		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770

Name	OJ990503_31.9819.C10.o9.ts	Method	TBLASTX:Soybean
Start	7843	End	9072
GI	none	Score	102
Exons	7843..8151, 7853..8152, 8350..8727, 8369..8521, 8716..9072		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o4.np	Method	AAT/NAP
Start	11803	End	15618
GI	6069653	Score	920
Exons	11803..11831, 12617..12776, 13026..13222, 13397..14322, 15537..15618		
GI Descrip.	(AP000616) hypothetical protein [Oryza sativa]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o4.gs	Method	GENSCAN
Start	13105	End	13904
GI	none	Score	.54
Exons	13105..13345, 13368..13529, 13570..13904		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o5.np	Method	AAT/NAP
Start	15321	End	16372
GI	4680186	Score	280
Exons	15321..15712, 16215..16372		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o5.gs	Method	GENSCAN
Start	16997	End	17993
GI	none	Score	.87
Exons	16997..17542, 17619..17993		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o9.tm	Method	TBLASTX:Maize
Start	16997	End	17491
GI	none	Score	240
Exons	16997..17029, 17026..17166, 17027..17209, 17028..17207, 17162..17203, 17333..17491, 17366..17482, 17440..17490		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o4.gp	Method	AAT/GAP
Start	18977	End	19446
GI	LIB3431-023-P1-N1-F10	Score	713
Exons	18977..19313, 19398..19446		
GI Descrip.	'4033838/emb|CAA77213| 2.0e-21 (Y18550) sigma-like factor		

[Arabidopsis thaliana] >gi_4972299_dbj_BAA78109.1_ (AB021120) RNA polymerase sigma subunit SigE [Arabidopsis thaliana]'

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o6.gs	Method	GENSCAN
Start	19119	End	21080
GI	none	Score	.99
Exons	19119..19313, 19398..19661, 19747..19983, 20069..20215, 20317..20604, 20709..21080		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o6.np	Method	AAT/NAP
Start	19119	End	20843
GI	4033838	Score	976
Exons	19119..19313, 19398..19652, 19738..19983, 20069..20215, 20317..20607, 20712..20843		
GI Descrip.	(Y18550) sigma-like factor [Arabidopsis thaliana] gi|4972299|dbj|BAA78109.1| (AB021120) RNA polymerase sigma subunit SigE [Arabidopsis thaliana]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o1.tc	Method	TBLASTX:Cress
Start	19122	End	20834
GI	none	Score	189
Exons	19122..19313, 19123..19314, 19395..19658, 19528..19662, 19745..19984, 19750..19986, 20069..20218, 20070..20207, 20296..20445, 20318..20419, 20712..20834		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o1.ts	Method	TBLASTX:Soybean
Start	19122	End	20445
GI	none	Score	173
Exons	19122..19313, 19132..19314, 19395..19658, 19546..19662, 19745..19984, 19750..19986, 20069..20182, 20073..20180, 20293..20445, 20318..20422		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o3.tm	Method	TBLASTX:Maize
Start	19281	End	19849
GI	none	Score	165
Exons	19281..19331, 19443..19661, 19444..19662, 19742..19849, 19750..19848		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o5.gp	Method	AAT/GAP

Start	19474	End	20021
GI	LIB3431-023-P1-K1-F10	Score	808
Exons	19474..19661, 19747..20021		
GI Descrip.	'4033838/emb|CAA77213| 3.0e-51 (Y18550) sigma-like factor [Arabidopsis thaliana] >gi_4972299_dbj_BAA78109.1_ (AB021120) RNA polymerase sigma subunit SigE [Arabidopsis thaliana]'		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o10.tm	Method	TBLASTX:Maize
Start	22011	End	22194
GI	none	Score	179
Exons	22011..22193, 22012..22194		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o3.tc	Method	TBLASTX:Cress
Start	22014	End	22383
GI	none	Score	239
Exons	22014..22382, 22018..22383		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o7.gs	Method	GENSCAN
Start	22014	End	35770
GI	none	Score	.69
Exons	22014..22640, 22724..22854, 23049..23235, 24008..24105, 24199..24429, 24523..24698, 29096..29361, 29398..29458, 30305..32367, 32503..32544, 32623..32663, 33760..33840, 35659..35770		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o3.ts	Method	TBLASTX:Soybean
Start	22014	End	23146
GI	none	Score	368
Exons	22014..22400, 22018..22560, 22458..22550, 22718..22855, 22728..22862, 23050..23136, 23057..23146		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o7.np	Method	AAT/NAP
Start	22026	End	24610
GI	6579208	Score	765
Exons	22026..22640, 22724..22854, 23049..23235, 24008..24099, 24193..24342, 24523..24610		
GI Descrip.	(AC011438) T23G18.9 [Arabidopsis thaliana]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o8.tm	Method	TBLASTX:Maize

Start	22395	End	22643
GI	none	Score	207
Exons	22395..22589, 22396..22641, 22458..22643		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o5.ts	Method	TBLASTX:Soybean
Start	23978	End	24563
GI	none	Score	72
Exons	23978..24106, 24014..24100, 24197..24277, 24198..24281, 24330..24431, 24338..24430, 24521..24556, 24522..24563		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o4.tc	Method	TBLASTX:Cress
Start	24005	End	24559
GI	none	Score	60
Exons	24005..24106, 24005..24106, 24197..24277, 24198..24284, 24330..24431, 24338..24430, 24521..24559, 24522..24557		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o6.gp	Method	AAT/GAP
Start	26666	End	27256
GI	none	Score	1073
Exons	26666..27256		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o4.tm	Method	TBLASTX:Maize
Start	27136	End	30711
GI	none	Score	72
Exons	27136..27219, 27159..27221, 29062..29325, 29096..29320, 29131..29346, 29398..29457, 29399..29458, 29404..29460, 30299..30562, 30301..30711, 30302..30559, 30304..30711		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o8.np	Method	AAT/NAP
Start	27171	End	32134
GI	6850858	Score	469
Exons	27171..27222, 29096..29319, 29398..29458, 30305..30479, 30507..30590, 30743..30998, 31350..31731, 32037..32134		
GI Descrip.	(AL132959) putative protein [Arabidopsis thaliana]		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o8.tc	Method	TBLASTX:Cress
Start	29095	End	29458
GI	none	Score	89
Exons	29095..29325, 29195..29320, 29398..29457, 29399..29458		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o8.ts	Method	TBLASTX:Soybean
Start	29095	End	30360
GI	none	Score	130
Exons	29095..29325, 29096..29320, 29398..29454, 29399..29458, 30304..30360		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o7.gp	Method	AAT/GAP
Start	30542	End	30973
GI	none	Score	798
Exons	30542..30973		

Seq. No.	9	Seq. ID	OJ990503_31.9819.C10
Gene No.	28	Strand	-
Start	6475	End	35770
Name	OJ990503_31.9819.C10.o7.tm	Method	TBLASTX:Maize
Start	31507	End	31789
GI	none	Score	273
Exons	31507..31788, 31523..31789, 31529..31789		

Seq. No.	10	Seq. ID	OJ990503_31.9819.C11
Gene No.	29	Strand	+
Start	235	End	748
Name	OJ990503_31.9819.C11.o1.gs	Method	GENSCAN
Start	235	End	748
GI	none	Score	.68
Exons	235..378, 648..748		

Seq. No.	11	Seq. ID	OJ990323_21.9819.C1
Gene No.	30	Strand	-
Start	268	End	600
Name	OJ990323_21.9819.C1.o1.gs	Method	GENSCAN
Start	268	End	600
GI	none	Score	.88
Exons	268..600		

Seq. No.	12	Seq. ID	OJ990323_21.9819.C2
Gene No.	31	Strand	-
Start	59	End	994
Name	OJ990323_21.9819.C2.o1.gs	Method	GENSCAN
Start	59	End	994
GI	none	Score	.82
Exons	59..192, 296..438, 444..624, 865..994		

Seq. No.	13	Seq. ID	OJ990323_21.9819.C3
Gene No.	32	Strand	+
Start	1076	End	2713
Name	OJ990323_21.9819.C3.o1.gs	Method	GENSCAN
Start	1076	End	2713
GI	none	Score	.54
Exons	1076..2449, 2558..2713		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	33	Strand	+
Start	1477	End	1997
Name	OJ990323_21.9819.C4.o1.gs	Method	GENSCAN
Start	1477	End	1997
GI	none	Score	.67
Exons	1477..1997		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	34	Strand	+
Start	2980	End	9641
Name	OJ990323_21.9819.C4.o2.gp	Method	AAT/GAP
Start	2875	End	3259
GI	uC-osflcyp033a04b1	Score	612
Exons	2875..3259		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	34	Strand	+
Start	2980	End	9641
Name	OJ990323_21.9819.C4.o3.gs	Method	GENSCAN
Start	2980	End	9641
GI	none	Score	.67
Exons	2980..3045, 4144..4909, 4948..4976, 5202..9641		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	34	Strand	+
Start	2980	End	9641
Name	OJ990323_21.9819.C4.o4.gp	Method	AAT/GAP
Start	4419	End	4873
GI	95437_1.R1084	Score	782
Exons	4419..4873		
GI Descrip.	'4512226/dbj|AB014738.1|AB014738 1.0e-134 Oryza sativa gypsy-type retrotransposon RIRE3 DNA, internal region, complete sequence'		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	34	Strand	+
Start	2980	End	9641
Name	OJ990323_21.9819.C4.o1.np	Method	AAT/NAP
Start	5199	End	9638
GI	4680179	Score	5396
Exons	5199..6203, 6237..9638		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	35	Strand	-
Start	2257	End	2430
Name	OJ990323_21.9819.C4.o2.gs	Method	GENSCAN
Start	2257	End	2430
GI	none	Score	.47
Exons	2257..2430		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	36	Strand	

Start	5281	End	5623
Name	OJ990323_21.9819.C4.o9.tw	Method	TBLASTX:Wheat
Start	5281	End	5623
GI	none	Score	211
Exons	5281..5313, 5397..5417, 5424..5621, 5426..5623, 5533..5622		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	37	Strand	
Start	5657	End	6008
Name	OJ990323_21.9819.C4.o7.tw	Method	TBLASTX:Wheat
Start	5657	End	6008
GI	none	Score	293
Exons	5657..5851, 5658..6008		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	37	Strand	
Start	5657	End	6008
Name	OJ990323_21.9819.C4.o6.tm	Method	TBLASTX:Maize
Start	5658	End	5963
GI	none	Score	232
Exons	5658..5963, 5672..5788		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	38	Strand	
Start	6228	End	6686
Name	OJ990323_21.9819.C4.o7.tm	Method	TBLASTX:Maize
Start	6228	End	6583
GI	none	Score	189
Exons	6228..6581, 6338..6400, 6491..6583		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	38	Strand	
Start	6228	End	6686
Name	OJ990323_21.9819.C4.o8.tw	Method	TBLASTX:Wheat
Start	6264	End	6686
GI	none	Score	166
Exons	6264..6473, 6332..6472, 6518..6631, 6519..6686		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	39	Strand	
Start	6797	End	7670
Name	OJ990323_21.9819.C4.o4.tw	Method	TBLASTX:Wheat
Start	6797	End	7283
GI	none	Score	52
Exons	6797..7240, 6801..6851, 6906..7283, 6915..7280		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	39	Strand	
Start	6797	End	7670
Name	OJ990323_21.9819.C4.o5.tm	Method	TBLASTX:Maize
Start	6812	End	7102
GI	none	Score	276
Exons	6812..7102, 6813..7100		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	39	Strand	
Start	6797	End	7670

Name	OJ990323_21.9819.C4.o3.tm	Method	TBLASTX:Maize
Start	7170	End	7670
GI	none	Score	167
Exons	7170..7349, 7178..7324, 7356..7670, 7496..7549, 7577..7663		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	39	Strand	
Start	6797	End	7670
Name	OJ990323_21.9819.C4.o1.ts	Method	TBLASTX:Soybean
Start	7224	End	7620
GI	none	Score	57
Exons	7224..7256, 7226..7255, 7260..7619, 7262..7300, 7328..7618, 7351..7620		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	39	Strand	
Start	6797	End	7670
Name	OJ990323_21.9819.C4.o5.tw	Method	TBLASTX:Wheat
Start	7332	End	7634
GI	none	Score	382
Exons	7332..7634, 7333..7413, 7334..7618		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	40	Strand	
Start	7635	End	8069
Name	OJ990323_21.9819.C4.o3.tw	Method	TBLASTX:Wheat
Start	7635	End	8057
GI	none	Score	598
Exons	7635..8057, 7667..8056		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	40	Strand	
Start	7635	End	8069
Name	OJ990323_21.9819.C4.o3.ts	Method	TBLASTX:Soybean
Start	7641	End	7886
GI	none	Score	210
Exons	7641..7886, 7658..7885		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	40	Strand	
Start	7635	End	8069
Name	OJ990323_21.9819.C4.o2.tm	Method	TBLASTX:Maize
Start	7706	End	8069
GI	none	Score	482
Exons	7706..8056, 7707..8060, 7707..8069		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	41	Strand	
Start	8060	End	9593
Name	OJ990323_21.9819.C4.o2.tw	Method	TBLASTX:Wheat
Start	8060	End	8627
GI	none	Score	646
Exons	8060..8623, 8091..8627, 8163..8627		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	41	Strand	
Start	8060	End	9593

Name	OJ990323_21.9819.C4.o1.tc	Method	TBLASTX:Cress
Start	8334	End	8651
GI	none	Score	90
Exons	8334..8507, 8508..8651, 8510..8650		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	41	Strand	
Start	8060	End	9593
Name	OJ990323_21.9819.C4.o2.ts	Method	TBLASTX:Soybean
Start	8415	End	8675
GI	none	Score	297
Exons	8415..8675, 8420..8674		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	41	Strand	
Start	8060	End	9593
Name	OJ990323_21.9819.C4.o4.tm	Method	TBLASTX:Maize
Start	8474	End	8765
GI	none	Score	375
Exons	8474..8761, 8475..8765		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	41	Strand	
Start	8060	End	9593
Name	OJ990323_21.9819.C4.o1.tw	Method	TBLASTX:Wheat
Start	8634	End	9260
GI	none	Score	707
Exons	8634..9260, 8690..9148, 9135..9257		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	41	Strand	
Start	8060	End	9593
Name	OJ990323_21.9819.C4.o1.tm	Method	TBLASTX:Maize
Start	8814	End	9398
GI	none	Score	231
Exons	8814..8975, 8822..8968, 8972..9397, 8973..9398		

Seq. No.	14	Seq. ID	OJ990323_21.9819.C4
Gene No.	41	Strand	
Start	8060	End	9593
Name	OJ990323_21.9819.C4.o6.tw	Method	TBLASTX:Wheat
Start	9260	End	9593
GI	none	Score	324
Exons	9260..9529, 9261..9593, 9264..9572		

Seq. No.	15	Seq. ID	OJ990323_21.9819.C5
Gene No.	42	Strand	+
Start	284	End	475
Name	OJ990323_21.9819.C5.o1.gs	Method	GENSCAN
Start	284	End	475
GI	none	Score	.65
Exons	284..475		

Seq. No.	15	Seq. ID	OJ990323_21.9819.C5
Gene No.	43	Strand	+
Start	1287	End	1671
Name	OJ990323_21.9819.C5.o1.gp	Method	AAT/GAP

Start	1287	End	1671
GI	uC-osflcyp033a04b1	Score	616
Exons	1287..1671		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	15	Seq. ID	OJ990323_21.9819.C5
Gene No.	44	Strand	-
Start	1	End	1567
Name	OJ990323_21.9819.C5.o1.np	Method	AAT/NAP
Start	1	End	1567
GI	5852180	Score	224
Exons	1..27, 156..356, 408..519, 1514..1567		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	45	Strand	+
Start	363	End	7901
Name	OJ990323_21.9819.C6.o1.gs	Method	GENSCAN
Start	363	End	7901
GI	none	Score	.68
Exons	363..1711, 1786..1927, 2053..2348, 2398..3035, 3145..3318, 3415..3525, 3610..3682, 3777..3902, 3955..4117, 6175..6318, 6555..6647, 7747..7901		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	45	Strand	+
Start	363	End	7901
Name	OJ990323_21.9819.C6.o1.np	Method	AAT/NAP
Start	382	End	4122
GI	4680204	Score	1123
Exons	382..1711, 1786..3035, 3145..3318, 3415..3634, 3985..4122		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	45	Strand	+
Start	363	End	7901
Name	OJ990323_21.9819.C6.o1.gp	Method	AAT/GAP
Start	4401	End	4545
GI	21474_1.R1084	Score	238
Exons	4401..4545		
GI Descrip.	'3894159 2.0e-10 (AC005312) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	46	Strand	+
Start	15852	End	19320
Name	OJ990323_21.9819.C6.o3.gp	Method	AAT/GAP
Start	15736	End	16247
GI	uC-osf1M202052c07b1	Score	999
Exons	15736..16247		
GI Descrip.	'4234848 1.0e-12 (AF082131) gag-pol polyprotein [Zea mays]'		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	46	Strand	+
Start	15852	End	19320
Name	OJ990323_21.9819.C6.o2.np	Method	AAT/NAP

Start	15846	End	19320
GI	4234852	Score	2246
Exons	15846..16022, 16056..19320		
GI Descrip.	(AF082133) gag-pol polyprotein [Zea mays]		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	46	Strand	+
Start	15852	End	19320
Name	OJ990323_21.9819.C6.o3.gs	Method	GENSCAN
Start	15852	End	17754
GI	none	Score	.71
Exons	15852..16543, 16587..16693, 17648..17754		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	46	Strand	+
Start	15852	End	19320
Name	OJ990323_21.9819.C6.o4.gp	Method	AAT/GAP
Start	16479	End	17052
GI	uC-osflcyp006a10b1	Score	834
Exons	16479..16693, 16801..17052		
GI Descrip.	'4234846 7.0e-13 (AF082130) gag-pol polyprotein [Zea mays]'		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	47	Strand	+
Start	20267	End	20890
Name	OJ990323_21.9819.C6.o4.gs	Method	GENSCAN
Start	20267	End	20890
GI	none	Score	.41
Exons	20267..20344, 20379..20714, 20783..20890		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	48	Strand	-
Start	7201	End	7728
Name	OJ990323_21.9819.C6.o2.gp	Method	AAT/GAP
Start	7201	End	7728
GI	none	Score	352
Exons	7201..7221, 7505..7728		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	49	Strand	-
Start	9211	End	14673
Name	OJ990323_21.9819.C6.o2.gs	Method	GENSCAN
Start	9211	End	14673
GI	none	Score	.55
Exons	9211..9287, 9845..9989, 10743..11290, 12783..13055, 13889..14016, 14534..14673		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	50	Strand	-
Start	21450	End	23544
Name	OJ990323_21.9819.C6.o3.np	Method	AAT/NAP
Start	21450	End	23544
GI	1353193	Score	161
Exons	21450..21601, 23505..23544		
GI Descrip.	O-METHYLTRANSFERASE ZRP4 (OMT) gi|542186|pir||JQ2268 O-methyltransferase (EC 2.1.1.-) - maize gi|404070 (L14063) O-methyltransferase [Zea mays]		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	51	Strand	-
Start	24041	End	27161
Name	OJ990323_21.9819.C6.o5.gs	Method	GENSCAN
Start	24041	End	27161
GI	none	Score	.65
Exons	24041..24214, 24765..24854, 25256..25347, 26572..26687, 27082..27161		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	52	Strand	-
Start	28412	End	36939
Name	OJ990323_21.9819.C6.o6.gs	Method	GENSCAN
Start	28412	End	36912
GI	none	Score	.48
Exons	28412..28446, 29706..29793, 32495..32636, 33093..33117, 33326..33458, 34650..34739, 36101..36325, 36337..36912		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	52	Strand	-
Start	28412	End	36939
Name	OJ990323_21.9819.C6.o4.np	Method	AAT/NAP
Start	34443	End	36939
GI	4098238	Score	819
Exons	34443..34739, 36101..36450, 36490..36939		
GI Descrip.	(U76384) o-methyltransferase [Triticum aestivum]		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	53	Strand	-
Start	38859	End	40303
Name	OJ990323_21.9819.C6.o7.gs	Method	GENSCAN
Start	38859	End	40303
GI	none	Score	.49
Exons	38859..38990, 39986..40119, 40243..40303		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o2.tw	Method	TBLASTX:Wheat
Start	918	End	1321
GI	none	Score	62
Exons	918..1058, 918..1034, 920..1156, 920..1069, 1021..1188, 1151..1321, 1226..1321		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o6.tw	Method	TBLASTX:Wheat
Start	2962	End	3484
GI	none	Score	61
Exons	2962..3042, 3131..3313, 3413..3484		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o1.tm	Method	TBLASTX:Maize

Start	15939	End	16541
GI	none	Score	475
Exons	15939..16517, 16061..16507, 16263..16541		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o6.tm	Method	TBLASTX:Maize
Start	17807	End	18111
GI	none	Score	131
Exons	17807..17998, 17815..17973, 17995..18111, 18003..18110		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o2.ts	Method	TBLASTX:Soybean
Start	17818	End	18225
GI	5509260	Score	117
Exons	17818..17850, 17842..17973, 17843..17998, 17986..18159, 17995..18225, 18003..18164		
GI Descrip.	-		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o1.tw	Method	TBLASTX:Wheat
Start	17936	End	18714
GI	none	Score	48
Exons	17936..17986, 17986..18210, 17995..18234, 18003..18221, 18221..18304, 18311..18529, 18339..18575, 18347..18529, 18508..18714, 18516..18710		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o5.tm	Method	TBLASTX:Maize
Start	18520	End	18804
GI	none	Score	228
Exons	18520..18804, 18654..18794		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o5.tw	Method	TBLASTX:Wheat
Start	18873	End	19269
GI	none	Score	137
Exons	18873..19046, 18905..19045, 19054..19269		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o4.tm	Method	TBLASTX:Maize
Start	19191	End	20889
GI	none	Score	71
Exons	19191..19349, 20325..20354, 20378..20416, 20394..20414, 20477..20683, 20478..20531, 20583..20741, 20588..20740, 20733..20759, 20782..20889		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o3.tm	Method	TBLASTX:Maize
Start	21392	End	34745
GI	none	Score	69
Exons	21392..21604, 21444..21605, 21473..21610, 21477..21605, 24739..24852, 24774..24857, 34385..34597, 34433..34732, 34437..34742, 34470..34598, 34622..34702, 34623..34745		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o1.ts	Method	TBLASTX:Soybean
Start	21447	End	36648
GI	none	Score	82
Exons	21447..21602, 21447..21602, 24745..24852, 24780..24863, 34432..34554, 34440..34595, 34440..34748, 34666..34737, 36101..36166, 36191..36310, 36343..36462, 36499..36588, 36607..36648		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o2.tm	Method	TBLASTX:Maize
Start	36134	End	36903
GI	none	Score	72
Exons	36134..36178, 36179..36313, 36180..36236, 36314..36433, 36316..36447, 36508..36576, 36607..36648, 36643..36903, 36671..36853		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o4.tw	Method	TBLASTX:Wheat
Start	36167	End	36447
GI	none	Score	49
Exons	36167..36223, 36179..36316, 36180..36236, 36319..36447, 36326..36442, 36334..36447		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o3.tw	Method	TBLASTX:Wheat
Start	36644	End	36903
GI	none	Score	158
Exons	36644..36859, 36664..36903		

Seq. No.	16	Seq. ID	OJ990323_21.9819.C6
Gene No.	54	Strand	-
Start	40695	End	40775
Name	OJ990323_21.9819.C6.o5.gp	Method	AAT/GAP
Start	40695	End	40775
GI	38012_1.R1084	Score	101
Exons	40695..40775		
GI Descrip.	'4097947/gb|U72255|OSU72255 2.0e-23 Oryza sativa		

beta-1,3-glucanase precursor (Gns9) gene, complete cds'

Seq. No.	17	Seq. ID	OJ990323_21.9819.C8
Gene No.	55	Strand	-
Start	2495	End	4661
Name	OJ990323_21.9819.C8.o1.gs	Method	GENSCAN
Start	2495	End	4661
GI	none	Score	.74
Exons	2495..2619, 2820..2930, 3076..3343, 3381..3407, 4539..4661		

Seq. No.	17	Seq. ID	OJ990323_21.9819.C8
Gene No.	55	Strand	-
Start	2495	End	4661
Name	OJ990323_21.9819.C8.o1.np	Method	AAT/NAP
Start	2889	End	3263
GI	2147956	Score	72
Exons	2889..2930, 3076..3263		
GI Descrip.	polygalacturonase (EC 3.2.1.15) - Prunus persica gi|479088|emb|CAA54448| (X77231) polygalacturonase [Prunus persica]		

Seq. No.	18	Seq. ID	OJ990323_21.9819.C9
Gene No.	56	Strand	-
Start	1	End	1101
Name	OJ990323_21.9819.C9.o1.np	Method	AAT/NAP
Start	1	End	1101
GI	5922634	Score	74
Exons	1..43, 1000..1101		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016867|dbj|BAA85210.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	19	Seq. ID	OJ990323_21.9819.C10
Gene No.	57	Strand	+
Start	270	End	7094
Name	OJ990323_21.9819.C10.o1.gs	Method	GENSCAN
Start	270	End	1070
GI	none	Score	.9
Exons	270..491, 776..1070		

Seq. No.	19	Seq. ID	OJ990323_21.9819.C10
Gene No.	57	Strand	+
Start	270	End	7094
Name	OJ990323_21.9819.C10.o1.np	Method	AAT/NAP
Start	344	End	7094
GI	6539553	Score	1215
Exons	344..500, 582..1115, 1582..1918, 4953..5098, 7052..7094		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	19	Seq. ID	OJ990323_21.9819.C10
Gene No.	58	Strand	-
Start	1115	End	1173
Name	OJ990323_21.9819.C10.o1.gp	Method	AAT/GAP
Start	1115	End	1173

GI	2721_1.R1084	Score	84
Exons	1115..1173		
GI Descrip.	'114622/sp|P12087|ATPF_ORYSA 1.0e-20 ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_67929_pir__LWRZ1 H+-transporting ATP synthase (EC 3.6.1.34) chain I - rice chloroplast >gi_669080_emb_CAA33992_ (X15901) ATPase I subunit [Oryza sativa] >gi_226695_prf__1603356W ATPase I [Oryza sativa]'		

Seq. No.	19	Seq. ID	OJ990323_21.9819.C10
Gene No.	59	Strand	-
Start	1211	End	1603
Name	OJ990323_21.9819.C10.o1.tw	Method	TBLASTX:Wheat
Start	1095	End	1518
GI	none	Score	71
Exons	1095..1160, 1100..1156, 1116..1160, 1157..1204, 1157..1195, 1194..1316, 1194..1316, 1195..1317, 1195..1317, 1196..1318, 1291..1401, 1320..1403, 1320..1400, 1321..1401, 1399..1518, 1401..1499, 1403..1516		

Seq. No.	19	Seq. ID	OJ990323_21.9819.C10
Gene No.	59	Strand	-
Start	1211	End	1603
Name	OJ990323_21.9819.C10.o1.tm	Method	TBLASTX:Maize
Start	1115	End	1587
GI	none	Score	103
Exons	1115..1192, 1116..1193, 1127..1204, 1170..1310, 1193..1309, 1194..1322, 1195..1332, 1201..1332, 1272..1418, 1314..1418, 1315..1419, 1412..1450, 1418..1486, 1419..1484, 1419..1487, 1423..1485, 1447..1560, 1480..1566, 1504..1587		

Seq. No.	19	Seq. ID	OJ990323_21.9819.C10
Gene No.	59	Strand	-
Start	1211	End	1603
Name	OJ990323_21.9819.C10.o2.gp	Method	AAT/GAP
Start	1211	End	1603
GI	2135_1.R1084	Score	714
Exons	1211..1603		
GI Descrip.	'11957/emb|X15901|CHOSXX 1.0e-159 Rice complete chloroplast genome'		

Seq. No.	19	Seq. ID	OJ990323_21.9819.C10
Gene No.	60	Strand	
Start	1684	End	1915
Name	OJ990323_21.9819.C10.o2.tm	Method	TBLASTX:Maize
Start	1684	End	1915
GI	none	Score	128
Exons	1684..1776, 1693..1776, 1704..1778, 1706..1789, 1707..1790, 1770..1898, 1777..1905, 1778..1915, 1779..1895		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	61	Strand	+
Start	1	End	3842
Name	OJ990323_21.9819.C11.o1.np	Method	AAT/NAP
Start	1	End	3842
GI	4680203	Score	1042
Exons	1..32, 793..2511, 3766..3842		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	61	Strand	+
Start	1	End	3842
Name	OJ990323_21.9819.C11.o2.np	Method	AAT/NAP
Start	1925	End	3842
GI	4680186	Score	145
Exons	1925..1959, 3675..3842		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	62	Strand	-
Start	2917	End	3422
Name	OJ990323_21.9819.C11.o1.tw	Method	TBLASTX:Wheat
Start	1344	End	1937
GI	none	Score	229
Exons	1344..1634, 1346..1636, 1692..1808, 1695..1793, 1812..1937, 1829..1936		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	62	Strand	-
Start	2917	End	3422
Name	OJ990323_21.9819.C11.o1.ts	Method	TBLASTX:Soybean
Start	1362	End	1634
GI	none	Score	292
Exons	1362..1634, 1379..1627		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	62	Strand	-
Start	2917	End	3422
Name	OJ990323_21.9819.C11.o2.ts	Method	TBLASTX:Soybean
Start	1677	End	1952
GI	none	Score	221
Exons	1677..1952, 1712..1951		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	62	Strand	-
Start	2917	End	3422
Name	OJ990323_21.9819.C11.o1.tc	Method	TBLASTX:Cress
Start	1701	End	2033
GI	none	Score	288
Exons	1701..2033, 1787..1837, 1871..1978		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	62	Strand	-
Start	2917	End	3422
Name	OJ990323_21.9819.C11.o1.tm	Method	TBLASTX:Maize
Start	1839	End	2324
GI	none	Score	102
Exons	1839..1943, 1847..1942, 1946..2038, 1950..2039, 2136..2183, 2184..2231, 2186..2236, 2231..2320, 2235..2324		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	62	Strand	-
Start	2917	End	3422
Name	OJ990323_21.9819.C11.o2.tw	Method	TBLASTX:Wheat
Start	1938	End	2273

GI	none	Score	57
Exons	1938..1979, 1983..2081, 1985..2080, 2127..2225, 2138..2209, 2235..2273		

Seq. No.	20	Seq. ID	OJ990323_21.9819.C11
Gene No.	62	Strand	-
Start	2917	End	3422
Name	OJ990323_21.9819.C11.o2.gs	Method	GENSCAN
Start	2917	End	3422
GI	none	Score	.71
Exons	2917..2983, 3346..3422		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	63	Strand	+
Start	1	End	2494
Name	OJ990323_21.9819.C12.o1.np	Method	AAT/NAP
Start	1	End	1030
GI	5852180	Score	206
Exons	1..269, 974..1030		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	63	Strand	+
Start	1	End	2494
Name	OJ990323_21.9819.C12.o2.np	Method	AAT/NAP
Start	1	End	1992
GI	6742729	Score	662
Exons	1..102, 1016..1992		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	63	Strand	+
Start	1	End	2494
Name	OJ990323_21.9819.C12.o1.gs	Method	GENSCAN
Start	77	End	2494
GI	none	Score	.42
Exons	77..245, 1416..2494		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	64	Strand	-
Start	3196	End	3315
Name	OJ990323_21.9819.C12.o1.tm	Method	TBLASTX:Maize
Start	1130	End	1513
GI	none	Score	59
Exons	1130..1198, 1198..1512, 1199..1513		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	64	Strand	-
Start	3196	End	3315
Name	OJ990323_21.9819.C12.o1.tw	Method	TBLASTX:Wheat
Start	1154	End	2287
GI	none	Score	551
Exons	1154..1870, 1207..1782, 1879..2061, 1889..2077, 2054..2155, 2065..2184, 2186..2287, 2188..2280		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	64	Strand	-

Start	3196	End	3315
Name	OJ990323_21.9819.C12.o1.tc	Method	TBLASTX:Cress
Start	1445	End	1870
GI	none	Score	317
Exons	1445..1870, 1453..1782		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	64	Strand	-
Start	3196	End	3315
Name	OJ990323_21.9819.C12.o2.tm	Method	TBLASTX:Maize
Start	1763	End	2053
GI	none	Score	146
Exons	1763..1933, 1811..1927, 1945..2052, 1946..2053		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	64	Strand	-
Start	3196	End	3315
Name	OJ990323_21.9819.C12.o1.ts	Method	TBLASTX:Soybean
Start	2135	End	2347
GI	none	Score	187
Exons	2135..2347, 2135..2293		

Seq. No.	21	Seq. ID	OJ990323_21.9819.C12
Gene No.	64	Strand	-
Start	3196	End	3315
Name	OJ990323_21.9819.C12.o2.gs	Method	GENSCAN
Start	3196	End	3315
GI	none	Score	.47
Exons	3196..3315		

Seq. No.	22	Seq. ID	OJ990323_21.9819.C13
Gene No.	65	Strand	+
Start	1	End	8488
Name	OJ990323_21.9819.C13.o1.np	Method	AAT/NAP
Start	1	End	1868
GI	4680179	Score	114
Exons	1..365, 1834..1868		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	22	Seq. ID	OJ990323_21.9819.C13
Gene No.	65	Strand	+
Start	1	End	8488
Name	OJ990323_21.9819.C13.o1.gs	Method	GENSCAN
Start	482	End	8488
GI	none	Score	.61
Exons	482..522, 1166..1370, 1461..3694, 3780..4031, 4312..4393, 4668..4834, 6873..7257, 7606..7636, 7992..8488		

Seq. No.	22	Seq. ID	OJ990323_21.9819.C13
Gene No.	66	Strand	+
Start	9630	End	12546
Name	OJ990323_21.9819.C13.o2.gs	Method	GENSCAN
Start	9630	End	12546
GI	none	Score	.4
Exons	9630..9804, 10265..10321, 12302..12546		

Seq. No.	22	Seq. ID	OJ990323_21.9819.C13

Gene No.	67	Strand	-
Start	497	End	13376
Name	OJ990323_21.9819.C13.o2.np	Method	AAT/NAP
Start	497	End	13376
GI	121640	Score	241
Exons	497..548, 2971..3151, 8273..8374, 10253..10369, 12960..13376		
GI Descrip.	GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR gi|72320|pir||KNMU glycine-rich cell wall protein precursor - Arabidopsis thaliana gi|16293|emb|CAA41249| (X58338) glycine rich protein [Arabidopsis thaliana]		

Seq. No.	22	Seq. ID	OJ990323_21.9819.C13
Gene No.	67	Strand	-
Start	497	End	13376
Name	OJ990323_21.9819.C13.o1.gp	Method	AAT/GAP
Start	7574	End	7735
GI	286806	Score	247
Exons	7574..7735		
GI Descrip.	5441872/dbj|AP000366.1|AP000366 2.0e-21 Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig a)		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	68	Strand	+
Start	864	End	5449
Name	OJ990323_21.9819.C14.o1.gp	Method	AAT/GAP
Start	864	End	1451
GI	2310235	Score	299
Exons	864..901, 1312..1451		
GI Descrip.	5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	68	Strand	+
Start	864	End	5449
Name	OJ990323_21.9819.C14.o1.gs	Method	GENSCAN
Start	1312	End	4536
GI	none	Score	.4
Exons	1312..2326, 2461..3147, 3213..4114, 4444..4536		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	68	Strand	+
Start	864	End	5449
Name	OJ990323_21.9819.C14.o1.np	Method	AAT/NAP
Start	1312	End	4495
GI	4680203	Score	3041
Exons	1312..3241, 3518..4495		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	68	Strand	+
Start	864	End	5449
Name	OJ990323_21.9819.C14.o2.gp	Method	AAT/GAP
Start	1316	End	5404
GI	342_1.R1084	Score	6275
Exons	1316..4588, 4624..4643, 4726..4820, 4930..5404		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	68	Strand	+
Start	864	End	5449
Name	OJ990323_21.9819.C14.o3.gp	Method	AAT/GAP
Start	1316	End	5276
GI	342_1.R1084	Score	6047
Exons	1316..4588, 4624..4643, 4726..4820, 4930..5276		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	68	Strand	+
Start	864	End	5449
Name	OJ990323_21.9819.C14.o5.gp	Method	AAT/GAP
Start	1355	End	5449
GI	342_1.R1084	Score	6321
Exons	1355..4588, 4624..4643, 4726..4820, 4930..5449		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o3.tw	Method	TBLASTX:Wheat
Start	1663	End	2014
GI	none	Score	103
Exons	1663..1770, 1753..2004, 1761..1994, 1762..2004, 1763..2014		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o1.ts	Method	TBLASTX:Soybean
Start	1935	End	2340
GI	none	Score	102
Exons	1935..1994, 1936..2010, 2011..2073, 2068..2340, 2100..2339, 2122..2340		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o2.tc	Method	TBLASTX:Cress
Start	2097	End	2444
GI	none	Score	206
Exons	2097..2249, 2104..2340, 2289..2348, 2340..2444, 2366..2425		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o2.tw	Method	TBLASTX:Wheat
Start	2233	End	2701
GI	none	Score	72
Exons	2233..2286, 2241..2285, 2287..2340, 2298..2348, 2316..2348, 2340..2390, 2340..2411, 2384..2485, 2394..2492, 2399..2491, 2401..2493, 2472..2696, 2493..2696, 2495..2701		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14

Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o1.tm	Method	TBLASTX:Maize
Start	2340	End	2735
GI	none	Score	215
Exons	2340..2531, 2340..2531, 2541..2735		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o2.ts	Method	TBLASTX:Soybean
Start	2565	End	2807
GI	none	Score	219
Exons	2565..2807		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o4.tw	Method	TBLASTX:Wheat
Start	2796	End	3131
GI	none	Score	106
Exons	2796..2918, 2798..2941, 2915..3094, 2916..3131, 2928..3098		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o1.tw	Method	TBLASTX:Wheat
Start	3132	End	4441
GI	none	Score	859
Exons	3132..3590, 3154..4026, 3155..4042, 4037..4081, 4041..4076, 4084..4146, 4088..4147, 4153..4254, 4154..4255, 4157..4270, 4278..4343, 4280..4360, 4349..4441, 4375..4440		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o2.tm	Method	TBLASTX:Maize
Start	3167	End	3481
GI	none	Score	311
Exons	3167..3481, 3178..3453, 3251..3481		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o1.tc	Method	TBLASTX:Cress
Start	3412	End	3859
GI	none	Score	164
Exons	3412..3849, 3412..3855, 3416..3859, 3710..3859		

Seq. No.	23	Seq. ID	OJ990323_21.9819.C14
Gene No.	69	Strand	-
Start	4135	End	4579
Name	OJ990323_21.9819.C14.o4.gp	Method	AAT/GAP
Start	4135	End	4579
GI	LIB3431-028-P1-N1-A10	Score	698
Exons	4135..4481, 4509..4579		
GI Descrip.	'4680203/gb|AAD27566.1|AF114171_7 3.0e-33 (AF114171) TNP2-like		

protein [Sorghum bicolor]'

Seq. No.	24	Seq. ID	OJ990323_21.9819.C16
Gene No.	70	Strand	-
Start	1178	End	1702
Name	OJ990323_21.9819.C16.o1.gs	Method	GENSCAN
Start	1178	End	1702
GI	none	Score	.78
Exons	1178..1226, 1346..1453, 1537..1702		

Seq. No.	25	Seq. ID	OJ990323_21.9819.C17
Gene No.	71	Strand	+
Start	777	End	982
Name	OJ990323_21.9819.C17.o1.np	Method	AAT/NAP
Start	777	End	982
GI	4680186	Score	203
Exons	777..982		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	25	Seq. ID	OJ990323_21.9819.C17
Gene No.	72	Strand	-
Start	526	End	910
Name	OJ990323_21.9819.C17.o1.gp	Method	AAT/GAP
Start	526	End	910
GI	uC-osflcyp033a04b1	Score	616
Exons	526..910		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	26	Seq. ID	OJ990323_22.9819.C1
Gene No.	73	Strand	+
Start	331	End	423
Name	OJ990323_22.9819.C1.o1.gs	Method	GENSCAN
Start	331	End	423
GI	none	Score	.42
Exons	331..423		

Seq. No.	27	Seq. ID	OJ990323_22.9819.C2
Gene No.	74	Strand	+
Start	1	End	746
Name	OJ990323_22.9819.C2.o1.np	Method	AAT/NAP
Start	1	End	746
GI	2498930	Score	58
Exons	1..31, 520..583, 694..746		
GI Descrip.	DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]		

Seq. No.	27	Seq. ID	OJ990323_22.9819.C2
Gene No.	74	Strand	+
Start	1	End	746
Name	OJ990323_22.9819.C2.o1.gs	Method	GENSCAN
Start	524	End	583
GI	none	Score	.94
Exons	524..583		

Seq. No.	28	Seq. ID	OJ990323_22.9819.C3
Gene No.	75	Strand	+

Start	1	End	704
Name	OJ990323_22.9819.C3.o1.np	Method	AAT/NAP
Start	1	End	704
GI	2498930	Score	1119
Exons	1..704		
GI Descrip.	DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]		

Seq. No.	28	Seq. ID	OJ990323_22.9819.C3
Gene No.	75	Strand	+
Start	1	End	704
Name	OJ990323_22.9819.C3.o1.gs	Method	GENSCAN
Start	3	End	644
GI	none	Score	.47
Exons	3..644		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	76	Strand	+
Start	1171	End	1362
Name	OJ990323_22.9819.C4.o1.gp	Method	AAT/GAP
Start	1171	End	1362
GI	uC-osf1M202088b07a1	Score	351
Exons	1171..1362		
GI Descrip.	'11957/emb|X15901|CHOSXX 2.0e-52 Rice complete chloroplast genome'		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	77	Strand	+
Start	1387	End	1872
Name	OJ990323_22.9819.C4.o1.gs	Method	GENSCAN
Start	1387	End	1872
GI	none	Score	.45
Exons	1387..1432, 1766..1872		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	78	Strand	+
Start	2069	End	3089
Name	OJ990323_22.9819.C4.o2.gs	Method	GENSCAN
Start	2069	End	3089
GI	none	Score	.88
Exons	2069..2461, 2526..3089		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	78	Strand	+
Start	2069	End	3089
Name	OJ990323_22.9819.C4.o2.np	Method	AAT/NAP
Start	2084	End	3089
GI	4514635	Score	1021
Exons	2084..3089		
GI Descrip.	(AB021175) root cap protein 1 [Zea mays]		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	79	Strand	+
Start	3948	End	4530
Name	OJ990323_22.9819.C4.o3.gs	Method	GENSCAN
Start	3948	End	4530
GI	none	Score	.76

Exons	3948..4189, 4458..4530		
Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o1.np	Method	AAT/NAP
Start	1	End	1047
GI	298750	Score	1791
Exons	1..1047		
GI Descrip.	photosystem I reaction center protein psaA product [Sorghum bicolor, Qiuji No. 5, Peptide Chloroplast, 750 aa]		
Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o1.tc	Method	TBLASTX:Cress
Start	49	End	622
GI	none	Score	372
Exons	49..411, 49..621, 53..622, 53..622		
Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o2.tm	Method	TBLASTX:Maize
Start	49	End	442
GI	none	Score	552
Exons	49..411, 49..411, 51..440, 168..440, 245..442		
Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o3.ts	Method	TBLASTX:Soybean
Start	61	End	282
GI	none	Score	112
Exons	61..231, 62..232, 235..282		
Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o2.ts	Method	TBLASTX:Soybean
Start	382	End	614
GI	none	Score	285
Exons	382..612, 383..610, 390..614		
Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o3.tc	Method	TBLASTX:Cress
Start	623	End	825
GI	none	Score	259
Exons	623..823, 623..823, 625..825, 637..825		
Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o1.tm	Method	TBLASTX:Maize
Start	642	End	1359

GI	none	Score	742
Exons	642..1094, 642..977, 643..1095, 643..1122, 1069..1182, 1072..1128, 1092..1169, 1144..1272, 1158..1274, 1164..1280, 1275..1304, 1276..1305, 1321..1359, 1326..1358		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o1.ts	Method	TBLASTX:Soybean
Start	775	End	1193
GI	none	Score	365
Exons	775..1092, 775..1110, 779..1111, 782..1111, 1164..1193		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	80	Strand	-
Start	1	End	1359
Name	OJ990323_22.9819.C4.o2.tc	Method	TBLASTX:Cress
Start	826	End	1193
GI	none	Score	361
Exons	826..1092, 826..1092, 1087..1170, 1164..1193		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	81	Strand	
Start	2258	End	2509
Name	OJ990323_22.9819.C4.o3.tm	Method	TBLASTX:Maize
Start	2258	End	2509
GI	none	Score	323
Exons	2258..2509, 2275..2376, 2422..2508		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	81	Strand	
Start	2258	End	2509
Name	OJ990323_22.9819.C4.o1.tw	Method	TBLASTX:Wheat
Start	2264	End	2470
GI	none	Score	103
Exons	2264..2350, 2336..2470, 2341..2376, 2419..2469		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	82	Strand	
Start	2694	End	3005
Name	OJ990323_22.9819.C4.o4.ts	Method	TBLASTX:Soybean
Start	2694	End	2936
GI	none	Score	203
Exons	2694..2936, 2747..2905		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	82	Strand	
Start	2694	End	3005
Name	OJ990323_22.9819.C4.o4.tc	Method	TBLASTX:Cress
Start	2700	End	3005
GI	none	Score	197
Exons	2700..3005, 2708..2971		

Seq. No.	29	Seq. ID	OJ990323_22.9819.C4
Gene No.	82	Strand	
Start	2694	End	3005
Name	OJ990323_22.9819.C4.o4.tm	Method	TBLASTX:Maize

Start	2832	End	3005
GI	none	Score	198
Exons	2832..3005, 2840..3004		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	83	Strand	+
Start	606	End	6091
Name	OJ990323_22.9819.C5.o1.gs	Method	GENSCAN
Start	606	End	6091
GI	none	Score	.76
Exons	606..782, 927..1722, 1966..2041, 2141..2229, 2328..2423, 2448..3200, 3835..3909, 5122..5326, 5601..6091		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	84	Strand	+
Start	19386	End	25468
Name	OJ990323_22.9819.C5.o3.gs	Method	GENSCAN
Start	19386	End	24389
GI	none	Score	.6
Exons	19386..19650, 21555..21632, 22624..22742, 22982..23110, 24246..24389		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	84	Strand	+
Start	19386	End	25468
Name	OJ990323_22.9819.C5.o4.gp	Method	AAT/GAP
Start	23900	End	24534
GI	23206_2.R1084	Score	749
Exons	23900..24015, 24149..24389, 24484..24534		
GI Descrip.	'2833374/sp|Q39236|T2AG_ARATH 2.0e-26 TRANSCRIPTION INITIATION FACTOR IIA GAMMA CHAIN (TFIIA-GAMMA) >gi_1429228_emb_CAA67369_ (X98862) putative small subunit [Arabidopsis thaliana]'		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	84	Strand	+
Start	19386	End	25468
Name	OJ990323_22.9819.C5.o2.np	Method	AAT/NAP
Start	24261	End	25468
GI	2826882	Score	223
Exons	24261..24389, 24484..24534, 25334..25468		
GI Descrip.	(AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana] gi|5051786|emb|CAB45079.1| (AL078637) transcription factor IIA small subunit [Arabidopsis thaliana]		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	85	Strand	-
Start	6084	End	6399
Name	OJ990323_22.9819.C5.o1.gp	Method	AAT/GAP
Start	6084	End	6399
GI	none	Score	628
Exons	6084..6399		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o4.tm	Method	TBLASTX:Maize
Start	925	End	1173

GI	none	Score	333
Exons	925..1173, 935..1168		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o6.tm	Method	TBLASTX:Maize
Start	1659	End	2620
GI	none	Score	72
Exons	1659..1703, 1660..1701, 1791..1871, 1792..1872, 1975..2040, 1977..2039, 1978..2040, 2139..2225, 2140..2232, 2326..2385, 2335..2385, 2531..2620		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o3.tm	Method	TBLASTX:Maize
Start	2760	End	5161
GI	none	Score	206
Exons	2760..3026, 2780..2950, 2785..3006, 3022..3198, 3026..3211, 3027..3200, 3831..3911, 3833..3910, 3835..3912, 3835..3912, 4640..4714, 4642..4716, 4643..4714, 4686..4715, 4776..4856, 4780..4857, 4798..4857, 4799..4858, 5120..5161		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o5.tm	Method	TBLASTX:Maize
Start	5163	End	5755
GI	none	Score	166
Exons	5163..5324, 5163..5327, 5185..5328, 5420..5458, 5421..5480, 5599..5694, 5600..5659, 5713..5754, 5723..5755		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o2.gp	Method	AAT/GAP
Start	8199	End	9874
GI	20712_1.R1084	Score	2104
Exons	8199..8679, 8859..8937, 9026..9078, 9173..9327, 9438..9644, 9740..9874		
GI Descrip.	'4490736/emb|CAB38898.1| 7.0e-61 (AL035708) putative protein [Arabidopsis thaliana]'		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o1.tm	Method	TBLASTX:Maize
Start	8563	End	14480
GI	none	Score	99
Exons	8563..8685, 8575..8721, 8859..8936, 8859..8939, 8863..8940, 9028..9078, 9029..9079, 9030..9080, 9167..9211, 9173..9298, 9174..9335, 9429..9656, 9434..9646, 9435..9653, 9436..9660, 9738..9848, 9738..9860, 9739..9849, 9740..9850, 9849..9881, 10263..10370, 10267..10374, 10301..10375, 13823..13849, 13847..14128, 13878..14066, 14273..14353, 14277..14354, 14372..14473, 14373..14480		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o1.tw	Method	TBLASTX:Wheat
Start	8581	End	14069
GI	none	Score	99
Exons	8581..8682, 8593..8682, 8859..8933, 8859..8939, 8863..8940, 9028..9078, 9029..9079, 9166..9225, 9173..9229, 9174..9233, 13847..14068, 13878..14069		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o2.gs	Method	GENSCAN
Start	8593	End	19074
GI	none	Score	.82
Exons	8593..8679, 8859..8951, 9173..9327, 9438..9644, 9740..9880, 10266..10424, 10518..10698, 11375..11474, 11803..11927, 12228..12318, 12586..12694, 12780..12879, 13365..13529, 13623..13728, 13833..14116, 14225..14463, 15258..15336, 15411..15549, 16538..16935, 17183..17380, 18434..18658, 18928..19074		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o5.ts	Method	TBLASTX:Soybean
Start	8881	End	14452
GI	none	Score	67
Exons	8881..8940, 8883..8939, 9427..9555, 9437..9556, 9468..9566, 9556..9633, 9557..9631, 9586..9633, 14273..14350, 14381..14452		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o1.tc	Method	TBLASTX:Cress
Start	9019	End	14389
GI	none	Score	60
Exons	9019..9078, 9020..9079, 9165..9218, 9173..9280, 9481..9552, 13862..14128, 13869..14072, 14189..14389, 14223..14384		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o1.ts	Method	TBLASTX:Soybean
Start	9019	End	14125
GI	none	Score	51
Exons	9019..9078, 9020..9064, 9165..9218, 9173..9256, 9257..9292, 13809..14072, 13810..14064, 13811..14119, 13811..14125		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o1.np	Method	AAT/NAP
Start	9161	End	19392
GI	4490736	Score	3712

Exons	9161..9326, 9434..9644, 9740..9852, 10232..10468, 10518..10825, 11371..11469, 11543..11656, 11753..11927, 12228..12318, 12586..12694, 12780..12934, 13307..13527, 13603..13728, 13812..14131, 14204..14421, 15258..15336, 15411..15549, 16538..16992, 17183..17380, 18434..18658, 18928..19210, 19331..19392		
GI Descrip.	(AL035708) putative protein [Arabidopsis thaliana]		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o3.ts	Method	TBLASTX:Soybean
Start	9738	End	16989
GI	none	Score	103
Exons	9738..9887, 10270..10431, 10275..10415, 10277..10432, 10301..10447, 10516..10698, 10517..10711, 10585..10755, 11372..11449, 11376..11450, 11506..11694, 11536..11691, 11537..11692, 11796..11840, 11800..11838, 11802..11927, 15256..15342, 16870..16989		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o2.tm	Method	TBLASTX:Maize
Start	10391	End	16989
GI	none	Score	66
Exons	10391..10444, 10395..10427, 10516..10698, 10517..10699, 10567..10740, 11352..11450, 11372..11449, 11536..11691, 11537..11686, 11537..11692, 11800..11937, 11801..11929, 11801..11941, 12224..12316, 12224..12316, 12225..12320, 12226..12321, 16729..16989		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o3.gp	Method	AAT/GAP
Start	10518	End	11848
GI	uC-osroM202035h07b1	Score	832
Exons	10518..10698, 11375..11447, 11543..11692, 11803..11848		
GI Descrip.	'4490736/emb|CAB38898.1| 2.0e-53 (AL035708) putative protein [Arabidopsis thaliana]'		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o2.ts	Method	TBLASTX:Soybean
Start	16537	End	16869
GI	none	Score	303
Exons	16537..16869, 16538..16867		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	86	Strand	-
Start	8593	End	19392
Name	OJ990323_22.9819.C5.o6.ts	Method	TBLASTX:Soybean
Start	17252	End	18565
GI	none	Score	109
Exons	17252..17383, 17257..17382, 17258..17422, 18434..18526,		

18434..18565, 18438..18563

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	87	Strand	
Start	24257	End	24536
Name	OJ990323_22.9819.C5.o8.tm	Method	TBLASTX:Maize
Start	24257	End	24536
GI	none	Score	188
Exons	24257..24382, 24260..24388, 24261..24398, 24474..24533, 24478..24534, 24483..24536		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	87	Strand	
Start	24257	End	24536
Name	OJ990323_22.9819.C5.o2.tc	Method	TBLASTX:Cress
Start	24260	End	24534
GI	none	Score	210
Exons	24260..24388, 24261..24398, 24261..24398, 24474..24533, 24478..24534		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	87	Strand	
Start	24257	End	24536
Name	OJ990323_22.9819.C5.o4.ts	Method	TBLASTX:Soybean
Start	24260	End	24534
GI	none	Score	109
Exons	24260..24382, 24260..24388, 24261..24398, 24261..24398, 24474..24533, 24478..24534		

Seq. No.	30	Seq. ID	OJ990323_22.9819.C5
Gene No.	88	Strand	
Start	25492	End	26022
Name	OJ990323_22.9819.C5.o7.tm	Method	TBLASTX:Maize
Start	25492	End	26022
GI	none	Score	68
Exons	25492..25530, 25525..25611, 25527..25613, 25640..25777, 25641..25847, 25876..25962, 25978..26022		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	89	Strand	+
Start	404	End	595
Name	OJ990323_22.9819.C6.o1.gs	Method	GENSCAN
Start	404	End	595
GI	none	Score	.47
Exons	404..595		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	90	Strand	+
Start	3276	End	3417
Name	OJ990323_22.9819.C6.o1.np	Method	AAT/NAP
Start	3276	End	3417
GI	2826882	Score	162
Exons	3276..3417		
GI Descrip.	(AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana] gi|5051786|emb|CAB45079.1| (AL078637) transcription factor IIA small subunit [Arabidopsis thaliana]		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	91	Strand	+
Start	5167	End	5600
Name	OJ990323_22.9819.C6.o3.gs	Method	GENSCAN
Start	5167	End	5600
GI	none	Score	.51
Exons	5167..5187, 5445..5600		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	92	Strand	+
Start	7017	End	9060
Name	OJ990323_22.9819.C6.o2.gp	Method	AAT/GAP
Start	6890	End	8794
GI	11753_1.R1084	Score	1092
Exons	6890..7082, 7843..7955, 8367..8444, 8603..8794		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	92	Strand	+
Start	7017	End	9060
Name	OJ990323_22.9819.C6.o4.gs	Method	GENSCAN
Start	7017	End	9060
GI	none	Score	.99
Exons	7017..7082, 7760..7778, 7843..7955, 8367..8444, 8750..8847, 8955..9060		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	93	Strand	+
Start	9689	End	9786
Name	OJ990323_22.9819.C6.o5.gs	Method	GENSCAN
Start	9689	End	9786
GI	none	Score	.45
Exons	9689..9715, 9757..9786		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	94	Strand	-
Start	855	End	1166
Name	OJ990323_22.9819.C6.o2.gs	Method	GENSCAN
Start	855	End	1166
GI	none	Score	.77
Exons	855..1166		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	95	Strand	-
Start	3271	End	3758
Name	OJ990323_22.9819.C6.o1.gp	Method	AAT/GAP
Start	3271	End	3758
GI	23206_1.R1084	Score	901
Exons	3271..3758		
GI Descrip.	'2826882/emb|CAA11524.1| 9.0e-47 (AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana] >gi_5051786_emb_CAB45079.1_ (AL078637) transcription factor IIA small subunit [Arabidopsis thaliana]'		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	96	Strand	-

Start	10502	End	10610
Name	OJ990323_22.9819.C6.o1.tm	Method	TBLASTX:Maize
Start	3257	End	3420
GI	none	Score	236
Exons	3257..3313, 3277..3420, 3279..3419		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	96	Strand	-
Start	10502	End	10610
Name	OJ990323_22.9819.C6.o1.ts	Method	TBLASTX:Soybean
Start	3270	End	3420
GI	none	Score	91
Exons	3270..3419, 3277..3420, 3279..3419		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	96	Strand	-
Start	10502	End	10610
Name	OJ990323_22.9819.C6.o1.tc	Method	TBLASTX:Cress
Start	3277	End	3432
GI	none	Score	204
Exons	3277..3432, 3277..3417, 3279..3431		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	96	Strand	-
Start	10502	End	10610
Name	OJ990323_22.9819.C6.o1.tw	Method	TBLASTX:Wheat
Start	7839	End	8711
GI	none	Score	221
Exons	7839..7958, 7849..7956, 7862..7957, 8366..8461, 8367..8462, 8368..8463, 8368..8463, 8673..8711		

Seq. No.	31	Seq. ID	OJ990323_22.9819.C6
Gene No.	96	Strand	-
Start	10502	End	10610
Name	OJ990323_22.9819.C6.o3.np	Method	AAT/NAP
Start	10502	End	10610
GI	3915195	Score	51
Exons	10502..10610		
GI Descrip.	PROBABLE TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) gi|2127807|pir||E64318 centromere/microtubule-binding protein homolog - Methanococcus jannaschii gi|1590909 (U67472) centromere/microtubule-binding protein (cbf5) [Methanococcus jannaschii]		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o1.np	Method	AAT/NAP
Start	1	End	1171
GI	2467224	Score	129
Exons	1..46, 192..312, 649..727, 917..999, 1082..1171		
GI Descrip.	(X92946) hypothetical protein [Lactococcus lactis]		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698

Name	OJ990323_22.9819.C7.o3.tm	Method	TBLASTX:Maize
Start	199	End	1798
GI	none	Score	183
Exons	199..312, 200..310, 202..312, 646..726, 648..743, 649..744, 901..1002, 913..1017, 1079..1138, 1080..1139, 1080..1139, 1694..1798, 1700..1798		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o1.gs	Method	GENSCAN
Start	202	End	8698
GI	none	Score	.58
Exons	202..312, 649..727, 1711..1778, 1826..2629, 3975..4049, 4137..4190, 4279..4345, 4637..4750, 4839..4939, 5104..5148, 5283..5366, 5720..5824, 6259..6367, 7320..7424, 7752..7930, 8612..8698		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o2.tm	Method	TBLASTX:Maize
Start	1814	End	2383
GI	none	Score	76
Exons	1814..1999, 1815..1910, 1871..1933, 2051..2275, 2052..2129, 2086..2133, 2199..2261, 2360..2383		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o1.gp	Method	AAT/GAP
Start	2283	End	2583
GI	2427556	Score	543
Exons	2283..2583		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o3.gp	Method	AAT/GAP
Start	3383	End	3747
GI	none	Score	684
Exons	3383..3747		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o1.tm	Method	TBLASTX:Maize
Start	3636	End	6354
GI	none	Score	128
Exons	3636..3752, 3643..3753, 3822..3875, 3831..3875, 3832..3876, 3833..3877, 3970..4050, 3975..4052, 3976..4050, 4132..4158, 4137..4196, 4138..4191, 4278..4343, 4279..4347, 4280..4342, 4285..4344, 4446..4556, 4447..4518, 4632..4748, 4636..4755, 4637..4756, 4822..4926, 4835..4930, 4836..4925, 5031..5126, 5032..5142, 5032..5160, 5033..5158, 5283..5366, 5284..5367, 5718..5867, 5720..5833, 6036..6176, 6043..6168, 6256..6354, 6257..6352		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o1.ts	Method	TBLASTX:Soybean
Start	3646	End	5830
GI	none	Score	84
Exons	3646..3753, 3648..3752, 3973..4050, 3975..4052, 3979..4050, 4137..4196, 4138..4191, 4279..4347, 4280..4342, 4285..4344, 4446..4514, 4446..4556, 4447..4521, 4629..4748, 4636..4755, 4639..4749, 4643..4756, 4835..4930, 4836..4925, 5032..5160, 5033..5146, 5283..5351, 5283..5366, 5284..5367, 5718..5819, 5720..5830		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o2.np	Method	AAT/NAP
Start	3654	End	6402
GI	4850384	Score	969
Exons	3654..3746, 3833..3874, 3975..4049, 4137..4190, 4279..4387, 4441..4515, 4637..4750, 4839..4939, 5033..5148, 5283..5366, 5720..5824, 6259..6402		
GI Descrip.	(AC007357) F3F19.3 [Arabidopsis thaliana]		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o2.tc	Method	TBLASTX:Cress
Start	3684	End	4327
GI	none	Score	65
Exons	3684..3752, 3685..3753, 3975..4052, 3982..4050, 4137..4196, 4138..4191, 4279..4326, 4280..4327		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o1.tc	Method	TBLASTX:Cress
Start	4714	End	5139
GI	none	Score	72
Exons	4714..4755, 4835..4927, 4835..4930, 5032..5139, 5032..5139		

Seq. No.	32	Seq. ID	OJ990323_22.9819.C7
Gene No.	97	Strand	-
Start	1	End	8698
Name	OJ990323_22.9819.C7.o4.gp	Method	AAT/GAP
Start	6123	End	7464
GI	none	Score	861
Exons	6123..6167, 6259..6367, 6462..6635, 7320..7464		

Seq. No.	33	Seq. ID	OJ990323_22.9819.C8
Gene No.	98	Strand	+
Start	262	End	7672
Name	OJ990323_22.9819.C8.o1.gs	Method	GENSCAN
Start	262	End	7672
GI	none	Score	.41
Exons	262..372, 1005..1039, 1274..1386, 7383..7487, 7564..7672		

Seq. No.	33	Seq. ID	OJ990323_22.9819.C8
Gene No.	99	Strand	-
Start	3665	End	9556
Name	OJ990323_22.9819.C8.o1.np	Method	AAT/NAP
Start	3665	End	9541
GI	5441880	Score	1426
Exons	3665..3697, 7831..8587, 9293..9541		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	33	Seq. ID	OJ990323_22.9819.C8
Gene No.	99	Strand	-
Start	3665	End	9556
Name	OJ990323_22.9819.C8.o3.gs	Method	GENSCAN
Start	8807	End	9556
GI	none	Score	.64
Exons	8807..8920, 9287..9396, 9439..9556		

Seq. No.	33	Seq. ID	OJ990323_22.9819.C8
Gene No.	100	Strand	-
Start	9553	End	9789
Name	OJ990323_22.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	7696	End	8270
GI	none	Score	71
Exons	7696..7758, 7813..8112, 7834..8031, 7874..8095, 8214..8270		

Seq. No.	33	Seq. ID	OJ990323_22.9819.C8
Gene No.	100	Strand	-
Start	9553	End	9789
Name	OJ990323_22.9819.C8.o1.tw	Method	TBLASTX:Wheat
Start	7696	End	7977
GI	none	Score	75
Exons	7696..7776, 7697..7762, 7774..7977, 7786..7977		

Seq. No.	33	Seq. ID	OJ990323_22.9819.C8
Gene No.	100	Strand	-
Start	9553	End	9789
Name	OJ990323_22.9819.C8.o2.np	Method	AAT/NAP
Start	9553	End	9789
GI	6721543	Score	145
Exons	9553..9789		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa]		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	101	Strand	+
Start	2693	End	4686
Name	OJ990323_22.9819.C10.o1.gp	Method	AAT/GAP
Start	2693	End	4686
GI	318_1.R1084	Score	1774
Exons	2693..3036, 3987..4053, 4173..4686		
GI Descrip.	'1345881/sp|P49100|CYB5_ORYSA 2.0e-75 CYTOCHROME B5 >gi_1076743_pir__S46307 cytochrome b5 - rice >gi_414705_emb_CAA53366_ (X75670) cytochrome b5 [Oryza sativa]'		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10

Gene No.	101	Strand	+
Start	2693	End	4686
Name	OJ990323_22.9819.C10.o1.np	Method	AAT/NAP
Start	2947	End	4426
GI	1345881	Score	655
Exons	2947..3036, 3987..4053, 4173..4426		
GI Descrip.	CYTOCHROME B5 gi|1076743|pir||S46307 cytochrome b5 - rice gi|414705|emb|CAA53366| (X75670) cytochrome b5 [Oryza sativa]		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	102	Strand	+
Start	16975	End	17883
Name	OJ990323_22.9819.C10.o3.gs	Method	GENSCAN
Start	16975	End	17883
GI	none	Score	.63
Exons	16975..17032, 17041..17266, 17318..17451, 17495..17883		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	103	Strand	-
Start	200	End	6290
Name	OJ990323_22.9819.C10.o1.gs	Method	GENSCAN
Start	200	End	6290
GI	none	Score	.45
Exons	200..366, 640..807, 887..1184, 2820..2976, 3080..3345, 3954..4007, 4164..4569, 5267..5476, 5718..5861, 6236..6290		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o2.tm	Method	TBLASTX:Maize
Start	2690	End	2908
GI	none	Score	217
Exons	2690..2908, 2690..2905		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o1.tm	Method	TBLASTX:Maize
Start	2908	End	4556
GI	none	Score	123
Exons	2908..3036, 2967..3032, 3984..4055, 3984..4040, 3986..4057, 4165..4437, 4166..4435, 4174..4446, 4439..4495, 4445..4504, 4539..4556		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o1.tw	Method	TBLASTX:Wheat
Start	2932	End	4452
GI	none	Score	130
Exons	2932..3036, 2973..3032, 3984..4052, 3984..4040, 3986..4051, 4163..4276, 4165..4428, 4165..4452, 4166..4429		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o1.ts	Method	TBLASTX:Soybean

Start	2947	End	4417
GI	none	Score	97
Exons	2947..3036, 3984..4055, 3986..4054, 4163..4264, 4165..4362, 4166..4384, 4358..4417, 4363..4416		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o1.tc	Method	TBLASTX:Cress
Start	2953	End	4420
GI	none	Score	94
Exons	2953..3036, 3984..4055, 3986..4054, 4165..4419, 4166..4420		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o2.gs	Method	GENSCAN
Start	7291	End	16459
GI	none	Score	.5
Exons	7291..7872, 8306..8520, 9342..9505, 9608..9746, 11864..11936, 12004..12285, 12538..12909, 12991..13202, 13290..14644, 15199..15233, 15277..15405, 15572..15624, 16177..16459		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o2.np	Method	AAT/NAP
Start	10477	End	13647
GI	4388821	Score	412
Exons	10477..10496, 12054..12700, 12793..12909, 12991..13202, 13290..13647		
GI Descrip.	(AC006528) Mutator-like transposase [Arabidopsis thaliana]		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o2.ts	Method	TBLASTX:Soybean
Start	12091	End	12432
GI	none	Score	86
Exons	12091..12225, 12091..12432, 12113..12355, 12301..12363		

Seq. No.	34	Seq. ID	OJ990323_22.9819.C10
Gene No.	104	Strand	-
Start	7291	End	16459
Name	OJ990323_22.9819.C10.o3.tm	Method	TBLASTX:Maize
Start	12160	End	12777
GI	none	Score	145
Exons	12160..12270, 12286..12375, 12436..12777		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	105	Strand	+
Start	6049	End	8443
Name	OJ990323_22.9819.C11.o2.gs	Method	GENSCAN
Start	6049	End	8443
GI	none	Score	.91
Exons	6049..6126, 6503..6575, 7312..7526, 7865..8443		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	106	Strand	-
Start	9454	End	9847
Name	OJ990323_22.9819.C11.o1.gp	Method	AAT/GAP
Start	9454	End	9847
GI	none	Score	695
Exons	9454..9847		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o1.tm	Method	TBLASTX:Maize
Start	9462	End	12518
GI	none	Score	65
Exons	9462..9509, 9872..10006, 9902..10018, 9916..10014, 10099..10275, 10101..10196, 10101..10280, 10102..10275, 10122..10268, 10125..10274, 10125..10262, 10248..10283, 10363..10608, 10406..10603, 10407..10604, 10407..10625, 11217..11255, 11239..11361, 11239..11352, 11241..11387, 11305..11352, 11434..11628, 11434..11568, 11443..11667, 11447..11656, 11452..11652, 12164..12283, 12176..12262, 12194..12289, 12195..12290, 12359..12508, 12368..12451, 12371..12496, 12371..12499, 12371..12517, 12378..12518, 12379..12513, 12399..12515		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o3.gs	Method	GENSCAN
Start	9961	End	12427
GI	none	Score	.65
Exons	9961..10004, 10100..10274, 10408..10602, 11239..11349, 11443..11646, 12182..12289, 12371..12427		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o1.np	Method	AAT/NAP
Start	10058	End	12517
GI	3980412	Score	1115
Exons	10058..10274, 10408..10602, 11239..11349, 11443..11655, 12182..12289, 12371..12517		
GI Descrip.	(AC004561) putative pumilio/Mpt5 family RNA-binding protein [Arabidopsis thaliana]		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o2.tc	Method	TBLASTX:Cress
Start	10093	End	10280
GI	none	Score	220
Exons	10093..10272, 10099..10278, 10101..10280		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o1.ts	Method	TBLASTX:Soybean

Start	10122	End	12457
GI	none	Score	47
Exons	10122..10268, 11296..11352, 11299..11352, 11443..11643, 11447..11644, 12176..12265, 12371..12457		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o2.ts	Method	TBLASTX:Soybean
Start	10354	End	11295
GI	none	Score	88
Exons	10354..10530, 10363..10608, 10412..10603, 11239..11295		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o3.tc	Method	TBLASTX:Cress
Start	10363	End	10546
GI	none	Score	92
Exons	10363..10545, 10378..10542, 10412..10546		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o1.tc	Method	TBLASTX:Cress
Start	10549	End	12514
GI	none	Score	66
Exons	10549..10608, 11239..11352, 11239..11352, 11443..11667, 11447..11656, 12176..12262, 12176..12244, 12368..12457, 12371..12514		

Seq. No.	35	Seq. ID	OJ990323_22.9819.C11
Gene No.	107	Strand	-
Start	9961	End	12518
Name	OJ990323_22.9819.C11.o2.gp	Method	AAT/GAP
Start	11491	End	12514
GI	uC-osflcyp175e01b1	Score	768
Exons	11491..11655, 12182..12289, 12371..12514		
GI Descrip.	'3980412 1.0e-73 (AC004561) pumilio-like protein [Arabidopsis thaliana]'		

Seq. No.	36	Seq. ID	OJ990323_22.9819.C12
Gene No.	108	Strand	+
Start	500	End	555
Name	OJ990323_22.9819.C12.o1.gs	Method	GENSCAN
Start	500	End	555
GI	none	Score	.51
Exons	500..555		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	109	Strand	+
Start	92	End	8716
Name	OJ990323_22.9819.C13.o1.gs	Method	GENSCAN
Start	92	End	8716
GI	none	Score	.68
Exons	92..145, 1115..1419, 2614..2841, 3151..3374, 3448..3605, 4300..4477, 4546..4626, 4721..4867, 4957..5598, 7859..7923,		

7925..8716

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	109	Strand	+
Start	92	End	8716
Name	OJ990323_22.9819.C13.o1.np	Method	AAT/NAP
Start	1455	End	5669
GI	4678362	Score	1200
Exons	1455..1523, 1635..1672, 2614..2841, 3151..3374, 3448..3605, 4300..4525, 4793..4867, 4957..5184, 5245..5386, 5507..5669		
GI Descrip.	(AL049659) protein kinase-like protein [Arabidopsis thaliana]		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	109	Strand	+
Start	92	End	8716
Name	OJ990323_22.9819.C13.o1.gp	Method	AAT/GAP
Start	8002	End	8334
GI	LIB3434-049-P1-K1-E10	Score	622
Exons	8002..8334		
GI Descrip.	'4713951/gb|AAD28297.1|AC007293_4 9.0e-10 (AC007293) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	110	Strand	+
Start	12152	End	12392
Name	OJ990323_22.9819.C13.o2.gp	Method	AAT/GAP
Start	12152	End	12392
GI	uC-osflcyp016e06b1	Score	315
Exons	12152..12392		
GI Descrip.	'5295936/dbj|AB026295.2|AB026295 3.0e-73 Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence'		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	111	Strand	+
Start	12582	End	14837
Name	OJ990323_22.9819.C13.o2.gs	Method	GENSCAN
Start	12582	End	14837
GI	none	Score	.87
Exons	12582..12614, 13260..13386, 13978..14097, 14716..14837		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	111	Strand	+
Start	12582	End	14837
Name	OJ990323_22.9819.C13.o3.gp	Method	AAT/GAP
Start	13284	End	14213
GI	none	Score	680
Exons	13284..13386, 13829..13899, 13978..14213		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	112	Strand	+
Start	15984	End	18241
Name	OJ990323_22.9819.C13.o5.gp	Method	AAT/GAP
Start	15912	End	16434
GI	26173_1.R1084	Score	978
Exons	15912..16434		
GI Descrip.	'4836904/gb|AAD30607.1|AC007369_17 3.0e-26 (AC007369) lcl_prt_seq No definition line found [Arabidopsis thaliana]'		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	112	Strand	+
Start	15984	End	18241
Name	OJ990323_22.9819.C13.o2.np	Method	AAT/NAP
Start	15984	End	17947
GI	4836904	Score	1193
Exons	15984..16844, 17735..17947		
GI Descrip.	(AC007369) lcl|prt_seq No definition line found [Arabidopsis thaliana] gi|6708183|gb|AAF25832.1|AF191028_1 (AF191028) papain-type cysteine endopeptidase XCP2 [Arabidopsis thaliana]		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	112	Strand	+
Start	15984	End	18241
Name	OJ990323_22.9819.C13.o3.gs	Method	GENSCAN
Start	15984	End	17950
GI	none	Score	.98
Exons	15984..16844, 17735..17950		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	112	Strand	+
Start	15984	End	18241
Name	OJ990323_22.9819.C13.o6.gp	Method	AAT/GAP
Start	16445	End	18241
GI	16092_1.R1084	Score	1698
Exons	16445..16844, 17735..18241		
GI Descrip.	'4836904/gb|AAD30607.1|AC007369_17 2.0e-86 (AC007369) lcl_prt_seq No definition line found [Arabidopsis thaliana]'		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o3.tc	Method	TBLASTX:Cress
Start	1488	End	2821
GI	none	Score	40
Exons	1488..1523, 1623..1676, 1634..1675, 2598..2660, 2615..2821, 2731..2820		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o3.ts	Method	TBLASTX:Soybean
Start	1599	End	2848
GI	5606266	Score	61
Exons	1599..1676, 2615..2842, 2615..2848		
GI Descrip.	3450842 4.0e-50 (AF080436) mitogen activated protein kinase kinase [Oryza sativa]		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o3.tm	Method	TBLASTX:Maize
Start	2786	End	4551
GI	none	Score	63
Exons	2786..2845, 3113..3331, 3140..3355, 3154..3336, 3441..3602, 3446..3601, 3702..3743, 4281..4430, 4291..4431, 4519..4551		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o2.ts	Method	TBLASTX:Soybean
Start	3136	End	3614
GI	none	Score	280
Exons	3136..3378, 3143..3376, 3441..3614, 3444..3599		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o2.tc	Method	TBLASTX:Cress
Start	3154	End	4476
GI	none	Score	267
Exons	3154..3336, 3155..3343, 3441..3602, 3444..3590, 3446..3598, 4305..4433, 4306..4476		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o4.ts	Method	TBLASTX:Soybean
Start	4798	End	5114
GI	none	Score	58
Exons	4798..4869, 4956..5114, 4956..5114		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o2.tm	Method	TBLASTX:Maize
Start	4953	End	5375
GI	none	Score	311
Exons	4953..5375, 4954..5349, 4956..5375		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o5.tm	Method	TBLASTX:Maize
Start	5451	End	6095
GI	none	Score	225
Exons	5451..5684, 5513..5680, 5579..5701, 5737..5772, 5742..5810, 5748..5810, 5919..5957, 5920..5952, 5955..5975, 6006..6095, 6069..6089		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o6.tm	Method	TBLASTX:Maize
Start	8052	End	8705
GI	none	Score	117
Exons	8052..8219, 8058..8168, 8180..8287, 8181..8270, 8280..8315, 8280..8312, 8328..8408, 8350..8397, 8475..8555, 8477..8557, 8574..8705, 8594..8662, 8637..8705		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678

Name	OJ990323_22.9819.C13.o7.tm	Method	TBLASTX:Maize
Start	13807	End	14147
GI	none	Score	34
Exons	13807..13899, 13841..13855, 13862..13897, 13863..13898, 13978..14016, 13979..14017, 13980..14147, 14003..14140		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o5.ts	Method	TBLASTX:Soybean
Start	13852	End	14147
GI	none	Score	44
Exons	13852..13899, 13865..13897, 13980..14147, 13980..14132, 14003..14140		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o4.tc	Method	TBLASTX:Cress
Start	13865	End	14162
GI	none	Score	59
Exons	13865..13900, 13865..13903, 13915..14004, 13929..14162		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	113	Strand	-
Start	14569	End	14678
Name	OJ990323_22.9819.C13.o4.gp	Method	AAT/GAP
Start	14569	End	14678
GI	uC-osflcyp082b07a1	Score	153
Exons	14569..14678		
GI Descrip.	'218221/dbj|D10675|RICSINE1R6 3.0e-30 Oryza sativa p-SINE1-r6 gene, repeat sequence'		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	114	Strand	
Start	16062	End	17949
Name	OJ990323_22.9819.C13.o1.tc	Method	TBLASTX:Cress
Start	16062	End	17940
GI	none	Score	335
Exons	16062..16370, 16076..16165, 16244..16321, 16400..16597, 16404..16595, 16596..16631, 16598..16630, 16623..16709, 16712..16843, 16719..16844, 17734..17928, 17735..17932, 17739..17939, 17740..17940		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	114	Strand	
Start	16062	End	17949
Name	OJ990323_22.9819.C13.o1.ts	Method	TBLASTX:Soybean
Start	16065	End	17932
GI	none	Score	324
Exons	16065..16343, 16247..16321, 16391..16669, 16401..16706, 16712..16843, 16716..16844, 17734..17928, 17735..17932		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	114	Strand	
Start	16062	End	17949
Name	OJ990323_22.9819.C13.o1.tm	Method	TBLASTX:Maize

Start	16074	End	16682
GI	none	Score	254
Exons	16074..16247, 16076..16168, 16242..16373, 16247..16342, 16386..16682, 16397..16678		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	114	Strand	
Start	16062	End	17949
Name	OJ990323_22.9819.C13.o1.tw	Method	TBLASTX:Wheat
Start	16377	End	16667
GI	none	Score	342
Exons	16377..16667, 16400..16663		

Seq. No.	37	Seq. ID	OJ990323_22.9819.C13
Gene No.	114	Strand	
Start	16062	End	17949
Name	OJ990323_22.9819.C13.o4.tm	Method	TBLASTX:Maize
Start	16788	End	17949
GI	none	Score	63
Exons	16788..16847, 17719..17928, 17739..17942, 17741..17932, 17746..17949		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o1.np	Method	AAT/NAP
Start	1	End	1970
GI	6572067	Score	241
Exons	1..79, 822..901, 1525..1618, 1793..1970		
GI Descrip.	(AL133452) putative protein [Arabidopsis thaliana]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o1.gs	Method	GENSCAN
Start	613	End	8003
GI	none	Score	.56
Exons	613..718, 822..894, 1525..1618, 1793..1882, 3149..3337, 5005..5183, 5255..5481, 5990..6266, 6965..7242, 7852..8003		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o1.gp	Method	AAT/GAP
Start	3167	End	3469
GI	none	Score	558
Exons	3167..3469		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o5.np	Method	AAT/NAP
Start	5039	End	55548
GI	1076802	Score	244
Exons	5039..5388, 17266..17624, 22406..22562, 26123..26259, 28756..29082, 46716..46831, 50566..50929, 55475..55548		
GI Descrip.	extensin-like protein - maize gi|600118|emb|CAA84230| (Z34465)		

extensin-like protein [Zea mays] gi|1096557|prf||2111476A extensin-like domain [Zea mays]

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o4.np	Method	AAT/NAP
Start	22716	End	25423
GI	6539570	Score	136
Exons	22716..22918, 23089..23155, 25337..25423		
GI Descrip.	(AP000836) hypothetical protein [Oryza sativa]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o3.gp	Method	AAT/GAP
Start	28791	End	29451
GI	uC-osf1cyp174f11b1	Score	1111
Exons	28791..29082, 29166..29451		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-50 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o6.np	Method	AAT/NAP
Start	35879	End	39939
GI	4680203	Score	295
Exons	35879..35978, 36015..36874, 38268..38373, 39908..39939		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o6.gs	Method	GENSCAN
Start	36324	End	40300
GI	none	Score	.57
Exons	36324..36464, 36829..37118, 37297..37369, 38164..38289, 38904..39056, 39075..39176, 39612..39783, 40290..40300		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o7.np	Method	AAT/NAP
Start	36558	End	38373
GI	99922	Score	163
Exons	36558..36874, 38268..38373		
GI Descrip.	hypothetical protein - soybean gi|930025|emb|CAA31883| (X13528) ORF (334 AA) [Glycine max]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o8.np	Method	AAT/NAP
Start	41871	End	47009
GI	4680203	Score	172
Exons	41871..41937, 45425..45796, 46966..47009		

GI Descrip. (AF114171) TNP2-like protein [Sorghum bicolor]

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o8.gs	Method	GENSCAN
Start	46380	End	53036
GI	none	Score	.82
Exons	46380..46385, 46406..46588, 46677..46853, 46869..47114, 47499..47619, 48370..48395, 48769..48828, 50357..50490, 50545..50662, 50796..50889, 50968..51137, 52073..52138, 52681..52791, 52884..53036		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o6.gp	Method	AAT/GAP
Start	50350	End	50523
GI	uC-osrocyp011c06b1	Score	324
Exons	50350..50523		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-50 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o7.gp	Method	AAT/GAP
Start	51610	End	51992
GI	3107859	Score	752
Exons	51610..51992		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o9.np	Method	AAT/NAP
Start	52681	End	55457
GI	1076641	Score	148
Exons	52681..52791, 52884..52987, 55433..55457		
GI Descrip.	tau-protein kinase (EC 2.7.1.135) homolog - common tobacco gi|456356|emb|CAA54803| (X77763) shaggy like protein kinase [Nicotiana tabacum] gi|1094395|prf||2106142A Ser/Thr protein kinase [Nicotiana tabacum]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	115	Strand	+
Start	1	End	55548
Name	OJ990323_28.9819.C1.o8.gp	Method	AAT/GAP
Start	52928	End	53593
GI	uC-osflcyp112h11a1	Score	878
Exons	52928..52987, 53099..53147, 53244..53593		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	116	Strand	+
Start	56838	End	60054
Name	OJ990323_28.9819.C1.o10.gs	Method	GENSCAN

Start	56838	End	60054
GI	none	Score	.72
Exons	56838..57325, 57352..58098, 58194..59903, 59940..60054		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	116	Strand	+
Start	56838	End	60054
Name	OJ990323_28.9819.C1.o10.np	Method	AAT/NAP
Start	56838	End	60051
GI	5803259	Score	5097
Exons	56838..58098, 58194..60051		
GI Descrip.	(AP000399) hypothetical protein [Oryza sativa]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	117	Strand	+
Start	72852	End	76140
Name	OJ990323_28.9819.C1.o12.gs	Method	GENSCAN
Start	72852	End	76140
GI	none	Score	.76
Exons	72852..72859, 73468..73561, 74786..74916, 75844..76035, 76098..76140		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	118	Strand	-
Start	9660	End	13297
Name	OJ990323_28.9819.C1.o2.np	Method	AAT/NAP
Start	9568	End	13297
GI	6006864	Score	1156
Exons	9568..9902, 10400..10552, 10777..10982, 11079..11319, 11528..11661, 11948..13002, 13039..13297		
GI Descrip.	(AC009540) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	118	Strand	-
Start	9660	End	13297
Name	OJ990323_28.9819.C1.o2.gs	Method	GENSCAN
Start	9660	End	13286
GI	none	Score	.88
Exons	9660..9896, 10400..10502, 10607..10653, 10771..10982, 11079..11319, 11528..11661, 11948..13286		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	119	Strand	-
Start	17118	End	17597
Name	OJ990323_28.9819.C1.o3.gs	Method	GENSCAN
Start	17118	End	17597
GI	none	Score	.74
Exons	17118..17255, 17505..17597		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	120	Strand	-
Start	18662	End	22450
Name	OJ990323_28.9819.C1.o3.np	Method	AAT/NAP
Start	18639	End	22450
GI	5922620	Score	186
Exons	18639..18792, 20236..20605, 21916..21941, 22301..22450		
GI Descrip.	(AP000492) EST D15357(C0514) corresponds to a region of the		

predicted gene.; hypothetical protein [Oryza sativa] gi|6016853|dbj|BAA85196.1| (AP000570) EST D15357(C0514) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	120	Strand	-
Start	18662	End	22450
Name	OJ990323_28.9819.C1.o4.gs	Method	GENSCAN
Start	18662	End	22062
GI	none	Score	.49
Exons	18662..18819, 19137..19351, 19962..20094, 20161..20254, 20334..20433, 20531..20629, 20693..20813, 20984..21160, 21334..21579, 21990..22062		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	121	Strand	-
Start	22751	End	33359
Name	OJ990323_28.9819.C1.o5.gs	Method	GENSCAN
Start	22751	End	33359
GI	none	Score	.45
Exons	22751..22939, 23768..23918, 24235..24354, 28807..29187, 33259..33359		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	121	Strand	-
Start	22751	End	33359
Name	OJ990323_28.9819.C1.o4.gp	Method	AAT/GAP
Start	30698	End	31220
GI	none	Score	1046
Exons	30698..31220		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	122	Strand	-
Start	38044	End	40277
Name	OJ990323_28.9819.C1.o5.gp	Method	AAT/GAP
Start	38044	End	40277
GI	2311800	Score	662
Exons	38044..38304, 40187..40277		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	123	Strand	-
Start	43177	End	45841
Name	OJ990323_28.9819.C1.o7.gs	Method	GENSCAN
Start	43177	End	45841
GI	none	Score	.88
Exons	43177..43278, 45103..45198, 45746..45841		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	124	Strand	-
Start	54851	End	55692
Name	OJ990323_28.9819.C1.o9.gs	Method	GENSCAN
Start	54851	End	55692
GI	none	Score	.75
Exons	54851..54853, 55194..55364, 55606..55692		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1

Gene No.	125	Strand	-
Start	60062	End	60523
Name	OJ990323_28.9819.C1.o9.gp	Method	AAT/GAP
Start	60062	End	60523
GI	2428323	Score	846
Exons	60062..60523		
GI Descrip.	5803242/dbj|AP000399.1|AP000399 0.0e+00 Oryza sativa genomic DNA, chromosome 6, clone:P0535G04		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	126	Strand	-
Start	60685	End	66332
Name	OJ990323_28.9819.C1.o11.np	Method	AAT/NAP
Start	60685	End	66332
GI	6498441	Score	6893
Exons	60685..60966, 61060..62457, 62629..63009, 63202..63544, 63719..63853, 64037..64410, 64474..64937, 65268..66332		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	127	Strand	-
Start	67064	End	73820
Name	OJ990323_28.9819.C1.o12.np	Method	AAT/NAP
Start	67064	End	73820
GI	5042454	Score	178
Exons	67064..67117, 67359..67540, 73766..73820		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o11.tm	Method	TBLASTX:Maize
Start	606	End	1857
GI	none	Score	62
Exons	606..716, 607..717, 607..717, 821..895, 822..896, 823..897, 824..898, 1517..1618, 1517..1618, 1525..1620, 1772..1855, 1792..1857, 1793..1855		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o1.tm	Method	TBLASTX:Maize
Start	7345	End	78662
GI	none	Score	103
Exons	7345..7452, 7450..7584, 7569..7775, 61222..61392, 78090..78458, 78090..78662, 78397..78585		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o1.ts	Method	TBLASTX:Soybean
Start	7450	End	78663
GI	none	Score	136
Exons	7450..7584, 7569..7640, 78318..78638, 78319..78663		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o3.tc	Method	TBLASTX:Cress
Start	9678	End	9932
GI	none	Score	78
Exons	9678..9818, 9690..9932, 9691..9837		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o9.tm	Method	TBLASTX:Maize
Start	10768	End	10994
GI	none	Score	130
Exons	10768..10869, 10769..10873, 10888..10977, 10888..10977, 10890..10994		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o4.ts	Method	TBLASTX:Soybean
Start	10789	End	11152
GI	none	Score	157
Exons	10789..10983, 10790..10984, 11077..11151, 11078..11152		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o1.tc	Method	TBLASTX:Cress
Start	10849	End	11662
GI	none	Score	65
Exons	10849..10980, 10871..10960, 11075..11164, 11080..11163, 11164..11319, 11165..11314, 11168..11329, 11534..11662		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o6.tm	Method	TBLASTX:Maize
Start	11245	End	12318
GI	none	Score	112
Exons	11245..11322, 11246..11320, 11248..11322, 11523..11603, 11525..11605, 11526..11603, 11528..11605, 11597..11662, 11619..11663, 11947..12318, 11951..12052, 11952..12062, 12125..12295, 12126..12296, 12130..12318		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o2.tc	Method	TBLASTX:Cress
Start	12192	End	12971
GI	none	Score	76
Exons	12192..12521, 12255..12296, 12348..12515, 12351..12533, 12402..12506, 12534..12971, 12555..12821, 12603..12839, 12670..12774, 12751..12864		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-

Start	77400	End	83325
Name	OJ990323_28.9819.C1.o3.ts	Method	TBLASTX:Soybean
Start	12204	End	12932
GI	none	Score	104
Exons	12204..12761, 12621..12932, 12729..12911, 12730..12909		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o5.tm	Method	TBLASTX:Maize
Start	12351	End	64715
GI	none	Score	137
Exons	12351..12524, 12351..12521, 12495..12998, 12607..12987, 64511..64585, 64574..64627, 64668..64715		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o10.tm	Method	TBLASTX:Maize
Start	52593	End	52988
GI	none	Score	135
Exons	52593..52814, 52594..52788, 52881..52988, 52883..52972		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o6.tw	Method	TBLASTX:Wheat
Start	60694	End	78296
GI	none	Score	81
Exons	60694..60819, 60698..60820, 60850..60921, 61000..61296, 61013..61156, 61193..61291, 61221..61292, 78222..78296		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o4.tw	Method	TBLASTX:Wheat
Start	61297	End	61678
GI	none	Score	169
Exons	61297..61677, 61328..61576, 61336..61581, 61622..61678		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o4.tm	Method	TBLASTX:Maize
Start	61492	End	61815
GI	none	Score	200
Exons	61492..61815, 61505..61786		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o9.tw	Method	TBLASTX:Wheat
Start	62008	End	62320
GI	none	Score	67
Exons	62008..62268, 62144..62320		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1

Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o5.ts	Method	TBLASTX:Soybean
Start	62068	End	62634
GI	5666795	Score	68
Exons	62068..62268, 62323..62460, 62536..62634		
GI Descrip.	4206306 2.0e-10 (AF049110) prpol [Zea mays]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o5.tw	Method	TBLASTX:Wheat
Start	62323	End	62757
GI	none	Score	88
Exons	62323..62472, 62324..62461, 62326..62463, 62506..62757, 62516..62692, 62560..62757		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o3.tm	Method	TBLASTX:Maize
Start	63409	End	79661
GI	none	Score	105
Exons	63409..63753, 79137..79421, 79207..79341, 79410..79661, 79417..79575		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o2.tw	Method	TBLASTX:Wheat
Start	63412	End	79736
GI	none	Score	313
Exons	63412..63831, 63419..63832, 79407..79736		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o2.ts	Method	TBLASTX:Soybean
Start	63490	End	79757
GI	none	Score	107
Exons	63490..63861, 79407..79757, 79414..79641		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o2.tm	Method	TBLASTX:Maize
Start	63772	End	80165
GI	none	Score	167
Exons	63772..64185, 79680..80165, 79699..80112		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o1.tw	Method	TBLASTX:Wheat
Start	63940	End	80203
GI	none	Score	230
Exons	63940..64401, 63946..64401, 63947..64402, 63960..64403,		

79851..80069, 80144..80203

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o6.ts	Method	TBLASTX:Soybean
Start	63997	End	80045
GI	none	Score	121
Exons	63997..64131, 64138..64362, 79905..80045		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o3.tw	Method	TBLASTX:Wheat
Start	64558	End	65053
GI	none	Score	74
Exons	64558..65052, 64594..64788, 64598..64858, 64916..65053		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o7.tw	Method	TBLASTX:Wheat
Start	65791	End	66183
GI	none	Score	96
Exons	65791..66048, 65825..66064, 66031..66129, 66032..66124, 66136..66183		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o12.tm	Method	TBLASTX:Maize
Start	65893	End	66178
GI	none	Score	107
Exons	65893..66141, 65894..66178		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o13.np	Method	AAT/NAP
Start	77386	End	83325
GI	6466937	Score	2239
Exons	77386..81504, 83302..83325		
GI Descrip.	(AC011621) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o13.gs	Method	GENSCAN
Start	77400	End	81891
GI	none	Score	.57
Exons	77400..77966, 77994..78101, 78228..79130, 79158..79494, 79627..80039, 80184..81311, 81325..81891		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325

Name	OJ990323_28.9819.C1.o7.tm	Method	TBLASTX:Maize
Start	77457	End	77813
GI	none	Score	132
Exons	77457..77813, 77478..77756, 77587..77796		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o8.tm	Method	TBLASTX:Maize
Start	78795	End	79085
GI	none	Score	90
Exons	78795..78938, 78939..79085, 78967..79068		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o8.tw	Method	TBLASTX:Wheat
Start	78960	End	79341
GI	none	Score	44
Exons	78960..79340, 79041..79148, 79261..79341		

Seq. No.	38	Seq. ID	OJ990323_28.9819.C1
Gene No.	128	Strand	-
Start	77400	End	83325
Name	OJ990323_28.9819.C1.o14.np	Method	AAT/NAP
Start	79907	End	81892
GI	2129478	Score	61
Exons	79907..80051, 80176..80303, 81536..81624, 81777..81892		
GI Descrip.	chitinase (EC 3.2.1.14) precursor - beet gi|488731|emb|CAA55883| (X79301) chitinase [Beta vulgaris] gi|829258|emb|CAA56946| (X81056) Chitinase [Beta vulgaris]		

Seq. No.	39	Seq. ID	OJ990323_28.9819.C2
Gene No.	129	Strand	-
Start	1	End	744
Name	OJ990323_28.9819.C2.o1.np	Method	AAT/NAP
Start	1	End	744
GI	6498441	Score	392
Exons	1..210, 541..744		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	39	Seq. ID	OJ990323_28.9819.C2
Gene No.	129	Strand	-
Start	1	End	744
Name	OJ990323_28.9819.C2.o1.tw	Method	TBLASTX:Wheat
Start	32	End	326
GI	none	Score	71
Exons	32..325, 189..326		

Seq. No.	39	Seq. ID	OJ990323_28.9819.C2
Gene No.	129	Strand	-
Start	1	End	744
Name	OJ990323_28.9819.C2.o1.gs	Method	GENSCAN
Start	47	End	539
GI	none	Score	.54

Exons	47..539		
Seq. No.	40	Seq. ID	OJ990323_28.9819.C3
Gene No.	130	Strand	+
Start	1	End	178
Name	OJ990323_28.9819.C3.o1.gp	Method	AAT/GAP
Start	1	End	178
GI	2311800	Score	239
Exons	1..178		
Seq. No.	41	Seq. ID	OJ990323_28.9819.C4
Gene No.	131	Strand	+
Start	79	End	142
Name	OJ990323_28.9819.C4.o1.gs	Method	GENSCAN
Start	79	End	142
GI	none	Score	.98
Exons	79..142		
Seq. No.	42	Seq. ID	OJ990323_28.9819.C6
Gene No.	132	Strand	-
Start	292	End	411
Name	OJ990323_28.9819.C6.o1.gs	Method	GENSCAN
Start	292	End	411
GI	none	Score	.52
Exons	292..411		
Seq. No.	42	Seq. ID	OJ990323_28.9819.C6
Gene No.	133	Strand	-
Start	547	End	627
Name	OJ990323_28.9819.C6.o1.gp	Method	AAT/GAP
Start	547	End	627
GI	LIB3477-003-P1-K1-E9	Score	100
Exons	547..627		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		
Seq. No.	43	Seq. ID	OJ990503_20.9819.C3
Gene No.	134	Strand	-
Start	447	End	935
Name	OJ990503_20.9819.C3.o1.gs	Method	GENSCAN
Start	447	End	935
GI	none	Score	.46
Exons	447..615, 690..935		
Seq. No.	44	Seq. ID	OJ990503_20.9819.C9
Gene No.	135	Strand	+
Start	55	End	565
Name	OJ990503_20.9819.C9.o1.gs	Method	GENSCAN
Start	55	End	565
GI	none	Score	.63
Exons	55..300, 375..565		
Seq. No.	45	Seq. ID	OJ990503_20.9819.C10
Gene No.	136	Strand	-
Start	693	End	979
Name	OJ990503_20.9819.C10.o1.gs	Method	GENSCAN

Start	693	End	979
GI	none	Score	.46
Exons	693..825, 900..979		

Seq. No.	46	Seq. ID	OJ990503_20.9819.C11
Gene No.	137	Strand	+
Start	273	End	1055
Name	OJ990503_20.9819.C11.o1.gs	Method	GENSCAN
Start	273	End	1055
GI	none	Score	.55
Exons	273..352, 427..530, 871..1055		

Seq. No.	47	Seq. ID	OJ990503_20.9819.C13
Gene No.	138	Strand	-
Start	1	End	781
Name	OJ990503_20.9819.C13.o1.np	Method	AAT/NAP
Start	1	End	781
GI	2498930	Score	720
Exons	1..429, 597..657, 762..781		
GI Descrip.	DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]		

Seq. No.	47	Seq. ID	OJ990503_20.9819.C13
Gene No.	138	Strand	-
Start	1	End	781
Name	OJ990503_20.9819.C13.o1.gs	Method	GENSCAN
Start	34	End	656
GI	none	Score	.98
Exons	34..429, 597..656		

Seq. No.	48	Seq. ID	OJ990503_20.9819.C16
Gene No.	139	Strand	-
Start	364	End	519
Name	OJ990503_20.9819.C16.o1.gs	Method	GENSCAN
Start	364	End	519
GI	none	Score	.89
Exons	364..519		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	140	Strand	+
Start	16269	End	16817
Name	OJ990323_17.9819.C1.o4.gp	Method	AAT/GAP
Start	16269	End	16817
GI	none	Score	770
Exons	16269..16582, 16729..16817		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	141	Strand	+
Start	16922	End	22916
Name	OJ990323_17.9819.C1.o5.gp	Method	AAT/GAP
Start	16922	End	17451
GI	uC-osf1M202091b10b1	Score	724
Exons	16922..17214, 17322..17451		
GI Descrip.	'4760544/dbj|AB019492.1|AB019492 5.0e-23 Homo sapiens IDN4-GGTR14 mRNA, partial cds'		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1

Gene No.	141	Strand	+
Start	16922	End	22916
Name	OJ990323_17.9819.C1.o3.np	Method	AAT/NAP
Start	16925	End	22916
GI	1814196	Score	42
Exons	16925..17118, 22850..22916		
GI Descrip.	(U39847) AO13 ankyrin [Caenorhabditis elegans]		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	141	Strand	+
Start	16922	End	22916
Name	OJ990323_17.9819.C1.o6.gp	Method	AAT/GAP
Start	17650	End	22301
GI	10494_1.R1084	Score	1495
Exons	17650..17702, 20947..21044, 21130..21179, 21433..21497, 21757..22301		
GI Descrip.	'5730046/ref|NM_006632.1|SLC17A3| 1.0e-09 Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545_HSU90545 Human sodium phosphate transporter (NPT4) mRNA, complete cds'		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	142	Strand	-
Start	694	End	3187
Name	OJ990323_17.9819.C1.o1.gp	Method	AAT/GAP
Start	694	End	3187
GI	none	Score	1292
Exons	694..1179, 3000..3187		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	143	Strand	-
Start	10462	End	12634
Name	OJ990323_17.9819.C1.o2.np	Method	AAT/NAP
Start	10462	End	12634
GI	6630546	Score	162
Exons	10462..10489, 12375..12634		
GI Descrip.	(AC011708) putative alpha/beta hydrolase [Arabidopsis thaliana]		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	143	Strand	-
Start	10462	End	12634
Name	OJ990323_17.9819.C1.o3.gp	Method	AAT/GAP
Start	10832	End	11001
GI	2796959	Score	272
Exons	10832..11001		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	143	Strand	-
Start	10462	End	12634
Name	OJ990323_17.9819.C1.o1.np	Method	AAT/NAP
Start	11643	End	11953
GI	6539553	Score	485
Exons	11643..11953		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	144	Strand	-
Start	22439	End	22607
Name	OJ990323_17.9819.C1.o2.tm	Method	TBLASTX:Maize
Start	447	End	11383
GI	none	Score	148
Exons	447..611, 447..611, 449..616, 460..621, 11220..11339, 11234..11341, 11234..11383		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	144	Strand	-
Start	22439	End	22607
Name	OJ990323_17.9819.C1.o1.tm	Method	TBLASTX:Maize
Start	674	End	11692
GI	none	Score	75
Exons	674..913, 675..761, 677..883, 708..929, 709..1119, 993..1127, 11445..11651, 11446..11673, 11449..11652, 11480..11692		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	144	Strand	-
Start	22439	End	22607
Name	OJ990323_17.9819.C1.o1.tw	Method	TBLASTX:Wheat
Start	11663	End	12022
GI	none	Score	148
Exons	11663..11818, 11669..11794, 11778..11963, 11780..11962, 11959..12006, 11966..12022		

Seq. No.	49	Seq. ID	OJ990323_17.9819.C1
Gene No.	144	Strand	-
Start	22439	End	22607
Name	OJ990323_17.9819.C1.o7.gp	Method	AAT/GAP
Start	22439	End	22607
GI	2796959	Score	271
Exons	22439..22607		

Seq. No.	50	Seq. ID	OJ990323_17.9819.C2
Gene No.	145	Strand	+
Start	1	End	579
Name	OJ990323_17.9819.C2.o1.np	Method	AAT/NAP
Start	1	End	579
GI	2498930	Score	45
Exons	1..27, 520..579		
GI Descrip.	DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]		

Seq. No.	50	Seq. ID	OJ990323_17.9819.C2
Gene No.	146	Strand	+
Start	520	End	579
Name	OJ990323_17.9819.C2.o1.gs	Method	GENSCAN
Start	520	End	579
GI	none	Score	.94
Exons	520..579		

Seq. No.	51	Seq. ID	OJ990323_17.9819.C3
Gene No.	147	Strand	+
Start	1	End	752

Name	OJ990323_17.9819.C3.o1.np	Method	AAT/NAP
Start	1	End	752
GI	2498930	Score	1184
Exons	1..752		
GI Descrip.	DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]		

Seq. No.	51	Seq. ID	OJ990323_17.9819.C3
Gene No.	147	Strand	+
Start	1	End	752
Name	OJ990323_17.9819.C3.o1.gs	Method	GENSCAN
Start	45	End	686
GI	none	Score	.83
Exons	45..686		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	148	Strand	+
Start	256	End	533
Name	OJ990323_17.9819.C4.o1.gp	Method	AAT/GAP
Start	256	End	533
GI	18282_1.R1084	Score	505
Exons	256..533		
GI Descrip.	'3805765 1.0e-123 (AC005693) putative protein kinase [Arabidopsis thaliana]'		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	149	Strand	+
Start	2766	End	3442
Name	OJ990323_17.9819.C4.o2.gp	Method	AAT/GAP
Start	2766	End	3442
GI	none	Score	1076
Exons	2766..3442		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	150	Strand	+
Start	15080	End	16766
Name	OJ990323_17.9819.C4.o3.gs	Method	GENSCAN
Start	15080	End	16766
GI	none	Score	.71
Exons	15080..15340, 16341..16766		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	151	Strand	+
Start	17215	End	23918
Name	OJ990323_17.9819.C4.o4.gs	Method	GENSCAN
Start	17215	End	23918
GI	none	Score	.42
Exons	17215..17319, 19413..19568, 21444..21734, 22814..23324, 23575..23918		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	151	Strand	+
Start	17215	End	23918
Name	OJ990323_17.9819.C4.o3.np	Method	AAT/NAP
Start	20774	End	23230
GI	3786008	Score	140
Exons	20774..20836, 21546..21734, 22814..22965, 23023..23230		

GI Descrip. (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	152	Strand	+
Start	32267	End	32545
Name	OJ990323_17.9819.C4.o5.np	Method	AAT/NAP
Start	32267	End	32545
GI	6539588	Score	152
Exons	32267..32545		

GI Descrip. (AP000837) hypothetical protein [Oryza sativa]

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	153	Strand	+
Start	36507	End	38568
Name	OJ990323_17.9819.C4.o7.gp	Method	AAT/GAP
Start	36425	End	36936
GI	uC-osflcyp089c04b1	Score	965
Exons	36425..36936		

GI Descrip. '3786008 9.0e-19 (AC005499) unknown protein [Arabidopsis thaliana]'

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	153	Strand	+
Start	36507	End	38568
Name	OJ990323_17.9819.C4.o7.gs	Method	GENSCAN
Start	36507	End	38568
GI	none	Score	.84
Exons	36507..37171, 37632..37711, 38423..38568		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	153	Strand	+
Start	36507	End	38568
Name	OJ990323_17.9819.C4.o6.np	Method	AAT/NAP
Start	36537	End	37139
GI	3786008	Score	282
Exons	36537..36908, 36948..37139		

GI Descrip. (AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	154	Strand	+
Start	40550	End	44581
Name	OJ990323_17.9819.C4.o8.gs	Method	GENSCAN
Start	40550	End	44581
GI	none	Score	.75
Exons	40550..40659, 41778..42713, 42798..43002, 43381..43599, 43687..43778, 43864..44581		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	154	Strand	+
Start	40550	End	44581
Name	OJ990323_17.9819.C4.o7.np	Method	AAT/NAP
Start	41905	End	44566
GI	4584542	Score	979
Exons	41905..43002, 43381..43599, 43687..43778, 43864..44137, 44207..44566		

GI Descrip. (AL049608) putative protein [Arabidopsis thaliana]

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	155	Strand	-
Start	7065	End	14147
Name	OJ990323_17.9819.C4.o2.gs	Method	GENSCAN
Start	7065	End	13880
GI	none	Score	.5
Exons	7065..7157, 8881..8968, 9754..10043, 10071..10377, 10403..10791, 10932..11378, 11458..11603, 11648..12188, 12236..12418, 12551..12685, 12753..13232, 13251..13880		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	155	Strand	-
Start	7065	End	14147
Name	OJ990323_17.9819.C4.o1.np	Method	AAT/NAP
Start	8505	End	14147
GI	6056391	Score	1944
Exons	8505..8540, 9768..11438, 11472..13191, 13349..14147		
GI Descrip.	(AC009324) Similar to retrotransposon proteins [Arabidopsis thaliana]		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	156	Strand	-
Start	17509	End	17964
Name	OJ990323_17.9819.C4.o4.gp	Method	AAT/GAP
Start	17509	End	17964
GI	none	Score	893
Exons	17509..17964		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	157	Strand	-
Start	19298	End	20836
Name	OJ990323_17.9819.C4.o2.np	Method	AAT/NAP
Start	19298	End	20770
GI	4503719	Score	222
Exons	19298..19406, 19494..19580, 19811..19957, 20669..20770		
GI Descrip.	fragile histidine triad gene gi|1706794|sp|P49789|FHIT_HUMAN BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE) (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE) (FRAGILE HISTIDINE TRIAD PROTEIN) gi|3114520|pdb|4FIT| Fhit-Apo gi|3114524|pdb|6FIT| Fhit-Transition State Analog gi|3318895|pdb|1FHI| Substrate Analog (Ib2) Complex W		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	157	Strand	-
Start	19298	End	20836
Name	OJ990323_17.9819.C4.o5.gp	Method	AAT/GAP
Start	20239	End	20836
GI	uC-osf1M202097d10b1	Score	918
Exons	20239..20551, 20671..20836		
GI Descrip.	'4062935/dbj|AB003495.1|AB003495 3.0e-14 Oryza sativa DNA for dihydroflavonol 4-reductase, complete cds'		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	158	Strand	-
Start	25276	End	28897
Name	OJ990323_17.9819.C4.o6.gp	Method	AAT/GAP

Start	25139	End	26003
GI	75776_1.R1084	Score	877
Exons	25139..25392, 25484..25582, 25868..26003		
GI Descrip.	'4503719/ref|NP_002003.1|pFHIT| 1.0e-23 fragile histidine triad gene >gi_1706794_sp_P49789_FHIT_HUMAN BIS(5''-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5'',5''''''-P1,P3-TRIPHOSPHATE HYDROLASE) (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE) (FRAGILE HISTIDINE TRIAD PROTEIN) >gi_3114520_pdb_4FIT_ Fhit-Apo >gi_3114524_pdb_6FIT_ Fhit-Transition State Analog >gi_3318895_pdb_1FHI_ Subst'		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	158	Strand	-
Start	25276	End	28897
Name	OJ990323_17.9819.C4.o5.gs	Method	GENSCAN
Start	25276	End	28897
GI	none	Score	.73
Exons	25276..25392, 25484..25591, 25868..25993, 26428..26593, 27233..27566, 28500..28551, 28886..28897		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	158	Strand	-
Start	25276	End	28897
Name	OJ990323_17.9819.C4.o4.np	Method	AAT/NAP
Start	25279	End	26109
GI	4503719	Score	233
Exons	25279..25375, 25488..25582, 25868..26109		
GI Descrip.	fragile histidine triad gene gi|1706794|sp|P49789|FHIT_HUMAN BIS(5'-ADENOSYL)-TRIPHOSPHATASE (DIADENOSINE 5',5'''-P1,P3-TRIPHOSPHATE HYDROLASE) (DINUCLEOSIDETRIPHOSPHATASE) (AP3A HYDROLASE) (AP3AASE) (FRAGILE HISTIDINE TRIAD PROTEIN) gi|3114520|pdb|4FIT| Fhit-Apo gi|3114524|pdb|6FIT| Fhit-Transition State Analog gi|3318895|pdb|1FHI| Substrate Analog (Ib2) Complex W		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	159	Strand	-
Start	45510	End	47348
Name	OJ990323_17.9819.C4.o9.gs	Method	GENSCAN
Start	45510	End	47348
GI	none	Score	.7
Exons	45510..45619, 46233..46307, 46598..47348		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o17.tm	Method	TBLASTX:Maize
Start	4984	End	5524
GI	none	Score	113
Exons	4984..5142, 5064..5141, 5133..5294, 5196..5267, 5268..5363, 5268..5360, 5405..5461, 5405..5524, 5421..5471		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o8.tw	Method	TBLASTX:Wheat

Start	9598	End	9959
GI	none	Score	104
Exons	9598..9633, 9730..9942, 9756..9959		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o7.tm	Method	TBLASTX:Maize
Start	9822	End	10127
GI	none	Score	88
Exons	9822..10127, 9823..10059, 9831..10118		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o1.ts	Method	TBLASTX:Soybean
Start	9825	End	10419
GI	none	Score	179
Exons	9825..10238, 9826..10227, 10351..10419		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o2.tm	Method	TBLASTX:Maize
Start	10128	End	10585
GI	none	Score	155
Exons	10128..10355, 10129..10356, 10345..10584, 10349..10585		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o6.tw	Method	TBLASTX:Wheat
Start	10185	End	10428
GI	none	Score	91
Exons	10185..10355, 10186..10344, 10345..10428, 10364..10423		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o7.ts	Method	TBLASTX:Soybean
Start	10266	End	10638
GI	none	Score	83
Exons	10266..10349, 10420..10638, 10421..10636		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o1.tw	Method	TBLASTX:Wheat
Start	10429	End	11133
GI	none	Score	141
Exons	10429..10563, 10582..10797, 10807..11133, 10815..11132		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o6.tc	Method	TBLASTX:Cress
Start	10444	End	10737

GI	none	Score	201
Exons	10444..10737		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o12.tm	Method	TBLASTX:Maize
Start	10591	End	10971
GI	none	Score	63
Exons	10591..10815, 10595..10693, 10785..10970, 10813..10971		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o2.ts	Method	TBLASTX:Soybean
Start	10821	End	11297
GI	5509260	Score	86
Exons	10821..11297, 10825..10974		
GI Descrip.	-		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o4.tc	Method	TBLASTX:Cress
Start	10914	End	11190
GI	none	Score	39
Exons	10914..11189, 10936..10980, 11044..11190		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o9.tm	Method	TBLASTX:Maize
Start	10971	End	11253
GI	none	Score	140
Exons	10971..11252, 10971..11252, 11101..11253		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o2.tc	Method	TBLASTX:Cress
Start	11796	End	12233
GI	none	Score	68
Exons	11796..12233, 11800..11937		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o3.tw	Method	TBLASTX:Wheat
Start	11796	End	12146
GI	none	Score	153
Exons	11796..12146, 11797..12105		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o4.ts	Method	TBLASTX:Soybean
Start	11811	End	12272

GI	none	Score	260
Exons	11811..12272		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o3.tm	Method	TBLASTX:Maize
Start	11821	End	12278
GI	none	Score	173
Exons	11821..12219, 11823..12200, 12043..12201, 12177..12278		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o5.tc	Method	TBLASTX:Cress
Start	12375	End	12671
GI	none	Score	203
Exons	12375..12458, 12462..12671		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o5.tw	Method	TBLASTX:Wheat
Start	12468	End	12917
GI	none	Score	78
Exons	12468..12581, 12478..12561, 12630..12725, 12732..12872, 12732..12917		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o11.tm	Method	TBLASTX:Maize
Start	12564	End	12893
GI	none	Score	54
Exons	12564..12674, 12610..12654, 12711..12890, 12711..12893, 12721..12891		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o14.tm	Method	TBLASTX:Maize
Start	13554	End	14057
GI	none	Score	95
Exons	13554..13865, 13642..13854, 13974..14057		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o10.tm	Method	TBLASTX:Maize
Start	15157	End	36812
GI	none	Score	275
Exons	15157..15342, 15158..15343, 21535..21579, 21536..21595, 21543..21737, 21545..21736, 21668..21790, 21670..21744, 22796..22873, 22801..22902, 36648..36701, 36726..36812		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-

Start	48413	End	61692
Name	OJ990323_17.9819.C4.o6.tm	Method	TBLASTX:Maize
Start	19286	End	27343
GI	none	Score	70
Exons	19286..19384, 19295..19375, 19479..19589, 19497..19583, 19811..19957, 19815..19955, 19841..19957, 20669..20782, 20670..20783, 25276..25392, 25276..25392, 25284..25394, 25287..25394, 25477..25584, 25481..25588, 25485..25583, 25866..26012, 25868..26014, 25872..26012, 27213..27320, 27253..27324, 27255..27338, 27256..27342, 27257..27343		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o3.tc	Method	TBLASTX:Cress
Start	19301	End	27332
GI	none	Score	97
Exons	19301..19384, 19497..19583, 19811..19957, 19815..19955, 19822..19962, 19823..19957, 20669..20770, 20670..20765, 25282..25380, 25282..25392, 25481..25588, 25485..25583, 25859..25987, 25868..26014, 25872..26012, 27207..27320, 27255..27332, 27256..27321		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o5.ts	Method	TBLASTX:Soybean
Start	19310	End	26014
GI	none	Score	95
Exons	19310..19387, 19494..19583, 19811..19957, 19815..19955, 20669..20764, 25278..25403, 25291..25383, 25485..25583, 25487..25588, 25859..25996, 25868..26014, 25872..26012		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o6.ts	Method	TBLASTX:Soybean
Start	42437	End	42743
GI	none	Score	47
Exons	42437..42499, 42502..42558, 42606..42731, 42607..42732, 42615..42743		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o4.tw	Method	TBLASTX:Wheat
Start	43358	End	43612
GI	none	Score	72
Exons	43358..43435, 43375..43443, 43375..43431, 43421..43435, 43426..43602, 43451..43612, 43455..43601, 43501..43611		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o4.tm	Method	TBLASTX:Maize
Start	46815	End	47078
GI	none	Score	375

Exons	46815..47078, 46874..47068		
Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o8.gp	Method	AAT/GAP
Start	47776	End	47916
GI	10494_1.R1084	Score	210
Exons	47776..47916		
GI Descrip.	'5730046/ref|NM_006632.1|SLC17A3| 1.0e-09 Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545_HSU90545 Human sodium phosphate transporter (NPT4) mRNA, complete cds'		
Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o9.gp	Method	AAT/GAP
Start	48054	End	48222
GI	2796959	Score	303
Exons	48054..48222		
Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o10.gs	Method	GENSCAN
Start	48413	End	55464
GI	none	Score	.73
Exons	48413..49184, 50141..50291, 51517..51624, 51681..52023, 53611..53910, 54012..54375, 54914..55161, 55297..55464		
Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o8.tm	Method	TBLASTX:Maize
Start	48673	End	49132
GI	none	Score	174
Exons	48673..48891, 48682..48897, 48716..49009, 48729..49007, 48998..49132, 49006..49122		
Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o8.np	Method	AAT/NAP
Start	53482	End	60455
GI	3522946	Score	687
Exons	53482..53910, 54012..54375, 54914..55161, 59031..59257, 60176..60455		
GI Descrip.	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]		
Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o1.tm	Method	TBLASTX:Maize
Start	53495	End	58234
GI	none	Score	69
Exons	53495..53584, 53503..53565, 53623..53682, 53710..53910,		

53753..53908, 53997..54200, 54013..54201, 57539..57709,
57656..57733, 57666..57737, 57761..57973, 57801..57971,
58120..58233, 58121..58234

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o3.ts	Method	TBLASTX:Soybean
Start	53500	End	60371
GI	none	Score	80
Exons	53500..53910, 53522..53671, 53780..53911, 53997..54191, 54946..55080, 55225..55389, 55444..55479, 56138..56269, 57534..57890, 57539..57961, 58741..58851, 59022..59123, 60240..60371		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o1.tc	Method	TBLASTX:Cress
Start	53509	End	57955
GI	none	Score	78
Exons	53509..53904, 53786..53893, 57560..57955, 57561..57944		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o7.tw	Method	TBLASTX:Wheat
Start	53623	End	57880
GI	none	Score	54
Exons	53623..53688, 53624..53674, 53680..53754, 53683..53829, 57662..57754, 57666..57722, 57732..57878, 57740..57880		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o2.tw	Method	TBLASTX:Wheat
Start	53830	End	58290
GI	none	Score	95
Exons	53830..53910, 53831..53908, 53833..53910, 54013..54207, 54048..54206, 57881..57961, 57882..57959, 58053..58121, 58054..58122, 58056..58184, 58058..58123, 58102..58290, 58103..58285		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o5.tm	Method	TBLASTX:Maize
Start	54896	End	59102
GI	none	Score	122
Exons	54896..55162, 54925..55164, 55300..55371, 58670..58936, 58687..58947, 58687..58935, 59031..59102, 59034..59096		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o13.tm	Method	TBLASTX:Maize
Start	56051	End	60360

GI	none	Score	103
Exons	56051..56119, 56084..56254, 56133..56246, 60174..60245, 60224..60331, 60237..60353, 60238..60360		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o12.gs	Method	GENSCAN
Start	57533	End	61649
GI	none	Score	.67
Exons	57533..57961, 58057..58393, 58688..58935, 59031..59257, 60176..60399, 61241..61365, 61391..61649		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o15.tm	Method	TBLASTX:Maize
Start	61224	End	61441
GI	none	Score	180
Exons	61224..61418, 61253..61441, 61254..61418, 61255..61428		

Seq. No.	52	Seq. ID	OJ990323_17.9819.C4
Gene No.	160	Strand	-
Start	48413	End	61692
Name	OJ990323_17.9819.C4.o16.tm	Method	TBLASTX:Maize
Start	61547	End	61692
GI	none	Score	143
Exons	61547..61690, 61549..61692, 61550..61690, 61572..61691		

Seq. No.	53	Seq. ID	OJ990323_17.9819.C6
Gene No.	161	Strand	-
Start	180	End	1175
Name	OJ990323_17.9819.C6.o1.gp	Method	AAT/GAP
Start	180	End	1175
GI	none	Score	564
Exons	180..281, 649..807, 882..991, 1139..1175		

Seq. No.	53	Seq. ID	OJ990323_17.9819.C6
Gene No.	161	Strand	-
Start	180	End	1175
Name	OJ990323_17.9819.C6.o1.np	Method	AAT/NAP
Start	627	End	946
GI	2245059	Score	77
Exons	627..946		
GI Descrip.	(Z97342) transcription factor like protein [Arabidopsis thaliana]		

Seq. No.	54	Seq. ID	OJ990323_17.9819.C7
Gene No.	162	Strand	-
Start	274	End	1755
Name	OJ990323_17.9819.C7.o1.gs	Method	GENSCAN
Start	274	End	1755
GI	none	Score	.79
Exons	274..331, 628..810, 1711..1755		

Seq. No.	55	Seq. ID	OJ990323_17.9819.C8
Gene No.	163	Strand	-

Start	1	End	750
Name	OJ990323_17.9819.C8.o1.np	Method	AAT/NAP
Start	1	End	750
GI	5902445	Score	1074
Exons	1..750		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	55	Seq. ID	OJ990323_17.9819.C8
Gene No.	163	Strand	-
Start	1	End	750
Name	OJ990323_17.9819.C8.o1.gs	Method	GENSCAN
Start	10	End	627
GI	none	Score	.68
Exons	10..279, 309..508, 536..627		

Seq. No.	55	Seq. ID	OJ990323_17.9819.C8
Gene No.	163	Strand	-
Start	1	End	750
Name	OJ990323_17.9819.C8.o1.tw	Method	TBLASTX:Wheat
Start	119	End	507
GI	none	Score	44
Exons	119..202, 120..164, 193..303, 193..504, 194..505, 340..507		

Seq. No.	55	Seq. ID	OJ990323_17.9819.C8
Gene No.	163	Strand	-
Start	1	End	750
Name	OJ990323_17.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	149	End	504
GI	none	Score	233
Exons	149..196, 187..504, 200..490		

Seq. No.	56	Seq. ID	OJ990323_17.9819.C9
Gene No.	164	Strand	-
Start	357	End	389
Name	OJ990323_17.9819.C9.o1.gs	Method	GENSCAN
Start	357	End	389
GI	none	Score	.92
Exons	357..389		

Seq. No.	57	Seq. ID	OJ990323_17.9819.C10
Gene No.	165	Strand	-
Start	361	End	513
Name	OJ990323_17.9819.C10.o1.gs	Method	GENSCAN
Start	361	End	513
GI	none	Score	.55
Exons	361..513		

Seq. No.	58	Seq. ID	OJ990323_17.9819.C13
Gene No.	166	Strand	-
Start	639	End	760
Name	OJ990323_17.9819.C13.o1.np	Method	AAT/NAP
Start	639	End	760
GI	4680186	Score	174
Exons	639..760		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	59	Seq. ID	OJ990323_19.9819.C2

Gene No.	167	Strand	+
Start	3637	End	4049
Name	OJ990323_19.9819.C2.o1.gp	Method	AAT/GAP
Start	3637	End	4049
GI	2315_6.R1084	Score	304
Exons	3637..3836, 4015..4049		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 4.0e-38 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	59	Seq. ID	OJ990323_19.9819.C2
Gene No.	168	Strand	+
Start	7098	End	10048
Name	OJ990323_19.9819.C2.o1.gs	Method	GENSCAN
Start	7098	End	10048
GI	none	Score	.46
Exons	7098..7304, 7395..7674, 7773..7872, 9128..9471, 9743..9852, 10016..10048		

Seq. No.	59	Seq. ID	OJ990323_19.9819.C2
Gene No.	169	Strand	-
Start	7348	End	7678
Name	OJ990323_19.9819.C2.o2.gp	Method	AAT/GAP
Start	7348	End	7678
GI	69014_1.R1084	Score	601
Exons	7348..7678		
GI Descrip.	'4680178/gb|AF111709.1|AF111709 1.0e-108 Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences; and unknown genes'		

Seq. No.	59	Seq. ID	OJ990323_19.9819.C2
Gene No.	170	Strand	-
Start	11919	End	13026
Name	OJ990323_19.9819.C2.o2.gs	Method	GENSCAN
Start	11919	End	13026
GI	none	Score	.77
Exons	11919..12301, 12720..13026		

Seq. No.	59	Seq. ID	OJ990323_19.9819.C2
Gene No.	171	Strand	-
Start	14590	End	15618
Name	OJ990323_19.9819.C2.o3.gs	Method	GENSCAN
Start	14590	End	15618
GI	none	Score	.54
Exons	14590..14679, 15538..15618		

Seq. No.	60	Seq. ID	OJ990323_19.9819.C3
Gene No.	172	Strand	-
Start	619	End	3094
Name	OJ990323_19.9819.C3.o1.gs	Method	GENSCAN
Start	619	End	3094
GI	none	Score	.49
Exons	619..709, 1826..1940, 2575..2590, 2978..3094		

Seq. No.	60	Seq. ID	OJ990323_19.9819.C3
Gene No.	173	Strand	-
Start	4190	End	4503
Name	OJ990323_19.9819.C3.o2.gs	Method	GENSCAN

Start	4190	End	4503
GI	none	Score	.93
Exons	4190..4321, 4431..4503		

Seq. No.	61	Seq. ID	OJ990323_19.9819.C4
Gene No.	174	Strand	-
Start	98	End	993
Name	OJ990323_19.9819.C4.o1.gs	Method	GENSCAN
Start	98	End	993
GI	none	Score	.42
Exons	98..647, 931..993		

Seq. No.	62	Seq. ID	OJ990323_19.9819.C5
Gene No.	175	Strand	+
Start	6239	End	7392
Name	OJ990323_19.9819.C5.o2.gs	Method	GENSCAN
Start	6239	End	7392
GI	none	Score	.92
Exons	6239..6244, 7258..7392		

Seq. No.	62	Seq. ID	OJ990323_19.9819.C5
Gene No.	176	Strand	-
Start	1	End	3323
Name	OJ990323_19.9819.C5.o1.np	Method	AAT/NAP
Start	1	End	3323
GI	5852175	Score	107
Exons	1..39, 1243..1413, 1990..2042, 3239..3323		
GI Descrip.	(AL117265) zhb0005.1 [Oryza sativa]		

Seq. No.	62	Seq. ID	OJ990323_19.9819.C5
Gene No.	176	Strand	-
Start	1	End	3323
Name	OJ990323_19.9819.C5.o1.gp	Method	AAT/GAP
Start	621	End	1220
GI	3761363	Score	865
Exons	621..1220		
GI Descrip.	5852170/emb|AL117265.1|OST17804 1.0e-151 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804		

Seq. No.	63	Seq. ID	OJ990323_19.9819.C6
Gene No.	177	Strand	-
Start	1250	End	2578
Name	OJ990323_19.9819.C6.o1.np	Method	AAT/NAP
Start	1078	End	1474
GI	2665788	Score	85
Exons	1078..1261, 1348..1474		
GI Descrip.	(AF035676) cellular nucleic acid binding protein [Gallus gallus]		

Seq. No.	63	Seq. ID	OJ990323_19.9819.C6
Gene No.	177	Strand	-
Start	1250	End	2578
Name	OJ990323_19.9819.C6.o1.gs	Method	GENSCAN
Start	1250	End	2578
GI	none	Score	.65
Exons	1250..2110, 2162..2578		

Seq. No.	64	Seq. ID	OJ990323_19.9819.C7

Gene No.	178	Strand	+
Start	435	End	594
Name	OJ990323_19.9819.C7.o1.gp	Method	AAT/GAP
Start	435	End	594
GI	LIB3433-006-Q6-K6-F12	Score	241
Exons	435..594		
GI Descrip.	'4388818/gb|AAD19773| 3.0e-40 (AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [Arabidopsis thaliana]'		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	179	Strand	+
Start	383	End	3222
Name	OJ990323_19.9819.C8.o1.gs	Method	GENSCAN
Start	383	End	3222
GI	none	Score	.84
Exons	383..1382, 3140..3222		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	180	Strand	+
Start	8084	End	9037
Name	OJ990323_19.9819.C8.o2.gs	Method	GENSCAN
Start	8084	End	9037
GI	none	Score	.98
Exons	8084..9037		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+
Start	10419	End	45124
Name	OJ990323_19.9819.C8.o3.gs	Method	GENSCAN
Start	10419	End	15717
GI	none	Score	.41
Exons	10419..10425, 14559..14710, 15086..15217, 15640..15717		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+
Start	10419	End	45124
Name	OJ990323_19.9819.C8.o5.np	Method	AAT/NAP
Start	11830	End	44677
GI	4982478	Score	203
Exons	11830..11863, 33953..34029, 41080..41173, 41643..41720, 44538..44677		
GI Descrip.	(AF069441) putative leucyl tRNA synthetase [Arabidopsis thaliana]		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+
Start	10419	End	45124
Name	OJ990323_19.9819.C8.o1.np	Method	AAT/NAP
Start	16320	End	19544
GI	6907089	Score	4136
Exons	16320..17581, 17675..19544		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+

Start	10419	End	45124
Name	OJ990323_19.9819.C8.o4.gs	Method	GENSCAN
Start	16320	End	19547
GI	none	Score	.95
Exons	16320..19547		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+
Start	10419	End	45124
Name	OJ990323_19.9819.C8.o3.np	Method	AAT/NAP
Start	26397	End	27915
GI	5922623	Score	409
Exons	26397..26477, 26853..27000, 27168..27243, 27842..27915		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016856|dbj|BAA85199.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+
Start	10419	End	45124
Name	OJ990323_19.9819.C8.o6.gs	Method	GENSCAN
Start	28360	End	29898
GI	none	Score	.53
Exons	28360..29518, 29813..29898		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+
Start	10419	End	45124
Name	OJ990323_19.9819.C8.o7.gs	Method	GENSCAN
Start	33302	End	35392
GI	none	Score	.96
Exons	33302..34529, 35307..35392		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	181	Strand	+
Start	10419	End	45124
Name	OJ990323_19.9819.C8.o9.gs	Method	GENSCAN
Start	43741	End	45124
GI	none	Score	.59
Exons	43741..43832, 43844..43930, 43951..44037, 44862..45023, 45121..45124		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	182	Strand	+
Start	47104	End	47582
Name	OJ990323_19.9819.C8.o1.gp	Method	AAT/GAP
Start	47104	End	47366
GI	2315_5.R1084	Score	355
Exons	47104..47366		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 1.0e-14 Oxyza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	182	Strand	+
Start	47104	End	47582
Name	OJ990323_19.9819.C8.o2.gp	Method	AAT/GAP
Start	47170	End	47582

GI	2315_6.R1084	Score	304
Exons	47170..47369, 47548..47582		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 4.0e-38 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	183	Strand	-
Start	20168	End	25814
Name	OJ990323_19:9819.C8.o2.np	Method	AAT/NAP
Start	20168	End	25814
GI	6498441	Score	6802
Exons	20168..20449, 20543..21940, 22112..22594, 22787..23027, 23202..23336, 23520..23893, 23957..24420, 24751..25814		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o5.tm	Method	TBLASTX:Maize
Start	20126	End	20308
GI	none	Score	122
Exons	20126..20308, 20127..20303		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o6.tw	Method	TBLASTX:Wheat
Start	20177	End	20779
GI	none	Score	85
Exons	20177..20302, 20181..20303, 20333..20392, 20489..20779, 20496..20774		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o4.tw	Method	TBLASTX:Wheat
Start	20780	End	21161
GI	none	Score	162
Exons	20780..21160, 20811..21059, 21105..21161		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o2.tm	Method	TBLASTX:Maize
Start	20975	End	21298
GI	none	Score	193
Exons	20975..21298, 20988..21269		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o8.tw	Method	TBLASTX:Wheat
Start	21491	End	21790
GI	none	Score	64
Exons	21491..21742, 21602..21790		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o5.tw	Method	TBLASTX:Wheat
Start	21806	End	22240
GI	none	Score	88
Exons	21806..21946, 21810..21944, 22002..22175, 22016..22225, 22016..22240		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o1.ts	Method	TBLASTX:Soybean
Start	22865	End	23236
GI	none	Score	90
Exons	22865..23236, 23076..23219		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o2.tw	Method	TBLASTX:Wheat
Start	22890	End	23314
GI	none	Score	283
Exons	22890..23216, 22895..23314, 23125..23313		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o3.tm	Method	TBLASTX:Maize
Start	22988	End	23372
GI	none	Score	166
Exons	22988..23371, 23007..23228, 23286..23372		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	23399	End	23755
GI	none	Score	110
Exons	23399..23701, 23399..23755, 23409..23720		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o1.tw	Method	TBLASTX:Wheat
Start	23423	End	23886
GI	none	Score	400
Exons	23423..23884, 23424..23885, 23443..23886		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o2.ts	Method	TBLASTX:Soybean
Start	23480	End	23845
GI	none	Score	117
Exons	23480..23614, 23621..23845		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o3.tw	Method	TBLASTX:Wheat
Start	24053	End	24536
GI	none	Score	165
Exons	24053..24535, 24081..24341, 24363..24536		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o7.tw	Method	TBLASTX:Wheat
Start	25274	End	25666
GI	none	Score	89
Exons	25274..25531, 25308..25547, 25514..25612, 25515..25595, 25619..25666		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o4.tm	Method	TBLASTX:Maize
Start	25376	End	25661
GI	none	Score	103
Exons	25376..25624, 25377..25661		

Seq. No.	65	Seq. ID	OJ990323_19.9819.C8
Gene No.	184	Strand	-
Start	26553	End	47815
Name	OJ990323_19.9819.C8.o4.np	Method	AAT/NAP
Start	26553	End	47815
GI	5042454	Score	131
Exons	26553..26608, 26838..27000, 47792..47815		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	66	Seq. ID	OJ990203_08.9819.C3
Gene No.	185	Strand	+
Start	1005	End	1075
Name	OJ990203_08.9819.C3.o1.gs	Method	GENSCAN
Start	1005	End	1075
GI	none	Score	.79
Exons	1005..1075		

Seq. No.	67	Seq. ID	OJ990203_08.9819.C5
Gene No.	186	Strand	+
Start	802	End	1056
Name	OJ990203_08.9819.C5.o1.gp	Method	AAT/GAP
Start	802	End	1056
GI	2311684	Score	478
Exons	802..1056		

Seq. No.	67	Seq. ID	OJ990203_08.9819.C5
Gene No.	187	Strand	-
Start	994	End	1078
Name	OJ990203_08.9819.C5.o1.gs	Method	GENSCAN
Start	994	End	1078
GI	none	Score	.5

Exons	994..1078		
Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	188	Strand	+
Start	2786	End	3315
Name	OJ990203_08.9819.C7.o1.gs	Method	GENSCAN
Start	2786	End	3315
GI	none	Score	.78
Exons	2786..3229, 3286..3315		
Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	189	Strand	+
Start	3915	End	6559
Name	OJ990203_08.9819.C7.o1.gp	Method	AAT/GAP
Start	3844	End	5966
GI	4464_1.R1084	Score	1573
Exons	3844..4037, 5147..5185, 5261..5488, 5602..5966		
GI Descrip.	'400989/sp|Q02764|RK24_TOBAC 2.0e-54 50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24) >gi_322771_pir__A45113 ribosomal protein L24 precursor - common tobacco >gi_170273 (M87838) ribosomal protein L24 [Nicotiana tabacum] >gi_170324 (M87839) ribosomal protein L24 [Nicotiana tabacum]'		
Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	189	Strand	+
Start	3915	End	6559
Name	OJ990203_08.9819.C7.o2.gs	Method	GENSCAN
Start	3915	End	5784
GI	none	Score	.83
Exons	3915..4037, 5147..5185, 5261..5488, 5602..5784		
Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	189	Strand	+
Start	3915	End	6559
Name	OJ990203_08.9819.C7.o2.np	Method	AAT/NAP
Start	4478	End	6559
GI	132819	Score	453
Exons	4478..4584, 5215..5482, 5596..5759, 6520..6559		
GI Descrip.	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24) gi|71307|pir||R5PM24 ribosomal protein L24 precursor, chloroplast - garden pea gi|20873|emb|CAA32185| (X14020) CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]		
Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	190	Strand	+
Start	6647	End	6763
Name	OJ990203_08.9819.C7.o2.tc	Method	TBLASTX:Cress
Start	967	End	1335
GI	none	Score	36
Exons	967..1023, 980..1024, 1117..1182, 1118..1183, 1263..1328, 1264..1335		
Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	190	Strand	+
Start	6647	End	6763
Name	OJ990203_08.9819.C7.o2.ts	Method	TBLASTX:Soybean
Start	967	End	1373

GI	none	Score	65
Exons	967..1023, 971..1027, 1099..1182, 1109..1177, 1263..1373, 1270..1308		

Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	190	Strand	+
Start	6647	End	6763
Name	OJ990203_08.9819.C7.o1.tm	Method	TBLASTX:Maize
Start	3912	End	5823
GI	none	Score	95
Exons	3912..3992, 3914..3991, 3970..4038, 3971..4039, 5146..5175, 5153..5182, 5231..5491, 5244..5366, 5254..5487, 5601..5819, 5602..5766, 5602..5823		

Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	190	Strand	+
Start	6647	End	6763
Name	OJ990203_08.9819.C7.o1.tc	Method	TBLASTX:Cress
Start	5247	End	5751
GI	none	Score	86
Exons	5247..5342, 5250..5465, 5258..5467, 5260..5466, 5599..5751, 5599..5751		

Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	190	Strand	+
Start	6647	End	6763
Name	OJ990203_08.9819.C7.o1.ts	Method	TBLASTX:Soybean
Start	5248	End	5760
GI	none	Score	144
Exons	5248..5454, 5250..5351, 5254..5466, 5255..5467, 5594..5752, 5599..5760, 5601..5750		

Seq. No.	68	Seq. ID	OJ990203_08.9819.C7
Gene No.	190	Strand	+
Start	6647	End	6763
Name	OJ990203_08.9819.C7.o3.np	Method	AAT/NAP
Start	6647	End	6763
GI	2911360	Score	93
Exons	6647..6763		
GI Descrip.	(AF041044) NADPH HC toxin reductase [Zea mays]		

Seq. No.	69	Seq. ID	OJ990203_08.9819.C8
Gene No.	191	Strand	+
Start	1	End	1324
Name	OJ990203_08.9819.C8.o1.np	Method	AAT/NAP
Start	1	End	1320
GI	3269286	Score	394
Exons	1..70, 205..431, 533..742, 806..1029, 1165..1320		
GI Descrip.	(AL030978) putative protein [Arabidopsis thaliana]		

Seq. No.	69	Seq. ID	OJ990203_08.9819.C8
Gene No.	191	Strand	+
Start	1	End	1324
Name	OJ990203_08.9819.C8.o1.gs	Method	GENSCAN
Start	205	End	1324
GI	none	Score	.81
Exons	205..431, 533..716, 806..932, 1153..1324		

Seq. No.	69	Seq. ID	OJ990203_08.9819.C8
Gene No.	192	Strand	-
Start	1823	End	2515
Name	OJ990203_08.9819.C8.o1.ts	Method	TBLASTX:Soybean
Start	1820	End	1993
GI	none	Score	99
Exons	1820..1993, 1823..1993		

Seq. No.	69	Seq. ID	OJ990203_08.9819.C8
Gene No.	192	Strand	-
Start	1823	End	2515
Name	OJ990203_08.9819.C8.o2.gs	Method	GENSCAN
Start	1823	End	2515
GI	none	Score	.56
Exons	1823..2275, 2366..2515		

Seq. No.	69	Seq. ID	OJ990203_08.9819.C8
Gene No.	192	Strand	-
Start	1823	End	2515
Name	OJ990203_08.9819.C8.o2.np	Method	AAT/NAP
Start	1826	End	2459
GI	3269285	Score	530
Exons	1826..2459		
GI Descrip.	(AL030978) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	69	Seq. ID	OJ990203_08.9819.C8
Gene No.	192	Strand	-
Start	1823	End	2515
Name	OJ990203_08.9819.C8.o1.tc	Method	TBLASTX:Cress
Start	1829	End	2284
GI	none	Score	79
Exons	1829..1930, 1970..2017, 2135..2200, 2174..2284, 2181..2282		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o2.gp	Method	AAT/GAP
Start	3028	End	4261
GI	38125_1.R1084	Score	901
Exons	3028..3249, 3875..4066, 4179..4261		
GI Descrip.	'3402751/emb|CAA20197.1| 8.0e-32 (AL031187) putative protein [Arabidopsis thaliana]'		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o2.gs	Method	GENSCAN
Start	3088	End	5153
GI	none	Score	.67
Exons	3088..3249, 3875..3997, 4179..4389, 4431..4454, 4710..4876, 5034..5153		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o2.np	Method	AAT/NAP

Start	3118	End	15715
GI	3402751	Score	749
Exons	3118..3221, 3850..4066, 4179..4389, 4653..4897, 4963..5097, 15678..15715		
GI Descrip.	(AL031187) putative protein [Arabidopsis thaliana]		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o3.gs	Method	GENSCAN
Start	5667	End	10878
GI	none	Score	.8
Exons	5667..5814, 5816..6049, 7864..7910, 8685..8804, 9315..9412, 9718..9926, 10088..10284, 10840..10878		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o4.gp	Method	AAT/GAP
Start	6198	End	6755
GI	none	Score	1088
Exons	6198..6755		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o5.gp	Method	AAT/GAP
Start	7114	End	7508
GI	none	Score	790
Exons	7114..7508		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o6.gp	Method	AAT/GAP
Start	9321	End	10185
GI	none	Score	822
Exons	9321..9412, 9544..9615, 9727..9926, 10088..10185		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o3.np	Method	AAT/NAP
Start	12657	End	15158
GI	2827514	Score	834
Exons	12657..13582, 14374..14584, 15129..15158		
GI Descrip.	(AL021633) predicted protein [Arabidopsis thaliana]		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	193	Strand	+
Start	3088	End	15942
Name	OJ990203_08.9819.C9.o4.gs	Method	GENSCAN
Start	12657	End	15942
GI	none	Score	.62
Exons	12657..13582, 14374..14579, 15353..15942		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9

Gene No.	194	Strand	+
Start	16945	End	17785
Name	OJ990203_08.9819.C9.o5.gs	Method	GENSCAN
Start	16945	End	17785
GI	none	Score	.85
Exons	16945..16960, 17649..17785		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	195	Strand	+
Start	19293	End	23401
Name	OJ990203_08.9819.C9.o6.gs	Method	GENSCAN
Start	19293	End	23401
GI	none	Score	.93
Exons	19293..20034, 22606..22766, 23360..23401		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	196	Strand	+
Start	25084	End	34630
Name	OJ990203_08.9819.C9.o7.gs	Method	GENSCAN
Start	25084	End	34630
GI	none	Score	.41
Exons	25084..25194, 25329..25412, 26197..26348, 27876..28091, 28942..29085, 30240..30459, 33004..33278, 33322..33425, 34067..34436, 34456..34630		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	196	Strand	+
Start	25084	End	34630
Name	OJ990203_08.9819.C9.o12.gp	Method	AAT/GAP
Start	29148	End	29765
GI	55573_1.R1084	Score	1151
Exons	29148..29765		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	197	Strand	-
Start	1	End	2063
Name	OJ990203_08.9819.C9.o1.np	Method	AAT/NAP
Start	1	End	2063
GI	3269285	Score	206
Exons	1..555, 598..855, 2016..2063		
GI Descrip.	(AL030978) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	197	Strand	-
Start	1	End	2063
Name	OJ990203_08.9819.C9.o1.gp	Method	AAT/GAP
Start	174	End	475
GI	none	Score	545
Exons	174..475		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	197	Strand	-
Start	1	End	2063
Name	OJ990203_08.9819.C9.o1.gs	Method	GENSCAN
Start	174	End	816

GI	none	Score	.62
Exons	174..816		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	198	Strand	-
Start	5189	End	5348
Name	OJ990203_08.9819.C9.o3.gp	Method	AAT/GAP
Start	5189	End	5348
GI	5005099	Score	289
Exons	5189..5348		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	199	Strand	-
Start	10838	End	11297
Name	OJ990203_08.9819.C9.o7.gp	Method	AAT/GAP
Start	10838	End	11297
GI	uC-osroM202001b09a1	Score	885
Exons	10838..11297		
GI Descrip.	'3789942 8.0e-27 (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]'		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	200	Strand	-
Start	17261	End	17428
Name	OJ990203_08.9819.C9.o8.gp	Method	AAT/GAP
Start	17261	End	17428
GI	3769020	Score	299
Exons	17261..17428		
GI Descrip.	3789942 8.0e-27 (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	201	Strand	-
Start	21609	End	21863
Name	OJ990203_08.9819.C9.o9.gp	Method	AAT/GAP
Start	21609	End	21863
GI	2311684	Score	478
Exons	21609..21863		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	202	Strand	-
Start	22281	End	22700
Name	OJ990203_08.9819.C9.o10.gp	Method	AAT/GAP
Start	22281	End	22700
GI	LIB3474-007-P1-K1-G11	Score	840
Exons	22281..22700		
GI Descrip.	'3789942 8.0e-27 (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]'		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o1.tm	Method	TBLASTX:Maize
Start	3043	End	5099
GI	none	Score	172
Exons	3043..3249, 3186..3251, 3872..4075, 3873..4073, 3874..4080, 4176..4379, 4176..4373, 4178..4384, 4178..4384, 4652..4882,		

4652..4882, 4744..4887, 5033..5098, 5034..5099

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o1.ts	Method	TBLASTX:Soybean
Start	3865	End	5096
GI	none	Score	257
Exons	3865..4077, 3866..4075, 3901..4077, 4176..4385, 4176..4364, 4178..4375, 4651..4881, 4652..4882, 4686..4889, 5034..5096		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o4.tm	Method	TBLASTX:Maize
Start	8600	End	10284
GI	none	Score	42
Exons	8600..8653, 8745..8804, 9310..9414, 9312..9413, 9318..9428, 9541..9615, 9542..9616, 9707..9802, 9725..9805, 9809..9871, 9812..9889, 9878..9940, 10069..10215, 10088..10252, 10088..10201, 10213..10284, 10228..10284		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o3.tm	Method	TBLASTX:Maize
Start	13386	End	14450
GI	none	Score	296
Exons	13386..13580, 13389..13580, 13409..13585, 13409..13582, 14365..14439, 14372..14449, 14373..14450		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o2.ts	Method	TBLASTX:Soybean
Start	13392	End	14539
GI	none	Score	245
Exons	13392..13589, 13409..13591, 14365..14442, 14372..14539, 14399..14536		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o2.tm	Method	TBLASTX:Maize
Start	15519	End	15849
GI	none	Score	241
Exons	15519..15845, 15522..15842, 15523..15846, 15598..15849		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o5.np	Method	AAT/NAP
Start	33491	End	35424
GI	6522536	Score	340
Exons	33491..33520, 34835..35424		
GI Descrip.	(AL132955) putative protein [Arabidopsis thaliana]		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o8.gs	Method	GENSCAN
Start	34812	End	35351
GI	none	Score	.88
Exons	34812..35351		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o5.tm	Method	TBLASTX:Maize
Start	34836	End	35195
GI	none	Score	58
Exons	34836..35195, 34864..34971, 35040..35186		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o1.tc	Method	TBLASTX:Cress
Start	35046	End	35381
GI	none	Score	69
Exons	35046..35198, 35223..35381, 35239..35376		

Seq. No.	70	Seq. ID	OJ990203_08.9819.C9
Gene No.	203	Strand	-
Start	33491	End	35424
Name	OJ990203_08.9819.C9.o3.ts	Method	TBLASTX:Soybean
Start	35058	End	35342
GI	none	Score	126
Exons	35058..35195, 35202..35342		

Seq. No.	71	Seq. ID	OJ990203_08.9819.C10
Gene No.	204	Strand	+
Start	267	End	1471
Name	OJ990203_08.9819.C10.o1.tc	Method	TBLASTX:Cress
Start	160	End	307
GI	none	Score	221
Exons	160..306, 161..307, 188..307		

Seq. No.	71	Seq. ID	OJ990203_08.9819.C10
Gene No.	204	Strand	+
Start	267	End	1471
Name	OJ990203_08.9819.C10.o1.np	Method	AAT/NAP
Start	267	End	1471
GI	1196998	Score	2044
Exons	267..1471		
GI Descrip.	(J01829) unknown protein [Transposon Tn10] gi|5103202|dbj|BAA78838.1| (AP000342) transposase of Tn10 [Plasmid R100] gi|5706382|dbj|BAA83097.1| (AB026428) transposase [Methylomonas aminofaciens] gi|5738092|gb|AAD50250.1|AF162223_9 (AF162223) IS10-right transposase [Shigella flexneri] gi|6721110|gb|AAF26764.1|AC007396_13 (AC007396) T4O12.21 [Arabidopsis thaliana]		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	205	Strand	+

Start	65	End	18984
Name	OJ990203_08.9819.C15.o1.gs	Method	GENSCAN
Start	65	End	11203
GI	none	Score	.72
Exons	65..109, 294..625, 2254..2379, 5000..5077, 6061..6165, 7606..7817, 7889..7962, 7980..8090, 8176..8414, 10984..11203		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	205	Strand	+
Start	65	End	18984
Name	OJ990203_08.9819.C15.o1.gp	Method	AAT/GAP
Start	7619	End	8408
GI	20679_1.R1084	Score	951
Exons	7619..7883, 7980..8170, 8252..8408		
GI Descrip.	'4204761 7.0e-65 (U51192) peroxidase precursor [Glycine max]'		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	205	Strand	+
Start	65	End	18984
Name	OJ990203_08.9819.C15.o2.gp	Method	AAT/GAP
Start	8332	End	18984
GI	19497_1.R1084	Score	1272
Exons	8332..8414, 18380..18984		
GI Descrip.	'678547 2.0e-42 (L13654) peroxidase [Lycopersicon esculentum]'		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	205	Strand	+
Start	65	End	18984
Name	OJ990203_08.9819.C15.o2.np	Method	AAT/NAP
Start	18529	End	18829
GI	2599086	Score	203
Exons	18529..18829		
GI Descrip.	(AF028073) peroxidase [Pinus taeda]		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	206	Strand	+
Start	20561	End	23538
Name	OJ990203_08.9819.C15.o3.gp	Method	AAT/GAP
Start	20561	End	22100
GI	none	Score	938
Exons	20561..20871, 21902..22100		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	206	Strand	+
Start	20561	End	23538
Name	OJ990203_08.9819.C15.o3.gs	Method	GENSCAN
Start	21907	End	23538
GI	none	Score	.74
Exons	21907..22479, 22570..22990, 23180..23538		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	206	Strand	+
Start	20561	End	23538
Name	OJ990203_08.9819.C15.o3.np	Method	AAT/NAP
Start	21958	End	23493
GI	6642657	Score	1134
Exons	21958..22479, 22570..22990, 23180..23493		

GI Descrip.	(AC012395) putative integral membrane protein [Arabidopsis thaliana]		
Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	207	Strand	-
Start	11301	End	20847
Name	OJ990203_08.9819.C15.o2.gs	Method	GENSCAN
Start	11301	End	20847
GI	none	Score	62
Exons	11301..11519, 11994..12111, 12306..16226, 16404..16451, 16456..16639, 16779..16983, 18388..18850, 19519..19640, 20590..20847		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	207	Strand	-
Start	11301	End	20847
Name	OJ990203_08.9819.C15.o1.np	Method	AAT/NAP
Start	12305	End	16210
GI	6539553	Score	6778
Exons	12305..16210		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o2.tm	Method	TBLASTX:Maize
Start	7745	End	18441
GI	none	Score	184
Exons	7745..7882, 7749..7883, 7980..8084, 7983..8111, 8023..8112, 8084..8197, 8093..8170, 8251..8331, 8252..8332, 8326..8427, 8327..8428, 18397..18441		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o2.ts	Method	TBLASTX:Soybean
Start	7755	End	18798
GI	none	Score	144
Exons	7755..7883, 7979..7996, 7980..8012, 8022..8084, 8089..8160, 8093..8161, 8233..8427, 8252..8428, 18376..18450, 18378..18440, 18451..18516, 18528..18578, 18532..18798, 18693..18788		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o6.tw	Method	TBLASTX:Wheat
Start	7755	End	18432
GI	none	Score	88
Exons	7755..7880, 7977..8018, 7980..8057, 8060..8167, 8086..8160, 8252..8428, 18376..18432		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793

Name	OJ990203_08.9819.C15.o2.tc	Method	TBLASTX:Cress
Start	7758	End	18798
GI	none	Score	140
Exons	7758..7883, 7980..8012, 7998..8084, 8061..8099, 8093..8161, 8104..8157, 8230..8427, 8252..8428, 18376..18465, 18451..18798, 18498..18578, 18702..18782		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o2.tw	Method	TBLASTX:Wheat
Start	12441	End	12917
GI	none	Score	376
Exons	12441..12827, 12442..12825, 12479..12826, 12520..12828, 12842..12916, 12846..12917		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o6.ts	Method	TBLASTX:Soybean
Start	12569	End	12910
GI	none	Score	79
Exons	12569..12778, 12648..12773, 12797..12910, 12804..12884		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o6.tm	Method	TBLASTX:Maize
Start	12773	End	13112
GI	none	Score	190
Exons	12773..13111, 12774..13112		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o3.ts	Method	TBLASTX:Soybean
Start	12923	End	13268
GI	none	Score	129
Exons	12923..13267, 13068..13268		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o3.tw	Method	TBLASTX:Wheat
Start	13121	End	13666
GI	none	Score	48
Exons	13121..13327, 13131..13253, 13322..13666, 13346..13519		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o5.tm	Method	TBLASTX:Maize
Start	13202	End	13667
GI	none	Score	55
Exons	13202..13666, 13305..13415, 13349..13531, 13485..13667		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15

Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o1.ts	Method	TBLASTX:Soybean
Start	13337	End	13801
GI	5509260	Score	58
Exons	13337..13801, 13356..13415, 13488..13583, 13632..13700		
GI Descrip.	-		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o3.tc	Method	TBLASTX:Cress
Start	13448	End	13708
GI	none	Score	62
Exons	13448..13708, 13629..13706		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o1.tw	Method	TBLASTX:Wheat
Start	13721	End	14476
GI	none	Score	200
Exons	13721..13960, 13722..13880, 13738..13968, 13741..13938, 13989..14468, 14012..14476		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o4.ts	Method	TBLASTX:Soybean
Start	14126	End	14524
GI	none	Score	38
Exons	14126..14299, 14253..14291, 14300..14524, 14346..14516		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o7.tm	Method	TBLASTX:Maize
Start	14312	End	14746
GI	none	Score	84
Exons	14312..14746, 14337..14537		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o5.tw	Method	TBLASTX:Wheat
Start	14477	End	14668
GI	none	Score	186
Exons	14477..14668, 14477..14668		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o7.ts	Method	TBLASTX:Soybean
Start	14534	End	14920
GI	none	Score	88
Exons	14534..14782, 14765..14920		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o3.tm	Method	TBLASTX:Maize
Start	14947	End	15269
GI	none	Score	395
Exons	14947..15114, 14948..15262, 14949..15242, 15015..15269		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o4.tm	Method	TBLASTX:Maize
Start	15768	End	16081
GI	none	Score	297
Exons	15768..16073, 15770..16081		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o4.tw	Method	TBLASTX:Wheat
Start	15829	End	16216
GI	none	Score	258
Exons	15829..16092, 15830..16216, 15831..16205		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o8.tm	Method	TBLASTX:Maize
Start	18376	End	18798
GI	none	Score	34
Exons	18376..18396, 18460..18504, 18504..18578, 18505..18798, 18621..18797		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o1.tm	Method	TBLASTX:Maize
Start	21901	End	22671
GI	none	Score	304
Exons	21901..22269, 21918..22238, 21919..22272, 22047..22271, 22266..22484, 22271..22333, 22275..22460, 22373..22483, 22506..22670, 22569..22667, 22570..22671		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o8.ts	Method	TBLASTX:Soybean
Start	21915	End	22170
GI	none	Score	190
Exons	21915..22166, 21949..22170		

Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o1.tc	Method	TBLASTX:Cress
Start	22242	End	22779
GI	none	Score	199

Exons	22242..22460, 22351..22479, 22509..22778, 22569..22697, 22570..22779		
Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o5.ts	Method	TBLASTX:Soybean
Start	22575	End	22845
GI	none	Score	113
Exons	22575..22775, 22575..22778, 22576..22779, 22783..22845		
Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o9.tm	Method	TBLASTX:Maize
Start	22750	End	23007
GI	none	Score	176
Exons	22750..22863, 22750..23007, 22754..22999, 22755..23006, 22933..23007		
Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o4.gs	Method	GENSCAN
Start	24365	End	26793
GI	none	Score	.63
Exons	24365..24996, 26613..26793		
Seq. No.	72	Seq. ID	OJ990203_08.9819.C15
Gene No.	208	Strand	-
Start	24365	End	26793
Name	OJ990203_08.9819.C15.o4.gp	Method	AAT/GAP
Start	26366	End	26441
GI	LIB3431-004-P1-K1-G12	Score	116
Exons	26366..26441		
GI Descrip.	'4680203/gb|AAD27566.1|AF114171_7 1.0e-39 (AF114171) TNP2-like protein [Sorghum bicolor]'		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	209	Strand	+
Start	1	End	5968
Name	OJ990203_08.9819.C16.o1.np	Method	AAT/NAP
Start	1	End	4978
GI	6069646	Score	1011
Exons	1..429, 2900..3728, 4011..4978		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	209	Strand	+
Start	1	End	5968
Name	OJ990203_08.9819.C16.o1.gs	Method	GENSCAN
Start	572	End	5968
GI	none	Score	.53

Exons	572..1375, 1555..3402, 3433..3787, 4364..4539, 4694..4724, 4744..4838, 5318..5968		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	209	Strand	+
Start	1	End	5968
Name	OJ990203_08.9819.C16.o3.np	Method	AAT/NAP
Start	1303	End	4978
GI	6069646	Score	1014
Exons	1303..1354, 2900..3728, 4011..4978		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	210	Strand	+
Start	24062	End	24316
Name	OJ990203_08.9819.C16.o6.gs	Method	GENSCAN
Start	24062	End	24316
GI	none	Score	.78
Exons	24062..24316		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	211	Strand	+
Start	25991	End	27172
Name	OJ990203_08.9819.C16.o6.np	Method	AAT/NAP
Start	25991	End	26727
GI	320608	Score	1119
Exons	25991..26727		
GI Descrip.	ubiquitin precursor - wild oat gi|15989|emb|CAA49200| (X69422) tetraubiquitin [Avena fatua] gi|777758 (L41658) polyubiquitin [Saccharum sp.]		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	211	Strand	+
Start	25991	End	27172
Name	OJ990203_08.9819.C16.o7.gs	Method	GENSCAN
Start	25991	End	27172
GI	none	Score	.85
Exons	25991..26676, 27136..27172		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	212	Strand	-
Start	6397	End	9284
Name	OJ990203_08.9819.C16.o2.gs	Method	GENSCAN
Start	6397	End	9284
GI	none	Score	.99
Exons	6397..6560, 7251..7422, 7513..7620, 7710..9284		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	213	Strand	-
Start	11978	End	13071
Name	OJ990203_08.9819.C16.o3.gs	Method	GENSCAN
Start	11978	End	12973
GI	none	Score	.58

Exons	11978..12388, 12475..12683, 12793..12973		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	213	Strand	-
Start	11978	End	13071
Name	OJ990203_08.9819.C16.o4.np	Method	AAT/NAP
Start	12181	End	12973
GI	3738326	Score	200
Exons	12181..12399, 12457..12683, 12793..12973		
GI Descrip.	(AC005170) nodulin-like protein [Arabidopsis thaliana]		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	213	Strand	-
Start	11978	End	13071
Name	OJ990203_08.9819.C16.o1.gp	Method	AAT/GAP
Start	12593	End	13071
GI	LIB3474-008-P1-K1-C12	Score	583
Exons	12593..12683, 12793..13071		
GI Descrip.	'3449320/dbj|AB016879.1|AB016879 5.0e-10 Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRB17, complete sequence'		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	214	Strand	-
Start	13811	End	19388
Name	OJ990203_08.9819.C16.o5.np	Method	AAT/NAP
Start	13811	End	15695
GI	2459428	Score	95
Exons	13811..13850, 15380..15493, 15638..15695		
GI Descrip.	(AC002332) unknown protein [Arabidopsis thaliana]		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	214	Strand	-
Start	13811	End	19388
Name	OJ990203_08.9819.C16.o4.gs	Method	GENSCAN
Start	14111	End	19341
GI	none	Score	.77
Exons	14111..14343, 14733..14882, 15450..15493, 15638..15713, 17551..17667, 18945..18988, 19256..19341		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	214	Strand	-
Start	13811	End	19388
Name	OJ990203_08.9819.C16.o2.gp	Method	AAT/GAP
Start	17924	End	19388
GI	1632667	Score	789
Exons	17924..18285, 18945..18988, 19357..19388		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	215	Strand	-
Start	20643	End	21106
Name	OJ990203_08.9819.C16.o5.gs	Method	GENSCAN
Start	20643	End	21106
GI	none	Score	.98
Exons	20643..20712, 20943..21106		
Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-

Start	26323	End	26915
Name	OJ990203_08.9819.C16.o4.tm	Method	TBLASTX:Maize
Start	1830	End	2109
GI	none	Score	176
Exons	1830..1991, 1831..1992, 1969..2109, 2022..2084		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o5.tm	Method	TBLASTX:Maize
Start	2740	End	3015
GI	none	Score	246
Exons	2740..3015, 2766..3014		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o3.tw	Method	TBLASTX:Wheat
Start	2821	End	3156
GI	none	Score	84
Exons	2821..2961, 2950..3156		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o2.tm	Method	TBLASTX:Maize
Start	3016	End	3951
GI	none	Score	264
Exons	3016..3429, 3499..3951		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o4.tw	Method	TBLASTX:Wheat
Start	3166	End	3485
GI	none	Score	179
Exons	3166..3471, 3171..3485		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o2.ts	Method	TBLASTX:Soybean
Start	3562	End	4101
GI	none	Score	165
Exons	3562..3888, 3969..4064, 3982..4101		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o2.tw	Method	TBLASTX:Wheat
Start	3583	End	4023
GI	none	Score	55
Exons	3583..3636, 3585..3854, 3691..3885, 3898..4023		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915

Name	OJ990203_08.9819.C16.o3.tm	Method	TBLASTX:Maize
Start	4408	End	18156
GI	none	Score	184
Exons	4408..4659, 4440..4658, 4629..4943, 4632..4883, 5363..5944, 5410..5673, 5741..5899, 17946..18152, 17947..18156		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o2.tc	Method	TBLASTX:Cress
Start	12430	End	12944
GI	none	Score	86
Exons	12430..12582, 12455..12574, 12598..12684, 12794..12883, 12861..12944		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o6.tm	Method	TBLASTX:Maize
Start	12613	End	12995
GI	none	Score	34
Exons	12613..12705, 12671..12703, 12788..12913, 12794..12901, 12804..12995		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o1.tc	Method	TBLASTX:Cress
Start	25969	End	26704
GI	none	Score	1091
Exons	25969..26673, 25969..26673, 25979..26041, 25983..26183, 25985..26644, 25988..26041, 25990..26673, 25990..26673, 25991..26644, 25991..26644, 25991..26644, 25991..26446, 26114..26227, 26338..26646, 26338..26457, 26342..26704, 26342..26704, 26345..26704, 26345..26683, 26345..26701, 26350..26646, 26447..26686, 26449..26646		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o1.tm	Method	TBLASTX:Maize
Start	25979	End	26707
GI	none	Score	1088
Exons	25979..26050, 25988..26644, 25990..26673, 25990..26499, 25990..26049, 25991..26503, 25992..26276, 26342..26707, 26342..26500, 26345..26704, 26447..26704, 26598..26657, 26598..26657		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o1.tw	Method	TBLASTX:Wheat
Start	25979	End	26704
GI	none	Score	1088
Exons	25979..26050, 25979..26050, 25983..26078, 25988..26644, 25988..26050, 25990..26673, 25990..26448, 25991..26449, 26342..26704, 26447..26704, 26598..26657, 26598..26651		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o1.ts	Method	TBLASTX:Soybean
Start	25985	End	26704
GI	none	Score	1089
Exons	25985..26644, 25990..26673, 25990..26673, 25990..26673, 25991..26644, 25991..26644, 25991..26446, 26342..26704, 26345..26695, 26345..26680, 26441..26704, 26447..26695, 26521..26646		

Seq. No.	73	Seq. ID	OJ990203_08.9819.C16
Gene No.	216	Strand	-
Start	26323	End	26915
Name	OJ990203_08.9819.C16.o3.gp	Method	AAT/GAP
Start	26323	End	26915
GI	3769020	Score	677
Exons	26323..26510, 26727..26915		
GI Descrip.	3789942 8.0e-27 (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]		

Seq. No.	74	Seq. ID	OJ990203_08.9819.C17
Gene No.	217	Strand	+
Start	361	End	852
Name	OJ990203_08.9819.C17.o1.np	Method	AAT/NAP
Start	361	End	852
GI	2827514	Score	648
Exons	361..852		
GI Descrip.	(AL021633) predicted protein [Arabidopsis thaliana]		

Seq. No.	74	Seq. ID	OJ990203_08.9819.C17
Gene No.	217	Strand	+
Start	361	End	852
Name	OJ990203_08.9819.C17.o1.tm	Method	TBLASTX:Maize
Start	435	End	765
GI	none	Score	241
Exons	435..761, 438..758, 514..765		

Seq. No.	75	Seq. ID	OJ990203_08.9819.C18
Gene No.	218	Strand	+
Start	775	End	890
Name	OJ990203_08.9819.C18.o1.gp	Method	AAT/GAP
Start	775	End	890
GI	none	Score	182
Exons	775..890		

Seq. No.	76	Seq. ID	OJ990203_08.9819.C19
Gene No.	219	Strand	+
Start	146	End	818
Name	OJ990203_08.9819.C19.o1.gs	Method	GENSCAN
Start	146	End	818
GI	none	Score	.7
Exons	146..207, 764..818		

Seq. No.	76	Seq. ID	OJ990203_08.9819.C19
Gene No.	220	Strand	-

Start	148	End	446
Name	OJ990203_08.9819.C19.o1.gp	Method	AAT/GAP
Start	148	End	446
GI	294_8.R1084	Score	491
Exons	148..446		
GI Descrip.	'1332579/emb|CAA66667| 3.0e-75 (X98063) polyubiquitin [Pinus sylvestris]'		

Seq. No.	77	Seq. ID	OJ990203_08.9819.C22
Gene No.	221	Strand	+
Start	432	End	732
Name	OJ990203_08.9819.C22.o1.gs	Method	GENSCAN
Start	432	End	732
GI	none	Score	.93
Exons	432..474, 515..732		

Seq. No.	77	Seq. ID	OJ990203_08.9819.C22
Gene No.	222	Strand	-
Start	1	End	277
Name	OJ990203_08.9819.C22.o1.np	Method	AAT/NAP
Start	1	End	277
GI	6539553	Score	90
Exons	1..81, 199..277		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	78	Seq. ID	OJ990203_08.9819.C26
Gene No.	223	Strand	-
Start	418	End	585
Name	OJ990203_08.9819.C26.o1.gp	Method	AAT/GAP
Start	418	End	585
GI	3769020	Score	295
Exons	418..585		
GI Descrip.	3789942 8.0e-27 (AF093505) polyubiquitin [Saccharum hybrid cultivar H32-8560]		

Seq. No.	79	Seq. ID	OJ990203_08.9819.C27
Gene No.	224	Strand	+
Start	323	End	482
Name	OJ990203_08.9819.C27.o1.gs	Method	GENSCAN
Start	323	End	482
GI	none	Score	.91
Exons	323..482		

Seq. No.	80	Seq. ID	OJ990203_08.9819.C28
Gene No.	225	Strand	-
Start	267	End	426
Name	OJ990203_08.9819.C28.o1.gp	Method	AAT/GAP
Start	267	End	426
GI	5005099	Score	288
Exons	267..426		

Seq. No.	81	Seq. ID	OJ990203_04.9819.C3
Gene No.	226	Strand	-
Start	127	End	1335

Name	OJ990203_04.9819.C3.o1.gs	Method	GENSCAN
Start	127	End	1335
GI	none	Score	.93
Exons	127..1335		

Seq. No.	81	Seq. ID	OJ990203_04.9819.C3
Gene No.	226	Strand	-
Start	127	End	1335
Name	OJ990203_04.9819.C3.o1.np	Method	AAT/NAP
Start	130	End	1335
GI	1196998	Score	2114
Exons	130..1335		
GI Descrip.	(J01829) unknown protein [Transposon Tn10] gi|5103202|dbj|BAA78838.1| (AP000342) transposase of Tn10 [Plasmid R100] gi|5706382|dbj|BAA83097.1| (AB026428) transposase [Methylomonas aminofaciens] gi|5738092|gb|AAD50250.1|AF162223_9 (AF162223) IS10-right transposase [Shigella flexneri] gi|6721110|gb|AAF26764.1|AC007396_13 (AC007396) T4O12.21 [Arabidopsis thaliana]		

Seq. No.	81	Seq. ID	OJ990203_04.9819.C3
Gene No.	227	Strand	
Start	1295	End	1467
Name	OJ990203_04.9819.C3.o1.tc	Method	TBLASTX:Cress
Start	1295	End	1467
GI	none	Score	221
Exons	1295..1453, 1295..1447, 1296..1466, 1297..1467		

Seq. No.	82	Seq. ID	OJ990203_04.9819.C4
Gene No.	228	Strand	-
Start	438	End	470
Name	OJ990203_04.9819.C4.o1.gs	Method	GENSCAN
Start	438	End	470
GI	none	Score	.73
Exons	438..470		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	229	Strand	+
Start	4692	End	7927
Name	OJ990203_04.9819.C5.o2.np	Method	AAT/NAP
Start	4692	End	7927
GI	5295955	Score	297
Exons	4692..4843, 5994..6110, 6653..6767, 7447..7927		
GI Descrip.	(AB026295) Similar to Epstein-Barr virus (EBV) genome.(V01555) [Oryza sativa]		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	229	Strand	+
Start	4692	End	7927
Name	OJ990203_04.9819.C5.o2.gs	Method	GENSCAN
Start	7716	End	7840
GI	none	Score	.99
Exons	7716..7840		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820

Name	OJ990203_04.9819.C5.o7.tm	Method	TBLASTX:Maize
Start	457	End	701
GI	none	Score	41
Exons	457..519, 489..701, 580..669		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o1.gs	Method	GENSCAN
Start	462	End	6820
GI	none	Score	.81
Exons	462..4507, 4606..5035, 5180..5225, 6753..6820		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o1.np	Method	AAT/NAP
Start	465	End	5038
GI	4680179	Score	6635
Exons	465..5038		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o6.tw	Method	TBLASTX:Wheat
Start	510	End	843
GI	none	Score	104
Exons	510..842, 574..843		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o1.tm	Method	TBLASTX:Maize
Start	702	End	1289
GI	none	Score	146
Exons	702..971, 703..963, 718..1014, 1032..1130, 1033..1128, 1062..1130, 1128..1289, 1135..1281, 1137..1283		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o1.tw	Method	TBLASTX:Wheat
Start	843	End	1469
GI	none	Score	351
Exons	843..1469, 844..1413		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o3.tm	Method	TBLASTX:Maize
Start	1338	End	1630
GI	none	Score	150
Exons	1338..1628, 1342..1527, 1347..1559, 1439..1630		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-

Start	462	End	6820
Name	OJ990203_04.9819.C5.o2.ts	Method	TBLASTX:Soybean
Start	1428	End	1688
GI	none	Score	52
Exons	1428..1496, 1428..1688, 1582..1683		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o1.tc	Method	TBLASTX:Cress
Start	1452	End	1778
GI	none	Score	90
Exons	1452..1595, 1596..1778		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o3.tw	Method	TBLASTX:Wheat
Start	1476	End	1955
GI	none	Score	219
Exons	1476..1955, 1477..1860, 1482..1937		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o2.tw	Method	TBLASTX:Wheat
Start	1959	End	2468
GI	none	Score	305
Exons	1959..2468, 2050..2436		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o2.tm	Method	TBLASTX:Maize
Start	2043	End	2396
GI	none	Score	137
Exons	2043..2396, 2058..2354, 2128..2394		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o3.ts	Method	TBLASTX:Soybean
Start	2217	End	2459
GI	none	Score	197
Exons	2217..2459		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o5.tm	Method	TBLASTX:Maize
Start	2397	End	2750
GI	none	Score	117
Exons	2397..2750, 2479..2739		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820

Name	OJ990203_04.9819.C5.o5.tw	Method	TBLASTX:Wheat
Start	2469	End	2771
GI	none	Score	201
Exons	2469..2771, 2470..2733		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o1.ts	Method	TBLASTX:Soybean
Start	2483	End	2879
GI	none	Score	126
Exons	2483..2836, 2484..2843, 2485..2727, 2702..2836, 2766..2840, 2847..2879, 2847..2879		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o4.tm	Method	TBLASTX:Maize
Start	2766	End	3237
GI	none	Score	100
Exons	2766..3233, 2799..3146, 2992..3237		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o4.tw	Method	TBLASTX:Wheat
Start	2820	End	3306
GI	none	Score	215
Exons	2820..3302, 2862..3302, 2863..3306		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o4.ts	Method	TBLASTX:Soybean
Start	2952	End	3233
GI	none	Score	66
Exons	2952..3233, 2953..3150		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o7.tw	Method	TBLASTX:Wheat
Start	3477	End	3831
GI	none	Score	79
Exons	3477..3830, 3513..3647, 3736..3831		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o6.tm	Method	TBLASTX:Maize
Start	3564	End	3884
GI	none	Score	209
Exons	3564..3884		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820

Name	OJ990203_04.9819.C5.o8.tm	Method	TBLASTX:Maize
Start	4230	End	4485
GI	none	Score	78
Exons	4230..4484, 4320..4484, 4339..4485		

Seq. No.	83	Seq. ID	OJ990203_04.9819.C5
Gene No.	230	Strand	-
Start	462	End	6820
Name	OJ990203_04.9819.C5.o8.tw	Method	TBLASTX:Wheat
Start	4407	End	4765
GI	none	Score	222
Exons	4407..4484, 4478..4765		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	231	Strand	+
Start	414	End	1600
Name	OJ990203_04.9819.C6.o1.gs	Method	GENSCAN
Start	414	End	1600
GI	none	Score	.54
Exons	414..732, 1359..1600		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	232	Strand	+
Start	6650	End	7408
Name	OJ990203_04.9819.C6.o1.gp	Method	AAT/GAP
Start	6650	End	7408
GI	5816562	Score	618
Exons	6650..6674, 6996..7408		
GI Descrip.	6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o1.np	Method	AAT/NAP
Start	1	End	6949
GI	5922631	Score	4548
Exons	1..32, 2310..3394, 4001..4926, 5053..5203, 5246..5818, 5864..6063, 6322..6566, 6825..6949		
GI Descrip.	(AP000492) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] gi|6016864|dbj|BAA85207.1| (AP000570) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativ		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o2.ts	Method	TBLASTX:Soybean
Start	2320	End	2708
GI	none	Score	114
Exons	2320..2568, 2322..2564, 2604..2708, 2614..2700		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-

Start	1	End	6949
Name	OJ990203_04.9819.C6.o4.tw	Method	TBLASTX:Wheat
Start	2331	End	2699
GI	none	Score	200
Exons	2331..2699, 2353..2694		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o3.tm	Method	TBLASTX:Maize
Start	2373	End	2646
GI	none	Score	90
Exons	2373..2471, 2475..2645, 2476..2646		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o3.tw	Method	TBLASTX:Wheat
Start	2736	End	3168
GI	none	Score	91
Exons	2736..3164, 2956..3168		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o1.tm	Method	TBLASTX:Maize
Start	2823	End	3267
GI	none	Score	128
Exons	2823..2849, 2847..2990, 3009..3266, 3012..3266, 3013..3267		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o1.ts	Method	TBLASTX:Soybean
Start	2934	End	3365
GI	none	Score	41
Exons	2934..3365, 2968..3108, 3160..3318		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o2.tw	Method	TBLASTX:Wheat
Start	3210	End	3629
GI	none	Score	228
Exons	3210..3629, 3211..3603		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o2.tm	Method	TBLASTX:Maize
Start	3498	End	3854
GI	none	Score	181
Exons	3498..3854, 3508..3813		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949

Name	OJ990203_04.9819.C6.o3.ts	Method	TBLASTX:Soybean
Start	3579	End	3944
GI	none	Score	129
Exons	3579..3713, 3720..3944		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o6.tw	Method	TBLASTX:Wheat
Start	3629	End	3863
GI	none	Score	134
Exons	3629..3790, 3630..3863, 3631..3861		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o1.tw	Method	TBLASTX:Wheat
Start	3864	End	4660
GI	none	Score	114
Exons	3864..4157, 3868..4029, 4204..4428, 4206..4427, 4484..4660		

Seq. No.	84	Seq. ID	OJ990203_04.9819.C6
Gene No.	233	Strand	-
Start	1	End	6949
Name	OJ990203_04.9819.C6.o5.tw	Method	TBLASTX:Wheat
Start	5240	End	5642
GI	none	Score	108
Exons	5240..5641, 5334..5642		

Seq. No.	85	Seq. ID	OJ990203_04.9819.C7
Gene No.	234	Strand	+
Start	384	End	1362
Name	OJ990203_04.9819.C7.o1.gs	Method	GENSCAN
Start	384	End	1362
GI	none	Score	.66
Exons	384..502, 1275..1362		

Seq. No.	86	Seq. ID	OJ990203_04.9819.C8
Gene No.	235	Strand	
Start	339	End	526
Name	OJ990203_04.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	339	End	499
GI	none	Score	131
Exons	339..491, 339..491, 349..492, 353..499, 377..499		

Seq. No.	86	Seq. ID	OJ990203_04.9819.C8
Gene No.	235	Strand	
Start	339	End	526
Name	OJ990203_04.9819.C8.o1.tc	Method	TBLASTX:Cress
Start	345	End	526
GI	none	Score	57
Exons	345..464, 349..492, 350..526		

Seq. No.	86	Seq. ID	OJ990203_04.9819.C8
Gene No.	235	Strand	
Start	339	End	526
Name	OJ990203_04.9819.C8.o1.ts	Method	TBLASTX:Soybean

Start	349	End	526
GI	none	Score	225
Exons	349..492, 350..526		

Seq. No.	87	Seq. ID	OJ990203_04.9819.C10
Gene No.	236	Strand	+
Start	403	End	609
Name	OJ990203_04.9819.C10.o1.tm	Method	TBLASTX:Maize
Start	375	End	609
GI	none	Score	333
Exons	375..599, 382..609		

Seq. No.	87	Seq. ID	OJ990203_04.9819.C10
Gene No.	236	Strand	+
Start	403	End	609
Name	OJ990203_04.9819.C10.o1.ts	Method	TBLASTX:Soybean
Start	400	End	609
GI	none	Score	331
Exons	400..609, 402..602		

Seq. No.	87	Seq. ID	OJ990203_04.9819.C10
Gene No.	236	Strand	+
Start	403	End	609
Name	OJ990203_04.9819.C10.o1.tw	Method	TBLASTX:Wheat
Start	400	End	609
GI	none	Score	208
Exons	400..609, 402..587		

Seq. No.	87	Seq. ID	OJ990203_04.9819.C10
Gene No.	236	Strand	+
Start	403	End	609
Name	OJ990203_04.9819.C10.o1.tc	Method	TBLASTX:Cress
Start	402	End	609
GI	none	Score	241
Exons	402..599, 403..609		

Seq. No.	87	Seq. ID	OJ990203_04.9819.C10
Gene No.	236	Strand	+
Start	403	End	609
Name	OJ990203_04.9819.C10.o1.gs	Method	GENSCAN
Start	403	End	609
GI	none	Score	1
Exons	403..609		

Seq. No.	88	Seq. ID	OJ990203_04.9819.C13
Gene No.	237	Strand	+
Start	1	End	2786
Name	OJ990203_04.9819.C13.o1.np	Method	AAT/NAP
Start	1	End	2786
GI	4680179	Score	786
Exons	1..90, 1053..2061, 2765..2786		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	88	Seq. ID	OJ990203_04.9819.C13
Gene No.	237	Strand	+
Start	1	End	2786
Name	OJ990203_04.9819.C13.o1.gp	Method	AAT/GAP

Start	178	End	449
GI	61605_1.R1084	Score	439
Exons	178..449		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	88	Seq. ID	OJ990203_04.9819.C13
Gene No.	237	Strand	+
Start	1	End	2786
Name	OJ990203_04.9819.C13.o1.gs	Method	GENSCAN
Start	1007	End	2122
GI	none	Score	.67
Exons	1007..2122		

Seq. No.	88	Seq. ID	OJ990203_04.9819.C13
Gene No.	237	Strand	+
Start	1	End	2786
Name	OJ990203_04.9819.C13.o1.tw	Method	TBLASTX:Wheat
Start	1169	End	1525
GI	none	Score	284
Exons	1169..1525, 1171..1347, 1376..1516, 1384..1524		

Seq. No.	88	Seq. ID	OJ990203_04.9819.C13
Gene No.	237	Strand	+
Start	1	End	2786
Name	OJ990203_04.9819.C13.o1.tm	Method	TBLASTX:Maize
Start	1406	End	1720
GI	none	Score	217
Exons	1406..1669, 1429..1593, 1634..1720		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	238	Strand	+
Start	1	End	4343
Name	OJ990203_04.9819.C14.o1.np	Method	AAT/NAP
Start	1	End	2216
GI	6063554	Score	311
Exons	1..22, 529..697, 1374..1405, 2043..2216		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	238	Strand	+
Start	1	End	4343
Name	OJ990203_04.9819.C14.o2.np	Method	AAT/NAP
Start	245	End	4340
GI	5902445	Score	2306
Exons	245..343, 2756..4340		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	238	Strand	+
Start	1	End	4343
Name	OJ990203_04.9819.C14.o1.gp	Method	AAT/GAP
Start	582	End	2858
GI	61605_1.R1084	Score	632
Exons	582..737, 1377..1457, 2589..2858		

GI Descrip. '5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	238	Strand	+
Start	1	End	4343
Name	OJ990203_04.9819.C14.o2.gs	Method	GENSCAN
Start	2875	End	4343
GI	none	Score	.51
Exons	2875..3256, 3380..3916, 3961..4343		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	239	Strand	+
Start	8630	End	18804
Name	OJ990203_04.9819.C14.o4.gs	Method	GENSCAN
Start	8630	End	18804
GI	none	Score	.47
Exons	8630..8677, 9389..9712, 9738..10094, 10618..10691, 10906..11957, 13172..13388, 13698..13810, 13884..13969, 14132..14234, 14352..14426, 14520..14602, 14899..15013, 15105..15361, 15695:.15877, 17079..17167, 18597..18804		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	240	Strand	-
Start	494	End	2028
Name	OJ990203_04.9819.C14.o1.gs	Method	GENSCAN
Start	494	End	2028
GI	none	Score	.49
Exons	494..1002, 1947..2028		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	241	Strand	-
Start	4685	End	7601
Name	OJ990203_04.9819.C14.o3.np	Method	AAT/NAP
Start	4685	End	7601
GI	6691716	Score	2492
Exons	4685..5124, 5198..5311, 5461..5563, 5638..5825, 5903..6088, 6165..6261, 6338..6515, 6713..7601		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	241	Strand	-
Start	4685	End	7601
Name	OJ990203_04.9819.C14.o3.gs	Method	GENSCAN
Start	4781	End	7601
GI	none	Score	.95
Exons	4781..5124, 5198..5311, 5374..5563, 5638..5825, 5903..6261, 6386..6630, 6717..7601		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	242	Strand	-
Start	8649	End	9058
Name	OJ990203_04.9819.C14.o2.gp	Method	AAT/GAP
Start	8649	End	9058
GI	5816562	Score	612

Exons	8649..9058		
GI Descrip.	6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10		
Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o4.tw	Method	TBLASTX:Wheat
Start	2914	End	3255
GI	none	Score	135
Exons	2914..3048, 3115..3255		
Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o3.tm	Method	TBLASTX:Maize
Start	3208	End	3573
GI	none	Score	419
Exons	3208..3516, 3211..3534, 3231..3533, 3526..3573		
Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o1.tw	Method	TBLASTX:Wheat
Start	3349	End	3731
GI	none	Score	407
Exons	3349..3729, 3349..3603, 3354..3731		
Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o2.tw	Method	TBLASTX:Wheat
Start	3733	End	4331
GI	none	Score	178
Exons	3733..3918, 3738..3827, 3868..3897, 3924..4208, 3935..4006, 4194..4331		
Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o6.tm	Method	TBLASTX:Maize
Start	4029	End	4292
GI	none	Score	167
Exons	4029..4211, 4151..4210, 4190..4264, 4191..4292		
Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o5.tw	Method	TBLASTX:Wheat
Start	7191	End	7481
GI	none	Score	200
Exons	7191..7481		
Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o6.tw	Method	TBLASTX:Wheat

Start	9596	End	11589
GI	none	Score	43
Exons	9596..9631, 9690..9761, 9707..9760, 11330..11581, 11426..11569, 11476..11589		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o4.tm	Method	TBLASTX:Maize
Start	9636	End	11689
GI	none	Score	48
Exons	9636..9683, 9690..9791, 9725..9814, 9792..9875, 9797..9865, 9891..10031, 9931..10035, 9985..10038, 10053..10139, 10054..10176, 10932..11096, 11423..11593, 11479..11589, 11618..11689, 11626..11688		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o2.ts	Method	TBLASTX:Soybean
Start	9699	End	11689
GI	none	Score	92
Exons	9699..9773, 9707..9772, 9792..9875, 9891..10028, 9902..10027, 10053..10175, 10054..10158, 11423..11572, 11479..11577, 11603..11689, 11623..11688		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o3.tc	Method	TBLASTX:Cress
Start	9792	End	11689
GI	none	Score	82
Exons	9792..9875, 9897..10022, 10054..10158, 11618..11689		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o7.tw	Method	TBLASTX:Wheat
Start	9798	End	10158
GI	none	Score	72
Exons	9798..9860, 9885..10025, 10078..10158		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o4.np	Method	AAT/NAP
Start	16199	End	26219
GI	6633835	Score	1641
Exons	16199..16284, 19760..19831, 20511..20674, 20763..21016, 21100..21266, 21339..21542, 21688..22054, 22130..22225, 22299..22380, 22457..22795, 23135..23206, 23328..23413, 23495..23578, 23663..23770, 24303..24407, 25020..25130, 25237..25364, 26087..26219		
GI Descrip.	(AC008047) F2K11.1 [Arabidopsis thaliana]		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-

Start	16199	End	34162
Name	OJ990203_04.9819.C14.o1.tm	Method	TBLASTX:Maize
Start	19176	End	21801
GI	none	Score	82
Exons	19176..19235, 19177..19317, 19177..19266, 19718..19792, 19719..19793, 19745..19834, 19777..19833, 19789..19836, 20455..20676, 20508..20684, 20558..20689, 20755..21015, 20755..21018, 20762..21019, 21102..21269, 21103..21270, 21104..21271, 21120..21302, 21130..21270, 21366..21542, 21370..21543, 21370..21543, 21688..21801, 21688..21795, 21690..21800		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o3.gp	Method	AAT/GAP
Start	19196	End	20588
GI	LIB3433-030-P1-K1-C5	Score	991
Exons	19196..19269, 19440..19831, 20511..20588		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o5.gs	Method	GENSCAN
Start	19403	End	34162
GI	none	Score	.82
Exons	19403..19831, 20511..20674, 20763..20933, 21711..21794, 21875..22054, 22130..22225, 22299..22380, 22457..22798, 23039..23068, 23161..23253, 23336..23413, 23495..23595, 24206..24431, 25020..25133, 25228..25382, 25663..25834, 27908..27976, 28190..28264, 29168..29221, 29486..29615, 29693..29812, 30877..31007, 34133..34162		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o3.tw	Method	TBLASTX:Wheat
Start	19757	End	20860
GI	none	Score	75
Exons	19757..19834, 19779..19832, 20458..20676, 20508..20684, 20558..20680, 20751..20846, 20755..20859, 20762..20860		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o1.tc	Method	TBLASTX:Cress
Start	20493	End	25124
GI	none	Score	68
Exons	20493..20663, 20508..20675, 20572..20676, 20728..21018, 20762..21010, 20773..21018, 21120..21236, 21130..21237, 21366..21527, 21382..21516, 21688..21792, 21701..21796, 21876..22061, 21889..22062, 22128..22226, 22129..22227, 25020..25124		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14

Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o1.ts	Method	TBLASTX:Soybean
Start	20611	End	21248
GI	none	Score	72
Exons	20611..20688, 20613..20675, 20728..21018, 20762..21019, 21120..21248, 21130..21234		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o3.ts	Method	TBLASTX:Soybean
Start	21365	End	22226
GI	none	Score	101
Exons	21365..21526, 21366..21512, 21366..21527, 21382..21513, 21688..21795, 21693..21755, 21701..21796, 21864..21926, 21978..22073, 21985..22062, 22128..22226		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o2.tm	Method	TBLASTX:Maize
Start	21864	End	22804
GI	none	Score	204
Exons	21864..22055, 21864..22061, 21865..22056, 22128..22226, 22128..22226, 22129..22227, 22130..22228, 22186..22227, 22298..22375, 22455..22757, 22455..22793, 22457..22804, 22603..22794		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o4.gp	Method	AAT/GAP
Start	22283	End	22543
GI	LIB3479-008-Q6-K1-F3	Score	292
Exons	22283..22380, 22457..22543		
GI Descrip.	'6015437/dbj|AB008112.1|AB008112 6.0e-11 Homo sapiens PEX1 mRNA, complete cds'		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o5.gp	Method	AAT/GAP
Start	23017	End	24432
GI	3761361	Score	1013
Exons	23017..23068, 23161..23253, 23336..23413, 23495..23577, 23663..23760, 24206..24432		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o2.tc	Method	TBLASTX:Cress
Start	23155	End	23747
GI	none	Score	51
Exons	23155..23265, 23166..23258, 23294..23416, 23327..23398, 23492..23581, 23493..23585, 23634..23747, 23657..23746		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o7.tm	Method	TBLASTX:Maize
Start	23179	End	23548
GI	none	Score	77
Exons	23179..23253, 23180..23251, 23182..23256, 23336..23419, 23385..23420, 23495..23548, 23496..23543		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o6.gp	Method	AAT/GAP
Start	25879	End	26151
GI	2427384	Score	480
Exons	25879..26151		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o7.gp	Method	AAT/GAP
Start	27809	End	27871
GI	4715947	Score	74
Exons	27809..27871		
GI Descrip.	2252840 3.0e-09 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi_6049882_gb_AAF02797.1_AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]		

Seq. No.	89	Seq. ID	OJ990203_04.9819.C14
Gene No.	243	Strand	-
Start	16199	End	34162
Name	OJ990203_04.9819.C14.o5.tm	Method	TBLASTX:Maize
Start	30713	End	31512
GI	none	Score	74
Exons	30713..30784, 30715..30780, 30876..31010, 30877..31008, 30891..31010, 31439..31507, 31441..31503, 31443..31505, 31444..31512		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	244	Strand	+
Start	1	End	10736
Name	OJ990203_04.9819.C15.o1.np	Method	AAT/NAP
Start	1	End	3425
GI	5902445	Score	577
Exons	1..470, 3394..3425		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	244	Strand	+
Start	1	End	10736
Name	OJ990203_04.9819.C15.o1.gs	Method	GENSCAN
Start	56	End	1115
GI	none	Score	.87
Exons	56..313, 738..1115		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	244	Strand	+
Start	1	End	10736
Name	OJ990203_04.9819.C15.o2.np	Method	AAT/NAP
Start	1786	End	10206
GI	6862928	Score	52
Exons	1786..1846, 2776..2919, 10143..10206		
GI Descrip.	(AC018907) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	244	Strand	+
Start	1	End	10736
Name	OJ990203_04.9819.C15.o2.gs	Method	GENSCAN
Start	2667	End	5189
GI	none	Score	.89
Exons	2667..4259, 4323..5189		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	244	Strand	+
Start	1	End	10736
Name	OJ990203_04.9819.C15.o4.np	Method	AAT/NAP
Start	3213	End	10736
GI	3643608	Score	214
Exons	3213..3234, 8978..9159, 9704..9762, 9847..9924, 10620..10736		
GI Descrip.	(AC005395) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	244	Strand	+
Start	1	End	10736
Name	OJ990203_04.9819.C15.o3.np	Method	AAT/NAP
Start	3927	End	4115
GI	6598344	Score	61
Exons	3927..4115		
GI Descrip.	(AC002335) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	245	Strand	+
Start	10649	End	11120
Name	OJ990203_04.9819.C15.o1.gp	Method	AAT/GAP
Start	10649	End	11120
GI	uC-osroM202017h10b1	Score	256
Exons	10649..10732, 10807..10872, 11088..11120		
GI Descrip.	'2252840 3.0e-09 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi_6049882_gb_AAF02797.1_AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]'		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	246	Strand	-
Start	5699	End	5935
Name	OJ990203_04.9819.C15.o3.gs	Method	GENSCAN
Start	5699	End	5935
GI	none	Score	.87
Exons	5699..5935		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15

Gene No.	247	Strand	-
Start	10918	End	11076
Name	OJ990203_04.9819.C15.o1.ts	Method	TBLASTX:Soybean
Start	8	End	325
GI	none	Score	194
Exons	8..238, 11..325		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	247	Strand	-
Start	10918	End	11076
Name	OJ990203_04.9819.C15.o1.tw	Method	TBLASTX:Wheat
Start	10	End	388
GI	none	Score	321
Exons	10..45, 11..388, 64..303, 80..370		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	247	Strand	-
Start	10918	End	11076
Name	OJ990203_04.9819.C15.o1.tm	Method	TBLASTX:Maize
Start	11	End	400
GI	none	Score	251
Exons	11..247, 16..246, 20..250, 269..400		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	247	Strand	-
Start	10918	End	11076
Name	OJ990203_04.9819.C15.o2.tm	Method	TBLASTX:Maize
Start	9735	End	10875
GI	none	Score	46
Exons	9735..9761, 9827..9925, 9847..9945, 9849..9926, 10610..10735, 10614..10733, 10618..10749, 10800..10871, 10805..10864, 10806..10871, 10807..10875		

Seq. No.	90	Seq. ID	OJ990203_04.9819.C15
Gene No.	247	Strand	-
Start	10918	End	11076
Name	OJ990203_04.9819.C15.o5.gs	Method	GENSCAN
Start	10918	End	11076
GI	none	Score	.69
Exons	10918..11076		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	248	Strand	+
Start	1	End	2745
Name	OJ990203_04.9819.C16.o1.np	Method	AAT/NAP
Start	1	End	2106
GI	3643608	Score	552
Exons	1..92, 447..535, 753..963, 1685..1848, 1974..2106		
GI Descrip.	(AC005395) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	248	Strand	+
Start	1	End	2745
Name	OJ990203_04.9819.C16.o1.gs	Method	GENSCAN
Start	210	End	2745
GI	none	Score	.72
Exons	210..354, 758..963, 1974..2005, 2212..2276, 2630..2745		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	249	Strand	+
Start	2904	End	12229
Name	OJ990203_04.9819.C16.o2.np	Method	AAT/NAP
Start	2904	End	6640
GI	4415916	Score	592
Exons	2904..2963, 3112..3235, 3674..3712, 3950..4115, 4229..4418, 4500..4706, 5973..6208, 6435..6640		
GI Descrip.	(AC006282) putative pectinesterase [Arabidopsis thaliana]		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	249	Strand	+
Start	2904	End	12229
Name	OJ990203_04.9819.C16.o2.gs	Method	GENSCAN
Start	3699	End	12229
GI	none	Score	.86
Exons	3699..3916, 3960..4115, 4183..4227, 4229..4418, 4500..4706, 5973..6208, 6435..6566, 6708..6815, 7377..7581, 7673..7885, 7909..8112, 9826..9893, 11199..11347, 11850..12229		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	249	Strand	+
Start	2904	End	12229
Name	OJ990203_04.9819.C16.o1.gp	Method	AAT/GAP
Start	10258	End	10667
GI	12650_1.R1084	Score	222
Exons	10258..10278, 10505..10667		
GI Descrip.	'5803242/dbj|AP000399.1|AP000399 2.0e-24 Oryza sativa genomic DNA, chromosome 6, clone:P0535G04'		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	249	Strand	+
Start	2904	End	12229
Name	OJ990203_04.9819.C16.o3.np	Method	AAT/NAP
Start	12060	End	12217
GI	6907084	Score	169
Exons	12060..12217		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	250	Strand	+
Start	12616	End	17256
Name	OJ990203_04.9819.C16.o4.np	Method	AAT/NAP
Start	12616	End	17256
GI	6016874	Score	2202
Exons	12616..12694, 12778..12915, 12980..13212, 13603..13762, 14156..14335, 14453..14793, 15260..15598, 17167..17256		
GI Descrip.	(AP000570) ESTs C19143(E10020),D25076(R3116) correspond to a region of the predicted gene.; Similar to putative AC9 transposase. (P03010) [Oryza sativa]		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	250	Strand	+
Start	12616	End	17256
Name	OJ990203_04.9819.C16.o2.gp	Method	AAT/GAP
Start	13305	End	13813

GI	uC-osflcyp110c07b1	Score	958
Exons	13305..13813		
GI Descrip.	'4680178/gb|AF111709.1|AF111709 5.0e-81 Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences; and unknown genes'		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o5.tm	Method	TBLASTX:Maize
Start	248	End	954
GI	none	Score	48
Exons	248..325, 255..326, 312..365, 315..434, 417..530, 442..531, 443..529, 712..894, 732..890, 733..894, 894..953, 895..954		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o2.ts	Method	TBLASTX:Soybean
Start	468	End	1828
GI	none	Score	96
Exons	468..530, 715..972, 750..971, 1682..1828, 1690..1815		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o1.tc	Method	TBLASTX:Cress
Start	750	End	1810
GI	none	Score	249
Exons	750..959, 751..972, 757..963, 1667..1771, 1675..1779, 1682..1810, 1690..1806		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o9.tm	Method	TBLASTX:Maize
Start	1790	End	2121
GI	none	Score	87
Exons	1790..1849, 1798..1851, 1798..1851, 1974..2090, 1975..2091, 1975..2121		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o1.tm	Method	TBLASTX:Maize
Start	4224	End	15455
GI	none	Score	131
Exons	4224..4313, 4226..4321, 4230..4325, 4328..4447, 4329..4427, 4472..4696, 4479..4706, 4536..4706, 4537..4719, 15321..15455		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o1.ts	Method	TBLASTX:Soybean
Start	4229	End	4706
GI	none	Score	120
Exons	4229..4318, 4230..4325, 4341..4418, 4343..4417, 4497..4706,		

4499..4699

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o1.tw	Method	TBLASTX:Wheat
Start	4230	End	4706
GI	none	Score	122
Exons	4230..4418, 4310..4399, 4497..4706, 4499..4684		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o2.tc	Method	TBLASTX:Cress
Start	4499	End	6164
GI	none	Score	247
Exons	4499..4696, 4500..4706, 5976..6077, 6045..6164		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o2.tm	Method	TBLASTX:Maize
Start	5976	End	6209
GI	none	Score	326
Exons	5976..6209, 6032..6208		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o8.tm	Method	TBLASTX:Maize
Start	6434	End	6587
GI	none	Score	235
Exons	6434..6463, 6436..6582, 6436..6582, 6450..6587		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o3.tm	Method	TBLASTX:Maize
Start	12964	End	13410
GI	none	Score	69
Exons	12964..13050, 13035..13244, 13036..13284, 13321..13377, 13372..13410		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o6.tm	Method	TBLASTX:Maize
Start	13504	End	13818
GI	none	Score	65
Exons	13504..13578, 13591..13818, 13599..13817		

Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o7.tm	Method	TBLASTX:Maize
Start	14023	End	14375
GI	none	Score	247

Exons	14023..14304, 14034..14375		
Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o4.tm	Method	TBLASTX:Maize
Start	14487	End	14730
GI	none	Score	282
Exons	14487..14645, 14497..14730		
Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o4.gs	Method	GENSCAN
Start	17065	End	17952
GI	none	Score	.91
Exons	17065..17694, 17779..17952		
Seq. No.	91	Seq. ID	OJ990203_04.9819.C16
Gene No.	251	Strand	-
Start	17065	End	18619
Name	OJ990203_04.9819.C16.o5.np	Method	AAT/NAP
Start	17123	End	18619
GI	4220443	Score	113
Exons	17123..17600, 17728..17952, 18597..18619		
GI Descrip.	(AC006216) Similar to gb|X74772 SF16 protein from Helianthus annuus and contains calmodulin-binding motif PF|00612. [Arabidopsis thaliana]		
Seq. No.	92	Seq. ID	OJ990203_04.9819.C17
Gene No.	252	Strand	-
Start	454	End	741
Name	OJ990203_04.9819.C17.o1.gs	Method	GENSCAN
Start	454	End	741
GI	none	Score	.64
Exons	454..741		
Seq. No.	93	Seq. ID	OJ990203_04.9819.C18
Gene No.	253	Strand	+
Start	1679	End	1730
Name	OJ990203_04.9819.C18.o1.gp	Method	AAT/GAP
Start	1679	End	1730
GI	4715947	Score	67
Exons	1679..1730		
GI Descrip.	2252840 3.0e-09 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi_6049882_gb_AAF02797.1_AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]		
Seq. No.	94	Seq. ID	OJ990203_04.9819.C21
Gene No.	254	Strand	+
Start	548	End	599
Name	OJ990203_04.9819.C21.o1.gs	Method	GENSCAN
Start	548	End	599
GI	none	Score	.98
Exons	548..599		

Seq. No.	95	Seq. ID	OJ990203_04.9819.C23
Gene No.	255	Strand	+
Start	51	End	741
Name	OJ990203_04.9819.C23.o1.np	Method	AAT/NAP
Start	51	End	741
GI	6721517	Score	822
Exons	51..741		
GI Descrip.	(AP001072) Similar to polyprotein. (AF061282) [Oryza sativa]		

Seq. No.	95	Seq. ID	OJ990203_04.9819.C23
Gene No.	255	Strand	+
Start	51	End	741
Name	OJ990203_04.9819.C23.o1.tw	Method	TBLASTX:Wheat
Start	64	End	540
GI	none	Score	408
Exons	64..540, 75..506		

Seq. No.	95	Seq. ID	OJ990203_04.9819.C23
Gene No.	255	Strand	+
Start	51	End	741
Name	OJ990203_04.9819.C23.o1.tm	Method	TBLASTX:Maize
Start	136	End	603
GI	none	Score	289
Exons	136..603		

Seq. No.	95	Seq. ID	OJ990203_04.9819.C23
Gene No.	255	Strand	+
Start	51	End	741
Name	OJ990203_04.9819.C23.o1.gs	Method	GENSCAN
Start	247	End	582
GI	none	Score	.91
Exons	247..582		

Seq. No.	95	Seq. ID	OJ990203_04.9819.C23
Gene No.	255	Strand	+
Start	51	End	741
Name	OJ990203_04.9819.C23.o1.ts	Method	TBLASTX:Soybean
Start	490	End	741
GI	none	Score	52
Exons	490..522, 492..521, 526..654, 533..568, 655..741, 659..739		

Seq. No.	96	Seq. ID	OJ990203_04.9819.C25
Gene No.	256	Strand	+
Start	142	End	809
Name	OJ990203_04.9819.C25.o1.gs	Method	GENSCAN
Start	142	End	809
GI	none	Score	.68
Exons	142..191, 540..595, 628..809		

Seq. No.	96	Seq. ID	OJ990203_04.9819.C25
Gene No.	257	Strand	-
Start	1	End	882
Name	OJ990203_04.9819.C25.o1.np	Method	AAT/NAP
Start	1	End	882
GI	5852179	Score	295
Exons	1..116, 529..882		

GI Descrip. (AL117265) zhb0009.1 [Oryza sativa]

Seq. No.	97	Seq. ID	OJ990203_04.9819.C26
Gene No.	258	Strand	-
Start	277	End	483
Name	OJ990203_04.9819.C26.o1.gs	Method	GENSCAN
Start	277	End	483
GI	none	Score	.53
Exons	277..483		

Seq. No.	97	Seq. ID	OJ990203_04.9819.C26
Gene No.	259	Strand	-
Start	547	End	742
Name	OJ990203_04.9819.C26.o1.np	Method	AAT/NAP
Start	547	End	742
GI	6016874	Score	169
Exons	547..742		

GI Descrip. (AP000570) ESTs C19143(E10020),D25076(R3116) correspond to a region of the predicted gene.; Similar to putative AC9 transposase. (P03010) [Oryza sativa]

Seq. No.	98	Seq. ID	OJ990203_04.9819.C27
Gene No.	260	Strand	-
Start	321	End	447
Name	OJ990203_04.9819.C27.o1.gs	Method	GENSCAN
Start	321	End	447
GI	none	Score	.49
Exons	321..447		

Seq. No.	99	Seq. ID	OJ990203_04.9819.C28
Gene No.	261	Strand	-
Start	199	End	358
Name	OJ990203_04.9819.C28.o1.gp	Method	AAT/GAP
Start	199	End	358
GI	jC-osleLIB3474037g11a1	Score	269
Exons	199..358		

GI Descrip. '5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]'

Seq. No.	99	Seq. ID	OJ990203_04.9819.C28
Gene No.	262	Strand	-
Start	413	End	569
Name	OJ990203_04.9819.C28.o2.gp	Method	AAT/GAP
Start	413	End	569
GI	jC-osleLIB3474037g11a1	Score	283
Exons	413..569		

GI Descrip. '5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]'

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	263	Strand	+
Start	28613	End	33904
Name	OJ990203_05.9819.C2.o3.gp	Method	AAT/GAP
Start	28363	End	28855
GI	uC-osroM202019e10b1	Score	953
Exons	28363..28855		

GI Descrip. '3228517 9.0e-10 (AF007788) ETTIN [Arabidopsis thaliana]'

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	263	Strand	+
Start	28613	End	33904
Name	OJ990203_05.9819.C2.o4.np	Method	AAT/NAP
Start	28573	End	33255
GI	2245390	Score	931
Exons	28573..28897, 28987..29074, 29174..29322, 29437..29521, 30147..30237, 30311..30475, 30899..31018, 31110..31182, 32061..32220, 32304..32417, 32532..32652, 32705..32839, 33029..33083, 33120..33255		
GI Descrip.	(U89296) auxin response transcription factor 3; ARF3 [Arabidopsis thaliana]		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	263	Strand	+
Start	28613	End	33904
Name	OJ990203_05.9819.C2.o4.gs	Method	GENSCAN
Start	28613	End	33565
GI	none	Score	.69
Exons	28613..28897, 28987..29043, 29122..29322, 29437..29521, 30382..30475, 30899..31018, 31110..31182, 32238..32360, 32417..33169, 33425..33565		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	263	Strand	+
Start	28613	End	33904
Name	OJ990203_05.9819.C2.o4.gp	Method	AAT/GAP
Start	32762	End	33904
GI	none	Score	1877
Exons	32762..33169, 33242..33372, 33459..33904		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	264	Strand	+
Start	37841	End	40567
Name	OJ990203_05.9819.C2.o6.gs	Method	GENSCAN
Start	37841	End	40567
GI	none	Score	.55
Exons	37841..37907, 38305..38408, 38413..38521, 39843..39957, 40411..40567		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	265	Strand	+
Start	40561	End	43434
Name	OJ990203_05.9819.C2.o5.np	Method	AAT/NAP
Start	40561	End	42159
GI	2129473	Score	467
Exons	40561..40633, 41429..42159		
GI Descrip.	arabinogalactan-like protein - loblolly pine gi|607774 (U09556) arabinogalactan-like protein [Pinus taeda]		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	265	Strand	+
Start	40561	End	43434
Name	OJ990203_05.9819.C2.o6.gp	Method	AAT/GAP
Start	41345	End	41766
GI	LIB3434-042-P1-K1-C1	Score	730

Exons	41345..41766		
GI Descrip.	'4204300 1.0e-21 (AC003027) Unknown protein [Arabidopsis thaliana]'		
Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	265	Strand	+
Start	40561	End	43434
Name	OJ990203_05.9819.C2.o7.gs	Method	GENSCAN
Start	41395	End	43434
GI	none	Score	.6
Exons	41395..42146, 42818..42912, 43208..43434		
Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	265	Strand	+
Start	40561	End	43434
Name	OJ990203_05.9819.C2.o7.gp	Method	AAT/GAP
Start	41885	End	42072
GI	none	Score	322
Exons	41885..42072		
Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	266	Strand	+
Start	45835	End	46653
Name	OJ990203_05.9819.C2.o8.gp	Method	AAT/GAP
Start	45799	End	46335
GI	33097_1.R1084	Score	1050
Exons	45799..46335		
GI Descrip.	'4204300 9.0e-26 (AC003027) Unknown protein [Arabidopsis thaliana]'		
Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	266	Strand	+
Start	45835	End	46653
Name	OJ990203_05.9819.C2.o8.gs	Method	GENSCAN
Start	45835	End	46653
GI	none	Score	.71
Exons	45835..46653		
Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	266	Strand	+
Start	45835	End	46653
Name	OJ990203_05.9819.C2.o6.np	Method	AAT/NAP
Start	45838	End	46644
GI	2129473	Score	416
Exons	45838..46644		
GI Descrip.	arabinogalactan-like protein - loblolly pine gi|607774 (U09556) arabinogalactan-like protein [Pinus taeda]		
Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	267	Strand	-
Start	1	End	12063
Name	OJ990203_05.9819.C2.o3.np	Method	AAT/NAP
Start	1	End	12047
GI	6630700	Score	576
Exons	1..201, 10853..11013, 11436..11499, 11573..12047		
GI Descrip.	(AP000969) Similar to hypothetical protein f678 - Escherichia coli. (A65193) [Oryza sativa] gi|6721537|dbj|BAA89567.1|		

(AP001073) Similar to hypothetical protein f678 - Escherichia coli. (A65193) [Oryza sativa]

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	267	Strand	-
Start	1	End	12063
Name	OJ990203_05.9819.C2.o1.gp	Method	AAT/GAP
Start	136	End	801
GI	none	Score	828
Exons	136..457, 535..612, 698..801		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	267	Strand	-
Start	1	End	12063
Name	OJ990203_05.9819.C2.o2.gp	Method	AAT/GAP
Start	221	End	779
GI	none	Score	677
Exons	221..457, 535..612, 698..779		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	267	Strand	-
Start	1	End	12063
Name	OJ990203_05.9819.C2.o1.gs	Method	GENSCAN
Start	239	End	12063
GI	none	Score	.67
Exons	239..457, 535..612, 698..1280, 1525..1547, 1650..1772, 1934..2068, 2264..2368, 3130..3315, 3894..3995, 4121..4234, 4344..4487, 5229..5390, 6002..6361, 7326..7452, 7688..7790, 10130..10251, 11510..11662, 11714..12063		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	268	Strand	-
Start	23233	End	27564
Name	OJ990203_05.9819.C2.o3.gs	Method	GENSCAN
Start	23233	End	27564
GI	none	Score	.4
Exons	23233..23324, 23915..24079, 25322..25464, 25784..25889, 27498..27564		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o2.tm	Method	TBLASTX:Maize
Start	119	End	27684
GI	none	Score	361
Exons	119..460, 123..458, 533..613, 534..614, 535..621, 535..615, 536..637, 695..829, 696..992, 697..990, 698..991, 820..993, 983..1150, 27517..27684		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o1.ts	Method	TBLASTX:Soybean
Start	132	End	1225
GI	none	Score	177
Exons	132..458, 143..472, 695..829, 698..1213, 750..1052, 983..1225		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o5.tm	Method	TBLASTX:Maize
Start	1151	End	2071
GI	none	Score	120
Exons	1151..1309, 1159..1311, 1462..1548, 1462..1533, 1464..1550, 1647..1775, 1648..1773, 1650..1775, 1898..2071, 1929..2069, 1976..2071		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o5.ts	Method	TBLASTX:Soybean
Start	1464	End	2062
GI	none	Score	77
Exons	1464..1550, 1465..1542, 1647..1775, 1659..1775, 1934..2023, 2015..2062		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o3.tc	Method	TBLASTX:Cress
Start	4419	End	5354
GI	none	Score	87
Exons	4419..4502, 4420..4488, 4424..4489, 4582..4653, 4591..4659, 4598..4660, 5186..5353, 5229..5354, 5230..5352, 5232..5354		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o2.tc	Method	TBLASTX:Cress
Start	28679	End	32385
GI	none	Score	146
Exons	28679..28810, 28723..28812, 29182..29322, 29217..29318, 29436..29522, 29437..29535, 30142..30234, 30146..30238, 30149..30259, 30279..30368, 30414..30476, 30897..31019, 32061..32138, 32121..32180, 32301..32366, 32308..32385		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o4.tm	Method	TBLASTX:Maize
Start	28780	End	29535
GI	none	Score	114
Exons	28780..28893, 28781..28894, 28956..29015, 28978..29067, 29197..29322, 29211..29324, 29436..29522, 29437..29535		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o3.ts	Method	TBLASTX:Soybean
Start	29233	End	29529
GI	4306688	Score	148
Exons	29233..29322, 29235..29324, 29437..29529		
GI Descrip.	-		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o1.tm	Method	TBLASTX:Maize
Start	30145	End	33312
GI	none	Score	117
Exons	30145..30234, 30158..30238, 30161..30238, 30268..30480, 30285..30476, 30314..30478, 30890..30979, 30897..31019, 30901..31017, 31107..31190, 31107..31184, 31108..31191, 32027..32218, 32061..32228, 32067..32219, 32292..32753, 32294..32725, 32301..32726, 32720..32860, 32724..32843, 32726..32866, 32855..32983, 32860..32982, 32967..33101, 32979..33113, 33014..33127, 33014..33112, 33131..33172, 33133..33171, 33242..33307, 33243..33311, 33243..33296, 33244..33312		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o4.ts	Method	TBLASTX:Soybean
Start	30145	End	32123
GI	none	Score	137
Exons	30145..30234, 30146..30238, 30309..30476, 30897..31019, 32061..32123		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o1.tw	Method	TBLASTX:Wheat
Start	30889	End	32609
GI	none	Score	187
Exons	30889..31020, 30891..31019, 31107..31190, 31107..31184, 31108..31191, 32027..32218, 32061..32219, 32061..32219, 32062..32223, 32301..32519, 32306..32488, 32462..32530, 32464..32529, 32530..32577, 32531..32578, 32535..32579, 32544..32609		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o5.gs	Method	GENSCAN
Start	34473	End	36614
GI	none	Score	.72
Exons	34473..34568, 35948..36058, 36184..36294, 36543..36614		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o6.tm	Method	TBLASTX:Maize
Start	35503	End	36638
GI	none	Score	172
Exons	35503..35652, 35504..35623, 35505..35624, 35508..35663, 35509..35625, 35948..36055, 35949..36056, 35961..36056, 36184..36297, 36374..36457, 36387..36458, 36519..36638, 36543..36620		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2

Gene No.	269	Strand	-
Start	34473	End	36729
Name	OJ990203_05.9819.C2.o5.gp	Method	AAT/GAP
Start	35939	End	36729
GI	26716_1.R1084	Score	783
Exons	35939..36058, 36184..36294, 36386..36457, 36543..36729		
GI Descrip.	'3821780/emb|AJ009303.1|XLAJ9303 6.0e-10 Xenopus laevis cDNA clone 27A6-1'		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	270	Strand	
Start	41527	End	46434
Name	OJ990203_05.9819.C2.o1.tc	Method	TBLASTX:Cress
Start	41527	End	46434
GI	none	Score	256
Exons	41527..41760, 41535..41687, 41760..41813, 41848..41970, 41916..41969, 45988..46227, 46279..46434		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	270	Strand	
Start	41527	End	46434
Name	OJ990203_05.9819.C2.o2.ts	Method	TBLASTX:Soybean
Start	41527	End	46434
GI	none	Score	294
Exons	41527..41814, 41631..41864, 41842..41970, 41919..41969, 45988..46281, 46279..46434		

Seq. No.	100	Seq. ID	OJ990203_05.9819.C2
Gene No.	270	Strand	
Start	41527	End	46434
Name	OJ990203_05.9819.C2.o3.tm	Method	TBLASTX:Maize
Start	41527	End	46434
GI	none	Score	143
Exons	41527..41625, 41535..41618, 41617..41970, 41628..41969, 45988..46095, 45990..46040, 46096..46320, 46110..46319, 46309..46434, 46314..46397, 46381..46431		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	271	Strand	+
Start	3502	End	11288
Name	OJ990203_05.9819.C3.o2.gs	Method	GENSCAN
Start	3502	End	10257
GI	none	Score	.56
Exons	3502..4924, 5691..5727, 5828..5976, 7832..9525, 9601..10257		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	271	Strand	+
Start	3502	End	11288
Name	OJ990203_05.9819.C3.o1.np	Method	AAT/NAP
Start	5214	End	11288
GI	4680183	Score	1228
Exons	5214..5327, 7808..9109, 9575..9616, 9704..10119, 11205..11288		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	272	Strand	-
Start	9557	End	14029

Name	OJ990203_05.9819.C3.o2.np	Method	AAT/NAP
Start	9557	End	11305
GI	6721558	Score	226
Exons	9557..9772, 10368..10505, 11206..11305		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa] gi|6815083|dbj|BAA90369.1| (AP001081) hypothetical protein [Oryza sativa]		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	272	Strand	-
Start	9557	End	14029
Name	OJ990203_05.9819.C3.o3.gs	Method	GENSCAN
Start	10324	End	14029
GI	none	Score	.45
Exons	10324..10505, 10672..11347, 11621..11793, 11999..12092, 13083..13280, 13863..14029		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	272	Strand	-
Start	9557	End	14029
Name	OJ990203_05.9819.C3.o3.np	Method	AAT/NAP
Start	10517	End	13839
GI	6721512	Score	70
Exons	10517..10548, 12116..12224, 13819..13839		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o3.tw	Method	TBLASTX:Wheat
Start	7885	End	8277
GI	none	Score	58
Exons	7885..7929, 7930..8043, 7941..7991, 8002..8277, 8049..8276		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o2.tm	Method	TBLASTX:Maize
Start	7924	End	8163
GI	none	Score	203
Exons	7924..8163		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o2.tw	Method	TBLASTX:Wheat
Start	8908	End	9363
GI	none	Score	148
Exons	8908..9090, 8916..9089, 9127..9363, 9129..9245, 9133..9348, 9288..9353		

Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o1.tw	Method	TBLASTX:Wheat
Start	9555	End	10011
GI	none	Score	541

Exons	9555..10010, 9556..10011		
Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o1.ts	Method	TBLASTX:Soybean
Start	9595	End	9960
GI	none	Score	105
Exons	9595..9819, 9826..9960		
Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o1.tm	Method	TBLASTX:Maize
Start	9685	End	10041
GI	none	Score	411
Exons	9685..10041, 9739..9987, 9747..10040		
Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o4.tw	Method	TBLASTX:Wheat
Start	10012	End	10248
GI	none	Score	247
Exons	10012..10248		
Seq. No.	101	Seq. ID	OJ990203_05.9819.C3
Gene No.	273	Strand	-
Start	14216	End	14416
Name	OJ990203_05.9819.C3.o1.gp	Method	AAT/GAP
Start	14216	End	14416
GI	2227_1.R1084	Score	301
Exons	14216..14416		
GI Descrip.	'6006355/dbj|AP000559.1|AP000559 2.0e-56 Oryza sativa genomic DNA, chromosome 6, clone:P0493C11'		
Seq. No.	102	Seq. ID	OJ990203_05.9819.C4
Gene No.	274	Strand	+
Start	1	End	596
Name	OJ990203_05.9819.C4.o1.np	Method	AAT/NAP
Start	1	End	596
GI	6560751	Score	288
Exons	1..46, 283..596		
GI Descrip.	(AC010155) F3M18.8 [Arabidopsis thaliana]		
Seq. No.	102	Seq. ID	OJ990203_05.9819.C4
Gene No.	274	Strand	+
Start	1	End	596
Name	OJ990203_05.9819.C4.o1.gp	Method	AAT/GAP
Start	309	End	457
GI	5004737	Score	241
Exons	309..457		
Seq. No.	102	Seq. ID	OJ990203_05.9819.C4
Gene No.	275	Strand	-
Start	378	End	1051
Name	OJ990203_05.9819.C4.o1.gs	Method	GENSCAN

Start	378	End	1051
GI	none	Score	.91
Exons	378..569, 896..1051		

Seq. No.	103	Seq. ID	OJ990203_05.9819.C8
Gene No.	276	Strand	-
Start	571	End	722
Name	OJ990203_05.9819.C8.o1.tw	Method	TBLASTX:Wheat
Start	72	End	214
GI	none	Score	183
Exons	72..212, 72..209, 74..214, 80..214		

Seq. No.	103	Seq. ID	OJ990203_05.9819.C8
Gene No.	276	Strand	-
Start	571	End	722
Name	OJ990203_05.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	136	End	551
GI	none	Score	137
Exons	136..261, 137..262, 138..278, 267..353, 267..344, 271..348, 397..519, 405..551, 453..518, 460..549		

Seq. No.	103	Seq. ID	OJ990203_05.9819.C8
Gene No.	276	Strand	-
Start	571	End	722
Name	OJ990203_05.9819.C8.o1.np	Method	AAT/NAP
Start	571	End	722
GI	5103193	Score	221
Exons	571..722		
GI Descrip.	(AP000342) transposase of Tn10 [Plasmid R100] gi|5738084|gb|AAD50242.1|AF162223_1 (AF162223) IS10-left transposase [Shigella flexneri]		

Seq. No.	104	Seq. ID	OJ990203_05.9819.C9
Gene No.	277	Strand	+
Start	1	End	572
Name	OJ990203_05.9819.C9.o1.np	Method	AAT/NAP
Start	1	End	569
GI	2119980	Score	825
Exons	1..569		
GI Descrip.	transposase (transposons) - Escherichia coli gi|43089|emb|CAA42760| (X60200) transposase [Escherichia coli] gi|303566|dbj|BAA03914| (D16449) transposase [Escherichia coli]		

Seq. No.	104	Seq. ID	OJ990203_05.9819.C9
Gene No.	277	Strand	+
Start	1	End	572
Name	OJ990203_05.9819.C9.o1.gs	Method	GENSCAN
Start	144	End	572
GI	none	Score	.98
Exons	144..572		

Seq. No.	105	Seq. ID	OJ990203_05.9819.C10
Gene No.	278	Strand	-
Start	421	End	588
Name	OJ990203_05.9819.C10.o1.gs	Method	GENSCAN
Start	421	End	588
GI	none	Score	.51

Exons	421..495, 539..588		
Seq. No.	106	Seq. ID	OJ990203_05.9819.C11
Gene No.	279	Strand	-
Start	467	End	631
Name	OJ990203_05.9819.C11.o1.gs	Method	GENSCAN
Start	467	End	631
GI	none	Score	.88
Exons	467..631		
Seq. No.	107	Seq. ID	OJ990203_05.9819.C12
Gene No.	280	Strand	+
Start	348	End	482
Name	OJ990203_05.9819.C12.o1.gs	Method	GENSCAN
Start	348	End	482
GI	none	Score	.42
Exons	348..482		
Seq. No.	108	Seq. ID	OJ990203_05.9819.C15
Gene No.	281	Strand	-
Start	1	End	357
Name	OJ990203_05.9819.C15.o1.np	Method	AAT/NAP
Start	1	End	357
GI	6721558	Score	115
Exons	1..69, 226..357		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa] gi|6815083|dbj|BAA90369.1| (AP001081) hypothetical protein [Oryza sativa]		
Seq. No.	108	Seq. ID	OJ990203_05.9819.C15
Gene No.	282	Strand	-
Start	258	End	357
Name	OJ990203_05.9819.C15.o1.gs	Method	GENSCAN
Start	258	End	357
GI	none	Score	.8
Exons	258..357		
Seq. No.	109	Seq. ID	OJ990203_05.9819.C16
Gene No.	283	Strand	+
Start	265	End	345
Name	OJ990203_05.9819.C16.o1.gs	Method	GENSCAN
Start	265	End	345
GI	none	Score	.77
Exons	265..345		
Seq. No.	110	Seq. ID	OJ990203_05.9819.C17
Gene No.	284	Strand	+
Start	124	End	729
Name	OJ990203_05.9819.C17.o1.np	Method	AAT/NAP
Start	124	End	729
GI	6815053	Score	435
Exons	124..439, 489..729		
GI Descrip.	(AP001080) hypothetical protein [Oryza sativa]		
Seq. No.	111	Seq. ID	OJ990203_05.9819.C18
Gene No.	285	Strand	+
Start	373	End	435

Name	OJ990203_05.9819.C18.o1.tw	Method	TBLASTX:Wheat
Start	245	End	434
GI	none	Score	227
Exons	245..331, 252..434, 276..434		

Seq. No.	111	Seq. ID	OJ990203_05.9819.C18
Gene No.	285	Strand	+
Start	373	End	435
Name	OJ990203_05.9819.C18.o1.gs	Method	GENSCAN
Start	373	End	435
GI	none	Score	.47
Exons	373..435		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	286	Strand	+
Start	120	End	1324
Name	OJ990203_05.9819.C19.o1.gp	Method	AAT/GAP
Start	120	End	632
GI	none	Score	734
Exons	120..206, 284..632		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	286	Strand	+
Start	120	End	1324
Name	OJ990203_05.9819.C19.o1.gs	Method	GENSCAN
Start	129	End	1324
GI	none	Score	.96
Exons	129..206, 284..1324		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	287	Strand	+
Start	1812	End	2134
Name	OJ990203_05.9819.C19.o2.gp	Method	AAT/GAP
Start	1812	End	2134
GI	none	Score	562
Exons	1812..2134		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	288	Strand	+
Start	9979	End	16823
Name	OJ990203_05.9819.C19.o3.gs	Method	GENSCAN
Start	9979	End	16814
GI	none	Score	.55
Exons	9979..9986, 10868..11062, 12639..12722, 15697..15956, 16069..16814		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	288	Strand	+
Start	9979	End	16823
Name	OJ990203_05.9819.C19.o4.np	Method	AAT/NAP
Start	15815	End	16823
GI	5051773	Score	379
Exons	15815..15910, 16278..16823		
GI Descrip.	(AL078637) putative protein [Arabidopsis thaliana]		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	289	Strand	+

Start	20361	End	26760
Name	OJ990203_05.9819.C19.o5.np	Method	AAT/NAP
Start	20076	End	26760
GI	6560763	Score	1446
Exons	20076..20254, 20491..20589, 20726..21484, 22452..22786, 22859..23336, 24098..24198, 24306..24392, 24743..24901, 24986..25141, 25749..25958, 26035..26760		
GI Descrip.	(AC010155) F3M18.14 [Arabidopsis thaliana]		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	289	Strand	+
Start	20361	End	26760
Name	OJ990203_05.9819.C19.o5.gs	Method	GENSCAN
Start	20361	End	26383
GI	none	Score	.75
Exons	20361..20589, 20726..21223, 21602..21678, 22115..22606, 22694..22786, 22859..23023, 23114..23336, 24098..24198, 24306..24392, 24743..24883, 24986..25141, 25749..25958, 26035..26383		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o1.tm	Method	TBLASTX:Maize
Start	104	End	1335
GI	none	Score	95
Exons	104..205, 120..206, 126..206, 281..937, 282..959, 282..941, 950..982, 953..994, 987..1049, 989..1051, 989..1051, 1043..1180, 1043..1165, 1169..1324, 1185..1322, 1216..1335, 1239..1325		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o1.ts	Method	TBLASTX:Soybean
Start	296	End	817
GI	none	Score	407
Exons	296..817, 310..453, 564..740		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o1.tc	Method	TBLASTX:Cress
Start	761	End	1321
GI	none	Score	156
Exons	761..1045, 1139..1321		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o2.gs	Method	GENSCAN
Start	1996	End	6028
GI	none	Score	.62
Exons	1996..2582, 2702..2897, 3076..3294, 4345..4511, 5521..5674, 5903..6028		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-

Start	1996	End	6028
Name	OJ990203_05.9819.C19.o3.np	Method	AAT/NAP
Start	2020	End	3237
GI	2842493	Score	845
Exons	2020..2582, 2702..2894, 3076..3237		
GI Descrip.	(AL021749) predicted protein [Arabidopsis thaliana]		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o2.ts	Method	TBLASTX:Soybean
Start	2242	End	2562
GI	none	Score	228
Exons	2242..2511, 2246..2488, 2485..2562, 2489..2554		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o3.tc	Method	TBLASTX:Cress
Start	2266	End	2584
GI	none	Score	70
Exons	2266..2364, 2267..2359, 2444..2488, 2485..2583, 2486..2584		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o3.tm	Method	TBLASTX:Maize
Start	2311	End	2572
GI	none	Score	119
Exons	2311..2514, 2320..2487, 2327..2488, 2480..2572, 2488..2571		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o3.ts	Method	TBLASTX:Soybean
Start	2700	End	2907
GI	none	Score	224
Exons	2700..2885, 2701..2907		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o4.tc	Method	TBLASTX:Cress
Start	2761	End	3270
GI	none	Score	159
Exons	2761..2904, 2763..2897, 3076..3111, 3202..3270		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	290	Strand	-
Start	1996	End	6028
Name	OJ990203_05.9819.C19.o3.gp	Method	AAT/GAP
Start	4026	End	4605
GI	none	Score	1081
Exons	4026..4605		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	291	Strand	

Start	16272	End	16562
Name	OJ990203_05.9819.C19.o2.tc	Method	TBLASTX:Cress
Start	16272	End	16562
GI	none	Score	154
Exons	16272..16397, 16274..16393, 16404..16484, 16497..16562		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	292	Strand	
Start	21033	End	22269
Name	OJ990203_05.9819.C19.o1.tw	Method	TBLASTX:Wheat
Start	21033	End	22269
GI	none	Score	236
Exons	21033..21119, 21040..21222, 21043..21222, 21600..21662, 21601..21678, 22097..22264, 22104..22265, 22105..22269, 22106..22267, 22114..22269		

Seq. No.	112	Seq. ID	OJ990203_05.9819.C19
Gene No.	293	Strand	
Start	22191	End	22952
Name	OJ990203_05.9819.C19.o2.tm	Method	TBLASTX:Maize
Start	22191	End	22952
GI	none	Score	137
Exons	22191..22316, 22192..22317, 22193..22333, 22322..22408, 22322..22399, 22326..22403, 22452..22574, 22460..22618, 22507..22659, 22508..22573, 22515..22604, 22670..22762, 22695..22769, 22702..22770, 22757..22786, 22807..22869, 22857..22952		

Seq. No.	113	Seq. ID	OJ990203_05.9819.C24
Gene No.	294	Strand	+
Start	156	End	312
Name	OJ990203_05.9819.C24.o1.gs	Method	GENSCAN
Start	156	End	312
GI	none	Score	.98
Exons	156..312		

Seq. No.	114	Seq. ID	OJ990203_05.9819.C27
Gene No.	295	Strand	-
Start	1	End	683
Name	OJ990203_05.9819.C27.o1.np	Method	AAT/NAP
Start	1	End	683
GI	5902444	Score	249
Exons	1..55, 167..683		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	114	Seq. ID	OJ990203_05.9819.C27
Gene No.	295	Strand	-
Start	1	End	683
Name	OJ990203_05.9819.C27.o1.gs	Method	GENSCAN
Start	229	End	540
GI	none	Score	.51
Exons	229..540		

Seq. No.	115	Seq. ID	OJ990203_05.9819.C28
Gene No.	296	Strand	+
Start	169	End	388
Name	OJ990203_05.9819.C28.o1.gs	Method	GENSCAN

Start	169	End	388
GI	none	Score	.45
Exons	169..220, 263..388		

Seq. No.	115	Seq. ID	OJ990203_05.9819.C28
Gene No.	297	Strand	-
Start	79	End	520
Name	OJ990203_05.9819.C28.o1.gp	Method	AAT/GAP
Start	79	End	520
GI	none	Score	602
Exons	79..335, 422..520		

Seq. No.	116	Seq. ID	OJ990203_05.9819.C29
Gene No.	298	Strand	-
Start	206	End	640
Name	OJ990203_05.9819.C29.o1.tm	Method	TBLASTX:Maize
Start	203	End	604
GI	none	Score	140
Exons	203..337, 204..500, 204..383, 491..604	205..498, 206..499, 328..501,	

Seq. No.	116	Seq. ID	OJ990203_05.9819.C29
Gene No.	298	Strand	-
Start	206	End	640
Name	OJ990203_05.9819.C29.o1.ts	Method	TBLASTX:Soybean
Start	203	End	640
GI	none	Score	75
Exons	203..337, 206..640, 258..560,	290..550	

Seq. No.	116	Seq. ID	OJ990203_05.9819.C29
Gene No.	298	Strand	-
Start	206	End	640
Name	OJ990203_05.9819.C29.o1.gp	Method	AAT/GAP
Start	206	End	287
GI	none	Score	120
Exons	206..287		

Seq. No.	116	Seq. ID	OJ990203_05.9819.C29
Gene No.	298	Strand	-
Start	206	End	640
Name	OJ990203_05.9819.C29.o1.gs	Method	GENSCAN
Start	206	End	628
GI	none	Score	.64
Exons	206..628		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	299	Strand	+
Start	13268	End	18414
Name	OJ990203_06.9819.C1.o3.gs	Method	GENSCAN
Start	13268	End	18414
GI	none	Score	.65
Exons	13268..13308, 13513..13588, 18343..18414	14091..14257, 14950..15022,	

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	300	Strand	+
Start	21765	End	24761

Name	OJ990203_06.9819.C1.o4.gs	Method	GENSCAN
Start	21765	End	24761
GI	none	Score	.7
Exons	21765..22398, 22565..22689, 22757..22900, 23007..23065, 23136..23769, 23817..23896, 24018..24163, 24262..24761		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	301	Strand	+
Start	28129	End	33584
Name	OJ990203_06.9819.C1.o2.np	Method	AAT/NAP
Start	28129	End	33584
GI	6498441	Score	7106
Exons	28129..29193, 29524..29987, 30051..30424, 30608..30742, 30917..31640, 31812..33209, 33303..33584		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	302	Strand	+
Start	38580	End	39027
Name	OJ990203_06.9819.C1.o4.np	Method	AAT/NAP
Start	38580	End	39027
GI	6498441	Score	676
Exons	38580..39027		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	303	Strand	-
Start	1681	End	12570
Name	OJ990203_06.9819.C1.o1.np	Method	AAT/NAP
Start	1151	End	12487
GI	5823335	Score	619
Exons	1151..1205, 1919..2061, 11730..12056, 12143..12265, 12351..12487		
GI Descrip.	(AF176001) putative transcription factor [Arabidopsis thaliana]		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	303	Strand	-
Start	1681	End	12570
Name	OJ990203_06.9819.C1.o1.gs	Method	GENSCAN
Start	1681	End	2516
GI	none	Score	.47
Exons	1681..1932, 2084..2247, 2495..2516		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	303	Strand	-
Start	1681	End	12570
Name	OJ990203_06.9819.C1.o2.gs	Method	GENSCAN
Start	6654	End	12487
GI	none	Score	.47
Exons	6654..6827, 7014..7786, 11362..12056, 12143..12272, 12355..12487		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	303	Strand	-
Start	1681	End	12570

Name	OJ990203_06.9819.C1.o3.gp	Method	AAT/GAP
Start	12355	End	12570
GI	3761372	Score	277
Exons	12355..12570		
GI Descrip.	1945282/emb|Y11351|OSMYB1402 2.0e-15 O.sativa mRNA for myb factor, 1402 bp		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	304	Strand	-
Start	25694	End	26335
Name	OJ990203_06.9819.C1.o5.gs	Method	GENSCAN
Start	25694	End	26335
GI	none	Score	.43
Exons	25694..26335		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	305	Strand	-
Start	34208	End	37848
Name	OJ990203_06.9819.C1.o7.gs	Method	GENSCAN
Start	34208	End	37848
GI	none	Score	.64
Exons	34208..35716, 35915..37469, 37640..37848		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	305	Strand	-
Start	34208	End	37848
Name	OJ990203_06.9819.C1.o3.np	Method	AAT/NAP
Start	34211	End	37450
GI	6907089	Score	4213
Exons	34211..36085, 36189..37450		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o5.tm	Method	TBLASTX:Maize
Start	7740	End	8114
GI	none	Score	159
Exons	7740..7976, 7767..7964, 7787..7975, 7967..8005, 8011..8112, 8049..8081, 8055..8114, 8072..8113		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o1.ts	Method	TBLASTX:Soybean
Start	11669	End	12449
GI	none	Score	143
Exons	11669..11704, 11777..11863, 11975..12034, 12140..12283, 12142..12282, 12341..12448, 12354..12449		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o1.tc	Method	TBLASTX:Cress
Start	11777	End	12488
GI	none	Score	124
Exons	11777..11860, 11963..12058, 11964..12059, 12140..12274,		

12142..12273, 12341..12487, 12350..12463, 12354..12488

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o5.tw	Method	TBLASTX:Wheat
Start	11967	End	12496
GI	none	Score	70
Exons	11967..12047, 11972..12058, 11973..12059, 12137..12277, 12137..12271, 12142..12276, 12341..12496, 12342..12488		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o1.tm	Method	TBLASTX:Maize
Start	11987	End	12533
GI	none	Score	91
Exons	11987..12058, 11988..12056, 12140..12274, 12142..12273, 12326..12463, 12341..12487, 12342..12488, 12513..12533		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o3.tw	Method	TBLASTX:Wheat
Start	25403	End	33575
GI	none	Score	64
Exons	25403..25534, 25404..25529, 25559..26011, 25755..25862, 25911..25997, 32967..33263, 32999..33262, 33345..33419, 33449..33571, 33450..33575		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o6.tm	Method	TBLASTX:Maize
Start	25439	End	33539
GI	none	Score	107
Exons	25439..25522, 25523..25687, 33345..33455, 33443..33538, 33456..33539		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o6.tw	Method	TBLASTX:Wheat
Start	26033	End	32945
GI	none	Score	186
Exons	26033..26386, 26043..26285, 26141..26386, 26331..26387, 32591..32647, 32592..32945, 32595..32933, 32693..32941		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o4.tm	Method	TBLASTX:Maize
Start	26213	End	32786
GI	none	Score	150
Exons	26213..26452, 26214..26450, 32454..32777, 32498..32764, 32574..32786		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o8.tw	Method	TBLASTX:Wheat
Start	28242	End	39009
GI	none	Score	55
Exons	28242..28325, 28332..28430, 28349..28429, 28397..28636, 28413..28670, 38692..38775, 38782..38880, 38799..38879, 38847..39008, 38863..39009		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o7.tm	Method	TBLASTX:Maize
Start	28320	End	39009
GI	none	Score	194
Exons	28320..28568, 28322..28567, 38770..39009, 38772..39008		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o4.tw	Method	TBLASTX:Wheat
Start	29408	End	29894
GI	none	Score	397
Exons	29408..29581, 29409..29894, 29603..29863		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o1.tw	Method	TBLASTX:Wheat
Start	30059	End	30521
GI	none	Score	563
Exons	30059..30514, 30060..30521, 30060..30515		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o2.tm	Method	TBLASTX:Maize
Start	30189	End	30545
GI	none	Score	384
Exons	30189..30545, 30224..30535, 30429..30545		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o3.tm	Method	TBLASTX:Maize
Start	30572	End	30956
GI	none	Score	362
Exons	30572..30937, 30573..30956		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o2.tw	Method	TBLASTX:Wheat
Start	30629	End	31049
GI	none	Score	489
Exons	30629..31024, 30630..31049		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o2.ts	Method	TBLASTX:Soybean
Start	30708	End	31079
GI	none	Score	274
Exons	30708..31079, 30725..30868		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o7.tw	Method	TBLASTX:Wheat
Start	31488	End	31946
GI	none	Score	233
Exons	31488..31742, 31512..31736, 31577..31753, 31797..31946, 31808..31945		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o3.ts	Method	TBLASTX:Soybean
Start	31635	End	32201
GI	5666795	Score	64
Exons	31635..31733, 31809..31946, 31962..32201		
GI Descrip.	4206306 2.0e-10 (AF049110) prpol [Zea mays]		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o9.tw	Method	TBLASTX:Wheat
Start	31949	End	32261
GI	none	Score	237
Exons	31949..32125, 31950..32261		

Seq. No.	117	Seq. ID	OJ990203_06.9819.C1
Gene No.	306	Strand	-
Start	38572	End	39009
Name	OJ990203_06.9819.C1.o8.gs	Method	GENSCAN
Start	38572	End	38910
GI	none	Score	.96
Exons	38572..38910		

Seq. No.	118	Seq. ID	OJ990203_06.9819.C2
Gene No.	307	Strand	+
Start	344	End	2342
Name	OJ990203_06.9819.C2.o1.gs	Method	GENSCAN
Start	344	End	2342
GI	none	Score	.47
Exons	344..472, 534..595, 2252..2342		

Seq. No.	118	Seq. ID	OJ990203_06.9819.C2
Gene No.	308	Strand	-
Start	1632	End	2154
Name	OJ990203_06.9819.C2.o1.gp	Method	AAT/GAP
Start	1632	End	2154
GI	LIB3434-038-P1-K1-F1	Score	737

Exons	1632..2154		
GI Descrip.	'5257255/dbj|AP000364.1|AP000364 0.0e+00 Oryza sativa genomic DNA, chromosome 8, clone:P0026F07'		
Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	309	Strand	+
Start	3795	End	11210
Name	OJ990203_06.9819.C3.o3.np	Method	AAT/NAP
Start	3795	End	11210
GI	6721512	Score	85
Exons	3795..3840, 6826..6961, 6990..7117, 11119..11210		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		
Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	309	Strand	+
Start	3795	End	11210
Name	OJ990203_06.9819.C3.o4.np	Method	AAT/NAP
Start	9213	End	10661
GI	6907088	Score	916
Exons	9213..9350, 9527..9764, 10258..10661		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		
Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	309	Strand	+
Start	3795	End	11210
Name	OJ990203_06.9819.C3.o5.np	Method	AAT/NAP
Start	10646	End	11210
GI	5734635	Score	179
Exons	10646..10756, 10809..11210		
GI Descrip.	(AP000391) hypothetical protein [Oryza sativa]		
Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o1.np	Method	AAT/NAP
Start	1	End	3655
GI	5902445	Score	1989
Exons	1..30, 1592..1777, 1817..3655		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		
Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o3.tm	Method	TBLASTX:Maize
Start	80	End	283
GI	none	Score	261
Exons	80..283, 81..278, 208..279		
Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o1.gs	Method	GENSCAN
Start	104	End	6791
GI	none	Score	.58
Exons	104..280, 282..496, 1603..1876, 2210..2647, 2903..3664, 3752..4220, 4274..5135, 5377..5660, 5733..5913, 6080..6791		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o6.tw	Method	TBLASTX:Wheat
Start	1865	End	2158
GI	none	Score	53
Exons	1865..2158, 1992..2024		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o4.tw	Method	TBLASTX:Wheat
Start	2162	End	2570
GI	none	Score	67
Exons	2162..2299, 2163..2297, 2343..2570, 2345..2569		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o1.ts	Method	TBLASTX:Soybean
Start	2660	End	3061
GI	none	Score	102
Exons	2660..3061, 2901..3059		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o2.tw	Method	TBLASTX:Wheat
Start	2720	End	3139
GI	none	Score	278
Exons	2720..3139, 2721..3092, 2750..3094		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o2.tm	Method	TBLASTX:Maize
Start	2813	End	3196
GI	none	Score	169
Exons	2813..3196, 2814..3092, 2924..3169		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o1.tm	Method	TBLASTX:Maize
Start	3224	End	3580
GI	none	Score	211
Exons	3224..3580, 3225..3518, 3278..3526		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o1.tw	Method	TBLASTX:Wheat
Start	3254	End	3710
GI	none	Score	362
Exons	3254..3709, 3255..3710		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3

Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o2.ts	Method	TBLASTX:Soybean
Start	3305	End	3670
GI	none	Score	96
Exons	3305..3439, 3446..3670		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o2.np	Method	AAT/NAP
Start	3722	End	5567
GI	5902444	Score	994
Exons	3722..5567		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o3.tw	Method	TBLASTX:Wheat
Start	3859	End	4306
GI	none	Score	38
Exons	3859..3912, 3902..4138, 3912..3977, 3917..4132, 4020..4136, 4175..4306		

Seq. No.	119	Seq. ID	OJ990203_06.9819.C3
Gene No.	310	Strand	-
Start	1	End	6791
Name	OJ990203_06.9819.C3.o5.tw	Method	TBLASTX:Wheat
Start	4987	End	5378
GI	none	Score	80
Exons	4987..5175, 4988..5185, 5175..5234, 5220..5333, 5272..5307, 5334..5378		

Seq. No.	120	Seq. ID	OJ990203_06.9819.C4
Gene No.	311	Strand	+
Start	868	End	2157
Name	OJ990203_06.9819.C4.o1.gs	Method	GENSCAN
Start	868	End	2157
GI	none	Score	.73
Exons	868..921, 1354..1482, 2114..2157		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	312	Strand	+
Start	31343	End	31740
Name	OJ990203_06.9819.C5.o3.gp	Method	AAT/GAP
Start	31343	End	31740
GI	none	Score	698
Exons	31343..31740		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	313	Strand	-
Start	1406	End	18914
Name	OJ990203_06.9819.C5.o1.gs	Method	GENSCAN
Start	1406	End	18914
GI	none	Score	.64
Exons	1406..1608, 9925..10081, 10685..10795, 10923..11093,		

11624..11704, 12906..13111, 14080..14589, 15799..15821,
15918..16077, 16450..16765, 18612..18914

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	313	Strand	-
Start	1406	End	18914
Name	OJ990203_06.9819.C5.o1.gp	Method	AAT/GAP
Start	11140	End	11602
GI	2428746	Score	863
Exons	11140..11602		
GI Descrip.	6041757/gb|AC011806.1|AC011806 7.0e-68 Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	313	Strand	-
Start	1406	End	18914
Name	OJ990203_06.9819.C5.o2.gp	Method	AAT/GAP
Start	13691	End	16692
GI	none	Score	2200
Exons	13691..13775, 13841..14540, 15918..16077, 16450..16692		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	313	Strand	-
Start	1406	End	18914
Name	OJ990203_06.9819.C5.o1.np	Method	AAT/NAP
Start	14078	End	16669
GI	6539264	Score	1034
Exons	14078..14540, 15918..16077, 16447..16669		
GI Descrip.	(AC011765) unknown protein [Arabidopsis thaliana]		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	314	Strand	-
Start	23689	End	32290
Name	OJ990203_06.9819.C5.o1.tm	Method	TBLASTX:Maize
Start	14065	End	16768
GI	none	Score	382
Exons	14065..14211, 14066..14542, 14069..14542, 14088..14546, 15913..15963, 15914..16078, 15920..16048, 16454..16624, 16455..16625, 16625..16768, 16625..16765		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	314	Strand	-
Start	23689	End	32290
Name	OJ990203_06.9819.C5.o1.ts	Method	TBLASTX:Soybean
Start	14108	End	15988
GI	none	Score	390
Exons	14108..14542, 14118..14555, 14223..14552, 15915..15980, 15920..15988, 15933..15983		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	314	Strand	-
Start	23689	End	32290
Name	OJ990203_06.9819.C5.o2.ts	Method	TBLASTX:Soybean
Start	16489	End	16652
GI	none	Score	94
Exons	16489..16650, 16490..16651, 16491..16652		

Seq. No.	121	Seq. ID	OJ990203_06.9819.C5
Gene No.	314	Strand	-
Start	23689	End	32290
Name	OJ990203_06.9819.C5.o3.gs	Method	GENSCAN
Start	23689	End	32290
GI	none	Score	.58
Exons	23689..23792, 25790..25998, 26202..26279, 30250..30428, 30998..31178, 31265..31325, 31405..31499, 31539..31936, 32149..32290		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	315	Strand	+
Start	1	End	3676
Name	OJ990203_06.9819.C6.o1.np	Method	AAT/NAP
Start	1	End	3357
GI	6665555	Score	581
Exons	1..72, 1677..1981, 2253..2651, 2758..2985, 3109..3357		
GI Descrip.	(AC013289) hypothetical protein [Arabidopsis thaliana] gi|6692256|gb|AAF24607.1|AC021046_5 (AC021046) unknown protein [Arabidopsis thaliana]		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	315	Strand	+
Start	1	End	3676
Name	OJ990203_06.9819.C6.o1.gp	Method	AAT/GAP
Start	1119	End	1484
GI	34521_1.R1084	Score	694
Exons	1119..1484		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	315	Strand	+
Start	1	End	3676
Name	OJ990203_06.9819.C6.o2.gp	Method	AAT/GAP
Start	2843	End	3676
GI	12188_1.R1084	Score	1304
Exons	2843..2985, 3109..3676		
GI Descrip.	'58067/emb|X52325|ARBLSKP 5.0e-55 pBluescript SK(+) vector DNA, phagemid excised from lambda ZAP'		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	316	Strand	+
Start	4979	End	6868
Name	OJ990203_06.9819.C6.o3.gp	Method	AAT/GAP
Start	4979	End	6868
GI	19006_1.R1084	Score	1150
Exons	4979..5155, 5271..5350, 6400..6509, 6594..6868		
GI Descrip.	'6041757/gb|AC011806.1|AC011806 7.0e-68 Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence'		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	317	Strand	+
Start	8128	End	10357
Name	OJ990203_06.9819.C6.o2.np	Method	AAT/NAP

Start	8128	End	10357
GI	6539261	Score	1441
Exons	8128..10357		
GI Descrip.	(AC011765) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o2.tw	Method	TBLASTX:Wheat
Start	596	End	1045
GI	none	Score	38
Exons	596..664, 599..625, 624..671, 627..668, 680..772, 700..729, 760..849, 761..850, 872..949, 968..1045, 968..1045		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o3.tm	Method	TBLASTX:Maize
Start	1268	End	2509
GI	none	Score	54
Exons	1268..1318, 1271..1321, 1374..1574, 1424..1582, 1429..1560, 1433..1579, 1719..1742, 1736..1975, 1747..1977, 1780..1887, 1844..1975, 1866..2009, 2232..2507, 2234..2305, 2239..2508, 2248..2508, 2372..2509		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o1.ts	Method	TBLASTX:Soybean
Start	1835	End	2660
GI	none	Score	177
Exons	1835..1981, 2232..2357, 2361..2576, 2378..2485, 2577..2660		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o1.tm	Method	TBLASTX:Maize
Start	2619	End	3394
GI	none	Score	41
Exons	2619..2651, 2621..2647, 2739..2891, 2748..2891, 2749..2895, 2755..2895, 2891..2983, 2892..2984, 2892..2984, 2893..2985, 3106..3378, 3106..3156, 3108..3392, 3230..3391, 3275..3394		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o4.ts	Method	TBLASTX:Soybean
Start	3106	End	3324
GI	none	Score	195
Exons	3106..3324, 3108..3182, 3237..3323		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o5.tm	Method	TBLASTX:Maize
Start	5023	End	6778
GI	none	Score	38

Exons	5023..5043, 5074..5157, 5076..5156, 5089..5166, 5257..5349, 5258..5353, 5270..5353, 6399..6509, 6400..6510, 6400..6510, 6591..6680, 6592..6648, 6593..6679, 6691..6777, 6696..6776, 6728..6778		
Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o2.tc	Method	TBLASTX:Cress
Start	5074	End	6674
GI	none	Score	122
Exons	5074..5157, 5076..5156, 5257..5349, 5258..5353, 6399..6509, 6400..6510, 6591..6674, 6592..6648		
Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o3.ts	Method	TBLASTX:Soybean
Start	5074	End	6680
GI	none	Score	133
Exons	5074..5157, 5076..5156, 5095..5166, 5257..5349, 5258..5353, 5272..5361, 6399..6509, 6399..6509, 6400..6510, 6400..6510, 6591..6680, 6592..6645		
Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o1.tw	Method	TBLASTX:Wheat
Start	8291	End	10057
GI	none	Score	92
Exons	8291..8497, 8378..8794, 8539..8661, 9434..9670, 9578..10057, 9950..10057		
Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o1.tc	Method	TBLASTX:Cress
Start	8294	End	10189
GI	none	Score	89
Exons	8294..8515, 8609..8818, 9203..9397, 9494..9667, 9791..10189, 9811..10149, 10052..10153		
Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o2.tm	Method	TBLASTX:Maize
Start	8327	End	9781
GI	none	Score	85
Exons	8327..8575, 8495..8881, 8497..8880, 9098..9421, 9440..9781		
Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o2.ts	Method	TBLASTX:Soybean
Start	8333	End	10150
GI	none	Score	92
Exons	8333..8497, 9215..9430, 9521..9667, 9829..10137, 9830..10150,		

9842..10150

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o3.np	Method	AAT/NAP
Start	9694	End	13071
GI	4262176	Score	208
Exons	9694..9734, 11285..11457, 11533..11649, 11739..11921, 13052..13071		
GI Descrip.	(AC005508) 18857 [Arabidopsis thaliana]		

Seq. No.	122	Seq. ID	OJ990203_06.9819.C6
Gene No.	318	Strand	-
Start	9694	End	13071
Name	OJ990203_06.9819.C6.o4.tm	Method	TBLASTX:Maize
Start	9781	End	10324
GI	none	Score	288
Exons	9781..9876, 9782..10228, 9785..9925, 9797..9943, 9863..10120, 9922..10233, 10238..10324		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	319	Strand	+
Start	1812	End	4244
Name	OJ990203_06.9819.C7.o1.gs	Method	GENSCAN
Start	1812	End	4244
GI	none	Score	.59
Exons	1812..1886, 4135..4244		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	320	Strand	+
Start	4186	End	4644
Name	OJ990203_06.9819.C7.o4.gp	Method	AAT/GAP
Start	4186	End	4644
GI	none	Score	918
Exons	4186..4644		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	321	Strand	+
Start	5307	End	8134
Name	OJ990203_06.9819.C7.o2.np	Method	AAT/NAP
Start	5307	End	8134
GI	6522544	Score	881
Exons	5307..5459, 6538..7173, 7590..7688, 7787..8134		
GI Descrip.	(AL132955) putative protein [Arabidopsis thaliana]		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	322	Strand	-
Start	1443	End	6943
Name	OJ990203_06.9819.C7.o1.gp	Method	AAT/GAP
Start	1443	End	2359
GI	LIB3431-022-P1-N1-G9	Score	752
Exons	1443..1653, 1877..1983, 2274..2359		
GI Descrip.	'1653513/dbj|BAA18426| 1.0e-08 (D90914) hypothetical protein [Synechocystis sp.]'		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7

Gene No.	322	Strand	-
Start	1443	End	6943
Name	OJ990203_06.9819.C7.o1.np	Method	AAT/NAP
Start	1871	End	6943
GI	1653513	Score	132
Exons	1871..1983, 2274..2365, 2486..2653, 3508..3592, 3897..4001, 4354..4494, 6913..6943		
GI Descrip.	(D90914) hypothetical protein [Synechocystis sp.]		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	322	Strand	-
Start	1443	End	6943
Name	OJ990203_06.9819.C7.o2.gp	Method	AAT/GAP
Start	2486	End	2692
GI	2797159	Score	208
Exons	2486..2578, 2669..2692		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	323	Strand	-
Start	9599	End	12787
Name	OJ990203_06.9819.C7.o3.np	Method	AAT/NAP
Start	9599	End	12787
GI	6522538	Score	606
Exons	9599..9715, 10108..10197, 10291..10368, 10488..10638, 10755..10816, 10901..10972, 12533..12787		
GI Descrip.	(AL132955) putative protein [Arabidopsis thaliana]		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o4.tm	Method	TBLASTX:Maize
Start	5265	End	6897
GI	none	Score	178
Exons	5265..5456, 5312..5419, 5370..5423, 6532..6810, 6536..6730, 6537..6731, 6721..6897, 6722..6889, 6723..6896, 6742..6897		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o1.tm	Method	TBLASTX:Maize
Start	6999	End	8140
GI	none	Score	43
Exons	6999..7022, 7000..7173, 7003..7173, 7062..7178, 7091..7174, 7579..7689, 7587..7694, 7588..7695, 7644..7691, 7765..8097, 7781..8140, 7781..8140		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o3.tc	Method	TBLASTX:Cress
Start	7587	End	8037
GI	none	Score	91
Exons	7587..7694, 7744..7851, 7781..7861, 7847..7978, 7930..8037, 7931..8017		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-

Start	18155	End	19684
Name	OJ990203_06.9819.C7.o3.tw	Method	TBLASTX:Wheat
Start	9586	End	9718
GI	none	Score	161
Exons	9586..9687, 9587..9700, 9590..9718		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o2.tm	Method	TBLASTX:Maize
Start	10141	End	13098
GI	none	Score	77
Exons	10141..10197, 10142..10198, 10289..10384, 10290..10382, 10291..10383, 10431..10640, 10483..10641, 10745..10819, 10757..10819, 10873..10974, 10888..11019, 10901..10978, 12511..12708, 12533..12709, 12534..12710, 12671..12790, 12706..12828, 12710..12790, 12742..12852, 12801..12863, 12810..12887, 12994..13044, 13017..13097, 13033..13098		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o2.ts	Method	TBLASTX:Soybean
Start	10578	End	12635
GI	none	Score	65
Exons	10578..10637, 10582..10638, 10754..10792, 10895..10975, 10901..10978, 12533..12634, 12537..12635		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o2.tw	Method	TBLASTX:Wheat
Start	10742	End	12787
GI	none	Score	92
Exons	10742..10819, 10849..10974, 10896..10973, 10901..10978, 12533..12634, 12534..12635, 12752..12787		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o4.np	Method	AAT/NAP
Start	18155	End	19661
GI	4415918	Score	921
Exons	18155..19661		
GI Descrip.	(AC006282) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o3.tm	Method	TBLASTX:Maize
Start	18180	End	19217
GI	none	Score	124
Exons	18180..18428, 18472..18888, 18480..19025, 18705..19025, 18741..19121, 18957..19205, 19008..19217, 19026..19211		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-

Start	18155	End	19684
Name	OJ990203_06.9819.C7.o1.ts	Method	TBLASTX:Soybean
Start	18189	End	18713
GI	none	Score	73
Exons	18189..18455, 18229..18360, 18465..18713		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o2.tc	Method	TBLASTX:Cress
Start	18279	End	18614
GI	none	Score	64
Exons	18279..18413, 18280..18399, 18471..18614, 18489..18566		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o1.tw	Method	TBLASTX:Wheat
Start	18594	End	19217
GI	none	Score	112
Exons	18594..18899, 18597..19058, 18598..18957, 18984..19217		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o1.tc	Method	TBLASTX:Cress
Start	18615	End	19217
GI	none	Score	104
Exons	18615..18734, 18654..18848, 18723..19046, 18732..18974, 18738..19172, 18960..19040, 19026..19214, 19044..19217		

Seq. No.	123	Seq. ID	OJ990203_06.9819.C7
Gene No.	324	Strand	-
Start	18155	End	19684
Name	OJ990203_06.9819.C7.o5.gp	Method	AAT/GAP
Start	19405	End	19684
GI	2442808	Score	456
Exons	19405..19684		

Seq. No.	124	Seq. ID	OJ990203_06.9819.C8
Gene No.	325	Strand	-
Start	498	End	2058
Name	OJ990203_06.9819.C8.o1.gs	Method	GENSCAN
Start	498	End	2058
GI	none	Score	.57
Exons	498..649, 1112..1170, 1819..1883, 1947..2058		

Seq. No.	125	Seq. ID	OJ990203_06.9819.C9
Gene No.	326	Strand	+
Start	69	End	159
Name	OJ990203_06.9819.C9.o1.gp	Method	AAT/GAP
Start	69	End	159
GI	LIB3431-022-P1-N1-G9	Score	128
Exons	69..159		
GI Descrip.	'1653513/dbj|BAA18426| 1.0e-08 (D90914) hypothetical protein [Synechocystis sp.]'		

Seq. No.	125	Seq. ID	OJ990203_06.9819.C9
Gene No.	327	Strand	+
Start	516	End	748
Name	OJ990203_06.9819.C9.o2.gp	Method	AAT/GAP
Start	516	End	748
GI	2428746	Score	412
Exons	516..748		
GI Descrip.	6041757/gb|AC011806.1|AC011806 7.0e-68 Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence		

Seq. No.	126	Seq. ID	OJ990203_06.9819.C10
Gene No.	328	Strand	+
Start	1	End	698
Name	OJ990203_06.9819.C10.o1.np	Method	AAT/NAP
Start	1	End	698
GI	6498441	Score	596
Exons	1..458, 677..698		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	126	Seq. ID	OJ990203_06.9819.C10
Gene No.	328	Strand	+
Start	1	End	698
Name	OJ990203_06.9819.C10.o1.gs	Method	GENSCAN
Start	134	End	602
GI	none	Score	.83
Exons	134..602		

Seq. No.	126	Seq. ID	OJ990203_06.9819.C10
Gene No.	329	Strand	-
Start	1	End	698
Name	OJ990203_06.9819.C10.o2.np	Method	AAT/NAP
Start	1	End	698
GI	5902445	Score	215
Exons	1..112, 501..698		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	126	Seq. ID	OJ990203_06.9819.C10
Gene No.	329	Strand	-
Start	1	End	698
Name	OJ990203_06.9819.C10.o1.tw	Method	TBLASTX:Wheat
Start	213	End	497
GI	none	Score	269
Exons	213..419, 216..497, 248..496		

Seq. No.	126	Seq. ID	OJ990203_06.9819.C10
Gene No.	329	Strand	-
Start	1	End	698
Name	OJ990203_06.9819.C10.o2.tw	Method	TBLASTX:Wheat
Start	501	End	695
GI	none	Score	78
Exons	501..695, 502..687		

Seq. No.	127	Seq. ID	OJ990203_06.9819.C14
Gene No.	330	Strand	-

Start	56	End	1264
Name	OJ990203_06.9819.C14.o1.gs	Method	GENSCAN
Start	56	End	1264
GI	none	Score	.92
Exons	56..1264		

Seq. No.	127	Seq. ID	OJ990203_06.9819.C14
Gene No.	330	Strand	-
Start	56	End	1264
Name	OJ990203_06.9819.C14.o1.np	Method	AAT/NAP
Start	59	End	1264
GI	1196998	Score	2083
Exons	59..1264		
GI Descrip.	(J01829) unknown protein [Transposon Tn10] gi|5103202|dbj|BAA78838.1| (AP000342) transposase of Tn10 [Plasmid R100] gi|5706382|dbj|BAA83097.1| (AB026428) transposase [Methylomonas aminofaciens] gi|5738092|gb|AAD50250.1|AF162223_9 (AF162223) IS10-right transposase [Shigella flexneri] gi|6721110|gb|AAF26764.1|AC007396_13 (AC007396) T4O12.21 [Arabidopsis thaliana]		

Seq. No.	127	Seq. ID	OJ990203_06.9819.C14
Gene No.	331	Strand	
Start	1224	End	1373
Name	OJ990203_06.9819.C14.o1.tc	Method	TBLASTX:Cress
Start	1224	End	1373
GI	none	Score	213
Exons	1224..1373, 1224..1370, 1225..1371, 1226..1372		

Seq. No.	128	Seq. ID	OJ990203_06.9819.C15
Gene No.	332	Strand	-
Start	545	End	658
Name	OJ990203_06.9819.C15.o1.gs	Method	GENSCAN
Start	545	End	658
GI	none	Score	.65
Exons	545..658		

Seq. No.	129	Seq. ID	OJ990203_06.9819.C18
Gene No.	333	Strand	-
Start	457	End	592
Name	OJ990203_06.9819.C18.o1.tm	Method	TBLASTX:Maize
Start	316	End	507
GI	none	Score	226
Exons	316..507, 322..381, 328..432, 360..434, 364..450, 382..432, 383..460		

Seq. No.	129	Seq. ID	OJ990203_06.9819.C18
Gene No.	333	Strand	-
Start	457	End	592
Name	OJ990203_06.9819.C18.o1.gs	Method	GENSCAN
Start	457	End	592
GI	none	Score	.5
Exons	457..521, 568..592		

Seq. No.	130	Seq. ID	OJ990203_06.9819.C19
Gene No.	334	Strand	-
Start	1	End	1002

Name	OJ990203_06.9819.C19.o1.np	Method	AAT/NAP
Start	1	End	1002
GI	6907086	Score	452
Exons	1..447, 507..1002		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	130	Seq. ID	OJ990203_06.9819.C19
Gene No.	334	Strand	-
Start	1	End	1002
Name	OJ990203_06.9819.C19.o1.gs	Method	GENSCAN
Start	541	End	752
GI	none	Score	.81
Exons	541..752		

Seq. No.	131	Seq. ID	OJ990203_06.9819.C20
Gene No.	335	Strand	-
Start	228	End	291
Name	OJ990203_06.9819.C20.o1.gs	Method	GENSCAN
Start	228	End	291
GI	none	Score	.69
Exons	228..291		

Seq. No.	132	Seq. ID	OJ990203_06.9819.C21
Gene No.	336	Strand	-
Start	313	End	597
Name	OJ990203_06.9819.C21.o1.gs	Method	GENSCAN
Start	313	End	597
GI	none	Score	.49
Exons	313..597		

Seq. No.	133	Seq. ID	OJ990203_06.9819.C23
Gene No.	337	Strand	
Start	326	End	517
Name	OJ990203_06.9819.C23.o1.tm	Method	TBLASTX:Maize
Start	326	End	517
GI	none	Score	178
Exons	326..517, 373..480, 431..484		

Seq. No.	134	Seq. ID	OJ990203_06.9819.C24
Gene No.	338	Strand	-
Start	511	End	619
Name	OJ990203_06.9819.C24.o1.gs	Method	GENSCAN
Start	511	End	619
GI	none	Score	.83
Exons	511..619		

Seq. No.	135	Seq. ID	OJ990203_06.9819.C26
Gene No.	339	Strand	-
Start	449	End	537
Name	OJ990203_06.9819.C26.o1.gp	Method	AAT/GAP
Start	449	End	537
GI	34521_1.R1084	Score	152
Exons	449..537		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	135	Seq. ID	OJ990203_06.9819.C26

Gene No.	340	Strand	-
Start	506	End	663
Name	OJ990203_06.9819.C26.o1.gs	Method	GENSCAN
Start	506	End	663
GI	none	Score	.7
Exons	506..663		

Seq. No.	136	Seq. ID	OJ990203_06.9819.C30
Gene No.	341	Strand	-
Start	226	End	984
Name	OJ990203_06.9819.C30.o1.gs	Method	GENSCAN
Start	226	End	940
GI	none	Score	.91
Exons	226..702, 842..940		

Seq. No.	136	Seq. ID	OJ990203_06.9819.C30
Gene No.	341	Strand	-
Start	226	End	984
Name	OJ990203_06.9819.C30.o1.np	Method	AAT/NAP
Start	725	End	984
GI	6721561	Score	175
Exons	725..984		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	137	Seq. ID	OJ990203_06.9819.C32
Gene No.	342	Strand	+
Start	260	End	333
Name	OJ990203_06.9819.C32.o1.gs	Method	GENSCAN
Start	260	End	333
GI	none	Score	.99
Exons	260..333		

Seq. No.	138	Seq. ID	OJ990203_06.9819.C34
Gene No.	343	Strand	+
Start	24	End	395
Name	OJ990203_06.9819.C34.o1.gs	Method	GENSCAN
Start	24	End	395
GI	none	Score	.4
Exons	24..169, 284..395		

Seq. No.	139	Seq. ID	OJ990203_06.9819.C36
Gene No.	344	Strand	+
Start	231	End	652
Name	OJ990203_06.9819.C36.o1.gp	Method	AAT/GAP
Start	231	End	652
GI	2428746	Score	204
Exons	231..248, 506..652		
GI Descrip.	6041757/gb|AC011806.1|AC011806 7.0e-68 Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence		

Seq. No.	139	Seq. ID	OJ990203_06.9819.C36
Gene No.	344	Strand	+

Start	231	End	652
Name	OJ990203_06.9819.C36.o1.gs	Method	GENSCAN
Start	486	End	566
GI	none	Score	.53
Exons	486..566		

Seq. No.	140	Seq. ID	OJ990203_06.9819.C40
Gene No.	345	Strand	+
Start	225	End	506
Name	OJ990203_06.9819.C40.o1.gs	Method	GENSCAN
Start	225	End	506
GI	none	Score	.61
Exons	225..506		

Seq. No.	141	Seq. ID	OJ990203_06.9819.C42
Gene No.	346	Strand	+
Start	88	End	736
Name	OJ990203_06.9819.C42.o1.gs	Method	GENSCAN
Start	88	End	220
GI	none	Score	.83
Exons	88..220		

Seq. No.	141	Seq. ID	OJ990203_06.9819.C42
Gene No.	346	Strand	+
Start	88	End	736
Name	OJ990203_06.9819.C42.o1.np	Method	AAT/NAP
Start	88	End	736
GI	3063470	Score	221
Exons	88..234, 683..736		
GI Descrip.	(AC003981) F22O13.32 [Arabidopsis thaliana]		

Seq. No.	141	Seq. ID	OJ990203_06.9819.C42
Gene No.	347	Strand	-
Start	82	End	315
Name	OJ990203_06.9819.C42.o1.gp	Method	AAT/GAP
Start	82	End	229
GI	3761372	Score	196
Exons	82..229		
GI Descrip.	1945282/emb|Y11351|OSMYB1402 2.0e-15 O.sativa mRNA for myb factor, 1402 bp		

Seq. No.	141	Seq. ID	OJ990203_06.9819.C42
Gene No.	347	Strand	-
Start	82	End	315
Name	OJ990203_06.9819.C42.o1.ts	Method	TBLASTX:Soybean
Start	84	End	234
GI	none	Score	251
Exons	84..221, 88..234		

Seq. No.	141	Seq. ID	OJ990203_06.9819.C42
Gene No.	347	Strand	-
Start	82	End	315
Name	OJ990203_06.9819.C42.o1.tc	Method	TBLASTX:Cress
Start	85	End	234
GI	none	Score	252
Exons	85..234, 87..221		

Seq. No.	141	Seq. ID	OJ990203_06.9819.C42
Gene No.	347	Strand	-
Start	82	End	315
Name	OJ990203_06.9819.C42.o1.tm	Method	TBLASTX:Maize
Start	87	End	315
GI	none	Score	254
Exons	87..233, 88..234, 109..315		

Seq. No.	141	Seq. ID	OJ990203_06.9819.C42
Gene No.	347	Strand	-
Start	82	End	315
Name	OJ990203_06.9819.C42.o1.tw	Method	TBLASTX:Wheat
Start	87	End	234
GI	none	Score	191
Exons	87..221, 88..234, 109..234		

Seq. No.	142	Seq. ID	OJ990203_06.9819.C43
Gene No.	348	Strand	-
Start	189	End	740
Name	OJ990203_06.9819.C43.o1.np	Method	AAT/NAP
Start	180	End	740
GI	5902444	Score	404
Exons	180..740		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	142	Seq. ID	OJ990203_06.9819.C43
Gene No.	348	Strand	-
Start	189	End	740
Name	OJ990203_06.9819.C43.o1.gs	Method	GENSCAN
Start	189	End	665
GI	none	Score	.92
Exons	189..665		

Seq. No.	142	Seq. ID	OJ990203_06.9819.C43
Gene No.	348	Strand	-
Start	189	End	740
Name	OJ990203_06.9819.C43.o1.tw	Method	TBLASTX:Wheat
Start	317	End	738
GI	none	Score	38
Exons	317..370, 360..596, 370..435, 375..590, 478..594, 688..738		

Seq. No.	143	Seq. ID	OJ990203_06.9819.C44
Gene No.	349	Strand	-
Start	156	End	557
Name	OJ990203_06.9819.C44.o1.gp	Method	AAT/GAP
Start	156	End	557
GI	5816562	Score	601
Exons	156..557		
GI Descrip.	6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10		

Seq. No.	144	Seq. ID	OJ990203_06.9819.C45
Gene No.	350	Strand	+
Start	425	End	900
Name	OJ990203_06.9819.C45.o1.tm	Method	TBLASTX:Maize
Start	422	End	784
GI	none	Score	189

Exons	422..634, 427..621, 600..749, 613..696, 672..722, 722..784, 730..783		
Seq. No.	144	Seq. ID	OJ990203_06.9819.C45
Gene No.	350	Strand	+
Start	425	End	900
Name	OJ990203_06.9819.C45.o1.np	Method	AAT/NAP
Start	425	End	900
GI	6522544	Score	261
Exons	425..900		
GI Descrip.	(AL132955) putative protein [Arabidopsis thaliana]		
Seq. No.	145	Seq. ID	OJ990203_06.9819.C46
Gene No.	351	Strand	-
Start	1	End	509
Name	OJ990203_06.9819.C46.o1.np	Method	AAT/NAP
Start	1	End	509
GI	5902445	Score	408
Exons	1..509		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		
Seq. No.	145	Seq. ID	OJ990203_06.9819.C46
Gene No.	351	Strand	-
Start	1	End	509
Name	OJ990203_06.9819.C46.o1.tm	Method	TBLASTX:Maize
Start	78	End	399
GI	none	Score	73
Exons	78..194, 78..398, 88..399		
Seq. No.	145	Seq. ID	OJ990203_06.9819.C46
Gene No.	351	Strand	-
Start	1	End	509
Name	OJ990203_06.9819.C46.o1.tw	Method	TBLASTX:Wheat
Start	102	End	410
GI	none	Score	148
Exons	102..410, 108..404, 109..408		
Seq. No.	145	Seq. ID	OJ990203_06.9819.C46
Gene No.	351	Strand	-
Start	1	End	509
Name	OJ990203_06.9819.C46.o1.gs	Method	GENSCAN
Start	199	End	406
GI	none	Score	.94
Exons	199..406		
Seq. No.	146	Seq. ID	OJ990203_06.9819.C47
Gene No.	352	Strand	+
Start	1	End	731
Name	OJ990203_06.9819.C47.o1.np	Method	AAT/NAP
Start	1	End	731
GI	5042454	Score	71
Exons	1..83, 287..351, 668..731		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		
Seq. No.	146	Seq. ID	OJ990203_06.9819.C47
Gene No.	353	Strand	-
Start	309	End	583

Name	OJ990203_06.9819.C47.o1.gs	Method	GENSCAN
Start	309	End	583
GI	none	Score	.79
Exons	309..348, 447..583		

Seq. No.	147	Seq. ID	OJ990203_07.9819.C1
Gene No.	354	Strand	+
Start	135	End	620
Name	OJ990203_07.9819.C1.o1.gp	Method	AAT/GAP
Start	135	End	620
GI	uC-osf1cyp110c07b1	Score	893
Exons	135..620		
GI Descrip.	'4680178/gb|AF111709.1|AF111709 5.0e-81 Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences; and unknown genes'		

Seq. No.	147	Seq. ID	OJ990203_07.9819.C1
Gene No.	354	Strand	+
Start	135	End	620
Name	OJ990203_07.9819.C1.o1.tm	Method	TBLASTX:Maize
Start	151	End	519
GI	none	Score	181
Exons	151..381, 228..374, 424..465, 427..519		

Seq. No.	148	Seq. ID	OJ990203_07.9819.C2
Gene No.	355	Strand	+
Start	455	End	528
Name	OJ990203_07.9819.C2.o1.gp	Method	AAT/GAP
Start	455	End	528
GI	LIB3433-030-P1-K1-C5	Score	125
Exons	455..528		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	149	Seq. ID	OJ990203_07.9819.C4
Gene No.	356	Strand	-
Start	1	End	1454
Name	OJ990203_07.9819.C4.o1.np	Method	AAT/NAP
Start	1	End	1454
GI	5852179	Score	408
Exons	1..224, 899..1135, 1210..1454		
GI Descrip.	(AL117265) zhb0009.1 [Oryza sativa]		

Seq. No.	149	Seq. ID	OJ990203_07.9819.C4
Gene No.	356	Strand	-
Start	1	End	1454
Name	OJ990203_07.9819.C4.o1.gs	Method	GENSCAN
Start	897	End	1329
GI	none	Score	.73
Exons	897..1163, 1186..1329		

Seq. No.	150	Seq. ID	OJ990203_07.9819.C5
Gene No.	357	Strand	-
Start	270	End	1248
Name	OJ990203_07.9819.C5.o1.gs	Method	GENSCAN
Start	270	End	1248
GI	none	Score	.56

Exons	270..357, 1130..1248		
Seq. No.	150	Seq. ID	OJ990203_07.9819.C5
Gene No.	358	Strand	-
Start	1776	End	1827
Name	OJ990203_07.9819.C5.o1.gp	Method	AAT/GAP
Start	1776	End	1827
GI	4715947	Score	67
Exons	1776..1827		
GI Descrip.	2252840 3.0e-09 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi_6049882_gb_AAF02797.1_AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]		
Seq. No.	151	Seq. ID	OJ990203_07.9819.C6
Gene No.	359	Strand	+
Start	1495	End	2190
Name	OJ990203_07.9819.C6.o1.gs	Method	GENSCAN
Start	1495	End	2190
GI	none	Score	.61
Exons	1495..1782, 2128..2190		
Seq. No.	152	Seq. ID	OJ990203_07.9819.C7
Gene No.	360	Strand	+
Start	200	End	494
Name	OJ990203_07.9819.C7.o1.gs	Method	GENSCAN
Start	200	End	494
GI	none	Score	.93
Exons	200..302, 420..494		
Seq. No.	153	Seq. ID	OJ990203_07.9819.C10
Gene No.	361	Strand	+
Start	362	End	586
Name	OJ990203_07.9819.C10.o1.gs	Method	GENSCAN
Start	362	End	586
GI	none	Score	.64
Exons	362..586		
Seq. No.	154	Seq. ID	OJ990203_07.9819.C11
Gene No.	362	Strand	+
Start	125	End	681
Name	OJ990203_07.9819.C11.o1.gs	Method	GENSCAN
Start	125	End	681
GI	none	Score	.69
Exons	125..227, 345..419, 513..681		
Seq. No.	155	Seq. ID	OJ990203_07.9819.C12
Gene No.	363	Strand	+
Start	1	End	698
Name	OJ990203_07.9819.C12.o1.np	Method	AAT/NAP
Start	1	End	397
GI	5902447	Score	307
Exons	1..397		
GI Descrip.	(AB030283) orf4 [Oryza sativa]		
Seq. No.	155	Seq. ID	OJ990203_07.9819.C12

Gene No.	363	Strand	+
Start	1	End	698
Name	OJ990203_07.9819.C12.o2.np	Method	AAT/NAP
Start	1	End	698
GI	6691716	Score	288
Exons	1..105, 182..367, 445..698		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	155	Seq. ID	OJ990203_07.9819.C12
Gene No.	363	Strand	+
Start	1	End	698
Name	OJ990203_07.9819.C12.o1.gs	Method	GENSCAN
Start	80	End	584
GI	none	Score	.73
Exons	80..367, 445..584		

Seq. No.	156	Seq. ID	OJ990203_07.9819.C13
Gene No.	364	Strand	-
Start	53	End	1261
Name	OJ990203_07.9819.C13.o1.gs	Method	GENSCAN
Start	53	End	1261
GI	none	Score	.93
Exons	53..1261		

Seq. No.	156	Seq. ID	OJ990203_07.9819.C13
Gene No.	364	Strand	-
Start	53	End	1261
Name	OJ990203_07.9819.C13.o1.np	Method	AAT/NAP
Start	56	End	1261
GI	1196998	Score	2114
Exons	56..1261		
GI Descrip.	(J01829) unknown protein [Transposon Tn10] gi|5103202|dbj|BAA78838.1| (AP000342) transposase of Tn10 [Plasmid R100] gi|5706382|dbj|BAA83097.1| (AB026428) transposase [Methylomonas aminofaciens] gi|5738092|gb|AAD50250.1|AF162223_9 (AF162223) IS10-right transposase [Shigella flexneri] gi|6721110|gb|AAF26764.1|AC007396_13 (AC007396) T4O12.21 [Arabidopsis thaliana]		

Seq. No.	156	Seq. ID	OJ990203_07.9819.C13
Gene No.	365	Strand	
Start	1221	End	1391
Name	OJ990203_07.9819.C13.o1.tc	Method	TBLASTX:Cress
Start	1221	End	1391
GI	none	Score	221
Exons	1221..1391, 1222..1368, 1223..1372		

Seq. No.	157	Seq. ID	OJ990203_07.9819.C14
Gene No.	366	Strand	-
Start	102	End	652
Name	OJ990203_07.9819.C14.o1.gs	Method	GENSCAN
Start	102	End	652
GI	none	Score	.89
Exons	102..652		

Seq. No.	158	Seq. ID	OJ990203_07.9819.C15
Gene No.	367	Strand	+
Start	267	End	501
Name	OJ990203_07.9819.C15.o1.gs	Method	GENSCAN
Start	267	End	501
GI	none	Score	.68
Exons	267..382, 405..501		

Seq. No.	159	Seq. ID	OJ990203_07.9819.C17
Gene No.	368	Strand	-
Start	282	End	367
Name	OJ990203_07.9819.C17.o1.gs	Method	GENSCAN
Start	282	End	367
GI	none	Score	.54
Exons	282..367		

Seq. No.	160	Seq. ID	OJ990203_07.9819.C18
Gene No.	369	Strand	+
Start	151	End	2538
Name	OJ990203_07.9819.C18.o1.np	Method	AAT/NAP
Start	151	End	2538
GI	6069653	Score	77
Exons	151..409, 458..699, 748..1038, 2506..2538		
GI Descrip.	(AP000616) hypothetical protein [Oryza sativa]		

Seq. No.	160	Seq. ID	OJ990203_07.9819.C18
Gene No.	370	Strand	+
Start	2508	End	5873
Name	OJ990203_07.9819.C18.o2.np	Method	AAT/NAP
Start	2508	End	5873
GI	3831457	Score	53
Exons	2508..2825, 5848..5873		
GI Descrip.	(AC005700) putative ligand-gated ion channel subunit [Arabidopsis thaliana]		

Seq. No.	160	Seq. ID	OJ990203_07.9819.C18
Gene No.	370	Strand	+
Start	2508	End	5873
Name	OJ990203_07.9819.C18.o2.gs	Method	GENSCAN
Start	5130	End	5358
GI	none	Score	.98
Exons	5130..5358		

Seq. No.	160	Seq. ID	OJ990203_07.9819.C18
Gene No.	370	Strand	+
Start	2508	End	5873
Name	OJ990203_07.9819.C18.o3.np	Method	AAT/NAP
Start	5130	End	5873
GI	6907105	Score	293
Exons	5130..5358, 5825..5873		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	161	Seq. ID	OJ990203_07.9819.C20
Gene No.	371	Strand	+
Start	95	End	1144
Name	OJ990203_07.9819.C20.o1.np	Method	AAT/NAP
Start	95	End	999

GI	6907105	Score	153
Exons	95..344, 469..571, 858..999		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	161	Seq. ID	OJ990203_07.9819.C20
Gene No.	371	Strand	+
Start	95	End	1144
Name	OJ990203_07.9819.C20.o1.gs	Method	GENSCAN
Start	502	End	1144
GI	none	Score	.45
Exons	502..561, 908..967, 1049..1144		

Seq. No.	162	Seq. ID	OJ990203_07.9819.C21
Gene No.	372	Strand	+
Start	335	End	2960
Name	OJ990203_07.9819.C21.o1.gs	Method	GENSCAN
Start	335	End	2262
GI	none	Score	.99
Exons	335..388, 573..712, 797..868, 1241..1315, 1501..2262		

Seq. No.	162	Seq. ID	OJ990203_07.9819.C21
Gene No.	372	Strand	+
Start	335	End	2960
Name	OJ990203_07.9819.C21.o1.np	Method	AAT/NAP
Start	578	End	2960
GI	6539581	Score	314
Exons	578..676, 1277..1305, 1509..1956, 2062..2117, 2751..2960		
GI Descrip.	(AP000837) Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10; hypothetical protein (AL035538) [Oryza sativa]		

Seq. No.	162	Seq. ID	OJ990203_07.9819.C21
Gene No.	373	Strand	-
Start	2262	End	2960
Name	OJ990203_07.9819.C21.o1.tm	Method	TBLASTX:Maize
Start	1594	End	1809
GI	none	Score	183
Exons	1594..1809, 1623..1763		

Seq. No.	162	Seq. ID	OJ990203_07.9819.C21
Gene No.	373	Strand	-
Start	2262	End	2960
Name	OJ990203_07.9819.C21.o2.np	Method	AAT/NAP
Start	2262	End	2960
GI	5042454	Score	138
Exons	2262..2322, 2684..2960		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	162	Seq. ID	OJ990203_07.9819.C21
Gene No.	373	Strand	-
Start	2262	End	2960
Name	OJ990203_07.9819.C21.o2.gs	Method	GENSCAN
Start	2601	End	2720
GI	none	Score	.97
Exons	2601..2720		

Seq. No.	163	Seq. ID	OJ990203_07.9819.C22
Gene No.	374	Strand	+

Start	1	End	2499
Name	OJ990203_07.9819.C22.o1.np	Method	AAT/NAP
Start	1	End	2499
GI	6539581	Score	1958
Exons	1..26, 559..2499		
GI Descrip.	(AP000837) Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10; hypothetical protein (AL035538) [Oryza sativa]		

Seq. No.	163	Seq. ID	OJ990203_07.9819.C22
Gene No.	374	Strand	+
Start	1	End	2499
Name	OJ990203_07.9819.C22.o1.gs	Method	GENSCAN
Start	557	End	1906
GI	none	Score	.88
Exons	557..1906		

Seq. No.	163	Seq. ID	OJ990203_07.9819.C22
Gene No.	374	Strand	+
Start	1	End	2499
Name	OJ990203_07.9819.C22.o2.tw	Method	TBLASTX:Wheat
Start	611	End	901
GI	none	Score	222
Exons	611..901, 737..895		

Seq. No.	163	Seq. ID	OJ990203_07.9819.C22
Gene No.	374	Strand	+
Start	1	End	2499
Name	OJ990203_07.9819.C22.o1.tc	Method	TBLASTX:Cress
Start	728	End	1048
GI	none	Score	225
Exons	728..1048, 755..949		

Seq. No.	163	Seq. ID	OJ990203_07.9819.C22
Gene No.	374	Strand	+
Start	1	End	2499
Name	OJ990203_07.9819.C22.o1.tm	Method	TBLASTX:Maize
Start	734	End	1117
GI	none	Score	282
Exons	734..1117, 737..1105		

Seq. No.	163	Seq. ID	OJ990203_07.9819.C22
Gene No.	374	Strand	+
Start	1	End	2499
Name	OJ990203_07.9819.C22.o1.ts	Method	TBLASTX:Soybean
Start	794	End	1336
GI	none	Score	383
Exons	794..1336, 794..1129		

Seq. No.	163	Seq. ID	OJ990203_07.9819.C22
Gene No.	374	Strand	+
Start	1	End	2499
Name	OJ990203_07.9819.C22.o1.tw	Method	TBLASTX:Wheat
Start	967	End	1399
GI	none	Score	236
Exons	967..1095, 968..1399, 1204..1398		

Seq. No.	164	Seq. ID	OJ990203_07.9819.C23

Gene No.	375	Strand	-
Start	172	End	358
Name	OJ990203_07.9819.C23.o1.gs	Method	GENSCAN
Start	172	End	358
GI	none	Score	.87
Exons	172..358		

Seq. No.	165	Seq. ID	OJ990203_07.9819.C25
Gene No.	376	Strand	+
Start	1	End	734
Name	OJ990203_07.9819.C25.o1.np	Method	AAT/NAP
Start	1	End	734
GI	6907086	Score	345
Exons	1..734		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	165	Seq. ID	OJ990203_07.9819.C25
Gene No.	377	Strand	-
Start	284	End	411
Name	OJ990203_07.9819.C25.o1.gs	Method	GENSCAN
Start	284	End	411
GI	none	Score	.4
Exons	284..411		

Seq. No.	166	Seq. ID	OJ990203_07.9819.C26
Gene No.	378	Strand	+
Start	531	End	668
Name	OJ990203_07.9819.C26.o1.gp	Method	AAT/GAP
Start	531	End	668
GI	61605_1.R1084	Score	183
Exons	531..668		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	167	Seq. ID	OJ990203_07.9819.C27
Gene No.	379	Strand	+
Start	1	End	890
Name	OJ990203_07.9819.C27.o1.np	Method	AAT/NAP
Start	1	End	890
GI	4220443	Score	103
Exons	1..53, 612..890		
GI Descrip.	(AC006216) Similar to gb|X74772 SF16 protein from Helianthus annuus and contains calmodulin-binding motif PF|00612. [Arabidopsis thaliana]		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	380	Strand	+
Start	81	End	587
Name	OJ990203_07.9819.C28.o1.gs	Method	GENSCAN
Start	81	End	587
GI	none	Score	.66
Exons	81..587		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	381	Strand	+
Start	22181	End	22754
Name	OJ990203_07.9819.C28.o5.gs	Method	GENSCAN

Start	22181	End	22754
GI	none	Score	.67
Exons	22181..22287, 22658..22754		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	382	Strand	+
Start	23600	End	23836
Name	OJ990203_07.9819.C28.o6.gs	Method	GENSCAN
Start	23600	End	23836
GI	none	Score	.54
Exons	23600..23836		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	383	Strand	-
Start	396	End	5036
Name	OJ990203_07.9819.C28.o1.np	Method	AAT/NAP
Start	396	End	5036
GI	6016874	Score	2202
Exons	396..485, 2054..2392, 2859..3199, 3317..3496, 3890..4049, 4440..4672, 4737..4874, 4958..5036		
GI Descrip.	(AP000570) ESTs C19143(E10020), D25076(R3116) correspond to a region of the predicted gene.; Similar to putative AC9 transposase. (P03010) [Oryza sativa]		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	383	Strand	-
Start	396	End	5036
Name	OJ990203_07.9819.C28.o1.gp	Method	AAT/GAP
Start	3839	End	4347
GI	uC-osflcyp110c07b1	Score	958
Exons	3839..4347		
GI Descrip.	'4680178/gb|AF111709.1|AF111709 5.0e-81 Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences; and unknown genes'		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	384	Strand	-
Start	5423	End	14747
Name	OJ990203_07.9819.C28.o3.gs	Method	GENSCAN
Start	5423	End	13952
GI	none	Score	.85
Exons	5423..5802, 6305..6453, 7759..7826, 9540..9743, 9767..9979, 10071..10275, 10837..10944, 11086..11217, 11444..11679, 12946..13152, 13234..13423, 13425..13469, 13537..13952		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	384	Strand	-
Start	5423	End	14747
Name	OJ990203_07.9819.C28.o2.np	Method	AAT/NAP
Start	5435	End	5592
GI	6907084	Score	169
Exons	5435..5592		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	384	Strand	-
Start	5423	End	14747

Name	OJ990203_07.9819.C28.o2.gp	Method	AAT/GAP
Start	6985	End	7394
GI	12650_1.R1084	Score	222
Exons	6985..7147, 7374..7394		
GI Descrip.	'5803242/dbj|AP000399.1|AP000399 2.0e-24 Oryza sativa genomic DNA, chromosome 6, clone:P0535G04'		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	384	Strand	-
Start	5423	End	14747
Name	OJ990203_07.9819.C28.o3.np	Method	AAT/NAP
Start	11012	End	14747
GI	4415916	Score	589
Exons	11012..11217, 11444..11679, 12946..13152, 13234..13423, 13537..13630, 13865..13977, 14416..14539, 14688..14747		
GI Descrip.	(AC006282) putative pectinesterase [Arabidopsis thaliana]		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	385	Strand	-
Start	14906	End	24825
Name	OJ990203_07.9819.C28.o4.gs	Method	GENSCAN
Start	14906	End	20941
GI	none	Score	.75
Exons	14906..15021, 15375..15439, 15646..15677, 16688..16893, 17297..17669, 17752..17853, 17885..17893, 18803..18878, 19611..19652, 20400..20720, 20880..20941		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	385	Strand	-
Start	14906	End	24825
Name	OJ990203_07.9819.C28.o4.np	Method	AAT/NAP
Start	15545	End	24825
GI	3643608	Score	942
Exons	15545..15677, 15803..15966, 16688..16898, 17116..17669, 17752..17853, 18803..18915, 19611..19688, 19773..19831, 20376..20557, 24770..24825		
GI Descrip.	(AC005395) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	385	Strand	-
Start	14906	End	24825
Name	OJ990203_07.9819.C28.o3.gp	Method	AAT/GAP
Start	17639	End	18886
GI	uC-osroM202017h10b1	Score	447
Exons	17639..17669, 17752..17853, 18663..18728, 18803..18886		
GI Descrip.	'2252840 3.0e-09 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi_6049882_gb_AAF02797.1_AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]'		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	386	Strand	-
Start	25213	End	26868
Name	OJ990203_07.9819.C28.o7.gs	Method	GENSCAN
Start	25213	End	26868
GI	none	Score	.51

Exons	25213..26868		
Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	386	Strand	-
Start	25213	End	26868
Name	OJ990203_07.9819.C28.o5.np	Method	AAT/NAP
Start	25420	End	25608
GI	6598344	Score	61
Exons	25420..25608		
GI Descrip.	(AC002335) hypothetical protein [Arabidopsis thaliana]		
Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o1.tm	Method	TBLASTX:Maize
Start	2197	End	13428
GI	none	Score	66
Exons	2197..2331, 12933..13091, 12946..13095, 12946..13173, 12956..13180, 13205..13324, 13225..13323, 13327..13422, 13331..13426, 13339..13428		
Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o4.tm	Method	TBLASTX:Maize
Start	2922	End	3165
GI	none	Score	97
Exons	2922..3155, 3007..3165		
Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o7.tm	Method	TBLASTX:Maize
Start	3277	End	3629
GI	none	Score	140
Exons	3277..3618, 3348..3629		
Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o6.tm	Method	TBLASTX:Maize
Start	3834	End	4148
GI	none	Score	109
Exons	3834..4061, 3835..4053, 4074..4148		
Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o3.tm	Method	TBLASTX:Maize
Start	4242	End	4688
GI	none	Score	110
Exons	4242..4280, 4275..4331, 4368..4616, 4408..4617, 4602..4688		
Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o8.tm	Method	TBLASTX:Maize

Start	11065	End	11218
GI	none	Score	174
Exons	11065..11202, 11070..11216, 11070..11216, 11189..11218		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o2.tm	Method	TBLASTX:Maize
Start	11443	End	11676
GI	none	Score	141
Exons	11443..11676, 11444..11620		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o2.tc	Method	TBLASTX:Cress
Start	11488	End	13153
GI	none	Score	167
Exons	11488..11607, 11575..11676, 12946..13152, 12956..13153		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o1.ts	Method	TBLASTX:Soybean
Start	12946	End	13423
GI	none	Score	239
Exons	12946..13155, 12953..13153, 13234..13311, 13235..13309, 13327..13422, 13334..13423		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o1.tw	Method	TBLASTX:Wheat
Start	12946	End	13422
GI	none	Score	150
Exons	12946..13155, 12968..13153, 13234..13422, 13253..13342		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o10.tm	Method	TBLASTX:Maize
Start	13536	End	13761
GI	none	Score	116
Exons	13536..13760, 13539..13742, 13693..13761		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o9.tm	Method	TBLASTX:Maize
Start	15530	End	15861
GI	none	Score	143
Exons	15530..15676, 15560..15676, 15561..15677, 15800..15853, 15800..15853, 15802..15861		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761

Name	OJ990203_07.9819.C28.o2.ts	Method	TBLASTX:Soybean
Start	15823	End	17183
GI	none	Score	118
Exons	15823..15969, 15836..15961, 16679..16936, 16680..16901, 17121..17183		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o1.tc	Method	TBLASTX:Cress
Start	15841	End	16901
GI	none	Score	106
Exons	15841..15969, 15845..15961, 16679..16900, 16688..16894, 16692..16901		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o5.tm	Method	TBLASTX:Maize
Start	16697	End	17403
GI	none	Score	69
Exons	16697..16756, 16698..16757, 16757..16918, 16757..16939, 16761..16919, 17120..17209, 17121..17234, 17122..17208, 17217..17336, 17286..17339, 17325..17396, 17326..17403		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o3.ts	Method	TBLASTX:Soybean
Start	17580	End	17861
GI	none	Score	56
Exons	17580..17666, 17584..17664, 17752..17856, 17753..17854, 17763..17861		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o11.tm	Method	TBLASTX:Maize
Start	17749	End	19800
GI	none	Score	126
Exons	17749..17856, 17750..17845, 17751..17861, 18660..18728, 18664..18729, 18664..18735, 18671..18730, 18786..18917, 18800..18925, 18802..18921, 19590..19688, 19609..19686, 19610..19708, 19774..19800		

Seq. No.	168	Seq. ID	OJ990203_07.9819.C28
Gene No.	387	Strand	-
Start	28420	End	28761
Name	OJ990203_07.9819.C28.o8.gs	Method	GENSCAN
Start	28420	End	28761
GI	none	Score	.5
Exons	28420..28761		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	388	Strand	+
Start	2327	End	18341
Name	OJ990203_07.9819.C29.o1.gs	Method	GENSCAN

Start	2327	End	15137
GI	none	Score	.81
Exons	2327..2416, 3533..3663, 4728..4847, 4925..5054, 5319..5372, 6276..6350, 6564..6632, 8706..8877, 9158..9312, 9407..9520, 10109..10334, 10945..11045, 11127..11204, 11287..11379, 11472..11501, 11742..12083, 12160..12241, 12315..12410, 12486..12665, 12746..12829, 13607..13777, 13866..14029, 14709..15137		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	388	Strand	+
Start	2327	End	18341
Name	OJ990203_07.9819.C29.o1.gp	Method	AAT/GAP
Start	6669	End	6731
GI	4715947	Score	74
Exons	6669..6731		
GI Descrip.	2252840 3.0e-09 (AF013293) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana] >gi_6049882_gb_AAF02797.1_AF195115_17 (AF195115) contains regions of similarity to Haemophilus influenzae permease (SP:P38767) [Arabidopsis thaliana]		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	388	Strand	+
Start	2327	End	18341
Name	OJ990203_07.9819.C29.o1.np	Method	AAT/NAP
Start	8321	End	18341
GI	6633835	Score	1641
Exons	8321..8453, 9176..9303, 9410..9520, 10133..10237, 10770..10877, 10962..11045, 11127..11212, 11334..11405, 11745..12083, 12160..12241, 12315..12410, 12486..12852, 12998..13201, 13274..13440, 13524..13777, 13866..14029, 14709..14780, 18256..18341		
GI Descrip.	(AC008047) F2K11.1 [Arabidopsis thaliana]		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	388	Strand	+
Start	2327	End	18341
Name	OJ990203_07.9819.C29.o2.gp	Method	AAT/GAP
Start	8389	End	8661
GI	2427384	Score	480
Exons	8389..8661		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	388	Strand	+
Start	2327	End	18341
Name	OJ990203_07.9819.C29.o3.gp	Method	AAT/GAP
Start	10108	End	11523
GI	3761361	Score	1013
Exons	10108..10334, 10780..10877, 10963..11045, 11127..11204, 11287..11379, 11472..11523		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	388	Strand	+
Start	2327	End	18341
Name	OJ990203_07.9819.C29.o4.gp	Method	AAT/GAP
Start	11997	End	12257

GI	LIB3479-008-Q6-K1-F3	Score	292
Exons	11997..12083, 12160..12257		
GI Descrip.	'6015437/dbj|AB008112.1|AB008112 6.0e-11 Homo sapiens PEX1 mRNA, complete cds'		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	388	Strand	+
Start	2327	End	18341
Name	OJ990203_07.9819.C29.o5.gp	Method	AAT/GAP
Start	13952	End	15344
GI	LIB3433-030-P1-K1-C5	Score	991
Exons	13952..14029, 14709..15100, 15271..15344		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	389	Strand	+
Start	25482	End	25891
Name	OJ990203_07.9819.C29.o6.gp	Method	AAT/GAP
Start	25482	End	25891
GI	5816562	Score	612
Exons	25482..25891		
GI Descrip.	6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	390	Strand	+
Start	26939	End	29855
Name	OJ990203_07.9819.C29.o3.gs	Method	GENSCAN
Start	26939	End	29759
GI	none	Score	.95
Exons	26939..27823, 27910..28154, 28279..28637, 28715..28902, 28977..29166, 29229..29342, 29416..29759		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	390	Strand	+
Start	26939	End	29855
Name	OJ990203_07.9819.C29.o5.np	Method	AAT/NAP
Start	26939	End	29855
GI	6691716	Score	2492
Exons	26939..27827, 28025..28202, 28279..28375, 28452..28637, 28715..28902, 28977..29079, 29229..29342, 29416..29855		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	391	Strand	-
Start	15736	End	25910
Name	OJ990203_07.9819.C29.o2.gs	Method	GENSCAN
Start	15736	End	25910
GI	none	Score	.47
Exons	15736..15943, 17373..17461, 18663..18845, 19179..19435, 19527..19641, 19938..20020, 20114..20188, 20306..20408, 20571..20656, 20730..20842, 21152..21368, 22583..23634, 23849..23922, 24446..24802, 24828..25151, 25863..25910		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	391	Strand	-
Start	15736	End	25910
Name	OJ990203_07.9819.C29.o2.np	Method	AAT/NAP
Start	18773	End	19894
GI	3335367	Score	208
Exons	18773..18845, 19102..19340, 19823..19894		
GI Descrip.	(AC003028) unknown protein [Arabidopsis thaliana]		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	391	Strand	-
Start	15736	End	25910
Name	OJ990203_07.9819.C29.o3.np	Method	AAT/NAP
Start	24367	End	24969
GI	4680501	Score	362
Exons	24367..24969		
GI Descrip.	(AF119222) hypothetical protein [Oryza sativa]		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	391	Strand	-
Start	15736	End	25910
Name	OJ990203_07.9819.C29.o4.np	Method	AAT/NAP
Start	24367	End	25166
GI	4680338	Score	355
Exons	24367..25166		
GI Descrip.	(AF128457) hypothetical protein [Oryza sativa subsp. indica]		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o5.tm	Method	TBLASTX:Maize
Start	3028	End	3827
GI	none	Score	89
Exons	3028..3096, 3033..3101, 3035..3097, 3037..3099, 3530..3664, 3530..3649, 3532..3663, 3756..3827, 3760..3825		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o1.tc	Method	TBLASTX:Cress
Start	9416	End	14047
GI	none	Score	74
Exons	9416..9520, 12313..12411, 12314..12412, 12478..12651, 12479..12664, 12744..12839, 12748..12852, 13013..13174, 13024..13158, 13303..13410, 13304..13420, 13521..13667, 13522..13812, 13522..13767, 13530..13778, 13864..13968, 13865..14032, 13877..14047		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o2.tc	Method	TBLASTX:Cress
Start	10793	End	11385
GI	none	Score	84
Exons	10793..10906, 10794..10883, 10955..11047, 10959..11048, 11124..11246, 11142..11213, 11275..11385, 11282..11374		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o7.tm	Method	TBLASTX:Maize
Start	10992	End	11361
GI	none	Score	76
Exons	10992..11045, 10997..11044, 11120..11155, 11121..11204, 11284..11358, 11287..11361, 11289..11360		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o2.tm	Method	TBLASTX:Maize
Start	11736	End	12676
GI	none	Score	358
Exons	11736..12083, 11746..11937, 11747..12085, 11783..12085, 12165..12242, 12312..12410, 12313..12354, 12313..12411, 12314..12412, 12479..12676, 12484..12675		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o3.ts	Method	TBLASTX:Soybean
Start	12314	End	13175
GI	none	Score	98
Exons	12314..12412, 12467..12562, 12478..12555, 12614..12676, 12744..12839, 12745..12852, 12785..12847, 13013..13174, 13014..13175, 13028..13174		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o1.tm	Method	TBLASTX:Maize
Start	12729	End	15364
GI	none	Score	142
Exons	12729..12851, 12739..12852, 12745..12852, 12997..13170, 12998..13174, 13238..13420, 13269..13436, 13270..13437, 13270..13410, 13271..13438, 13521..13778, 13521..13778, 13522..13785, 13525..13785, 13851..13982, 13856..14032, 13864..14085, 14704..14751, 14706..14795, 14707..14763, 14747..14821, 14748..14822, 15223..15363, 15305..15364		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o1.ts	Method	TBLASTX:Soybean
Start	13292	End	13929
GI	none	Score	138
Exons	13292..13420, 13306..13410, 13521..13778, 13522..13812, 13852..13929, 13865..13927		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o3.tw	Method	TBLASTX:Wheat
Start	13680	End	14783
GI	none	Score	142

Exons	13680..13778, 13681..13785, 13681..13785, 13694..13789, 13856..14032, 13860..13982, 13864..14082, 14706..14783, 14708..14761		
Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o2.ts	Method	TBLASTX:Soybean
Start	22851	End	24841
GI	none	Score	63
Exons	22851..22937, 22852..22917, 22963..23061, 22968..23117, 24365..24487, 24382..24486, 24512..24649, 24513..24638, 24665..24748, 24767..24841, 24768..24833		
Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o3.tc	Method	TBLASTX:Cress
Start	22851	End	24748
GI	none	Score	82
Exons	22851..22922, 24382..24486, 24518..24643, 24665..24748		
Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o4.tm	Method	TBLASTX:Maize
Start	22851	End	24904
GI	none	Score	59
Exons	22851..22922, 22852..22914, 22947..23117, 22951..23061, 23444..23608, 24364..24486, 24401..24487, 24502..24555, 24505..24609, 24509..24649, 24665..24748, 24675..24743, 24726..24815, 24749..24850, 24857..24904		
Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o6.tw	Method	TBLASTX:Wheat
Start	22951	End	24944
GI	none	Score	115
Exons	22951..23064, 22959..23210, 22971..23114, 24779..24850, 24780..24833, 24909..24944		
Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o7.tw	Method	TBLASTX:Wheat
Start	24382	End	24742
GI	none	Score	72
Exons	24382..24462, 24515..24655, 24680..24742		
Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o5.tw	Method	TBLASTX:Wheat
Start	27059	End	27349
GI	none	Score	200
Exons	27059..27349		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o4.gs	Method	GENSCAN
Start	30197	End	31665
GI	none	Score	.4
Exons	30197..30579, 30624..31160, 31284..31665		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o6.np	Method	AAT/NAP
Start	30200	End	32510
GI	5902445	Score	2300
Exons	30200..31796, 32420..32510		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o2.tw	Method	TBLASTX:Wheat
Start	30209	End	30807
GI	none	Score	56
Exons	30209..30346, 30332..30616, 30534..30605, 30622..30807, 30643..30672, 30713..30802		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o6.tm	Method	TBLASTX:Maize
Start	30248	End	30511
GI	none	Score	70
Exons	30248..30349, 30276..30350, 30329..30511, 30330..30389		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o1.tw	Method	TBLASTX:Wheat
Start	30809	End	31191
GI	none	Score	236
Exons	30809..31186, 30811..31191, 30937..31191		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o3.tm	Method	TBLASTX:Maize
Start	30967	End	31332
GI	none	Score	241
Exons	30967..31014, 31006..31329, 31007..31309, 31024..31332		

Seq. No.	169	Seq. ID	OJ990203_07.9819.C29
Gene No.	392	Strand	-
Start	30197	End	32510
Name	OJ990203_07.9819.C29.o4.tw	Method	TBLASTX:Wheat
Start	31285	End	31626
GI	none	Score	135

Exons 31285..31425, 31492..31626

Seq. No. 169 Seq. ID OJ990203_07.9819.C29
Gene No. 392 Strand -
Start 30197 End 32510
Name OJ990203_07.9819.C29.o7.gp Method AAT/GAP
Start 31682 End 31951
GI 61605_1.R1084 Score 443
Exons 31682..31951
GI Descrip. '5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'

Seq. No. 169 Seq. ID OJ990203_07.9819.C29
Gene No. 392 Strand -
Start 30197 End 32510
Name OJ990203_07.9819.C29.o7.np Method AAT/NAP
Start 32324 End 32510
GI 6063554 Score 124
Exons 32324..32510
GI Descrip. (AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No. 170 Seq. ID OJ990203_07.9819.C31
Gene No. 393 Strand +
Start 4362 End 8871
Name OJ990203_07.9819.C31.o2.np Method AAT/NAP
Start 4362 End 7660
GI 5295955 Score 445
Exons 4362..4734, 4975..5044, 5587..5701, 6381..6484, 6623..6959, 7057..7660
GI Descrip. (AB026295) Similar to Epstein-Barr virus (EBV) genome.(V01555) [Oryza sativa]

Seq. No. 170 Seq. ID OJ990203_07.9819.C31
Gene No. 393 Strand +
Start 4362 End 8871
Name OJ990203_07.9819.C31.o2.gs Method GENSCAN
Start 7181 End 8871
GI none Score .6
Exons 7181..7500, 7919..8096, 8866..8871

Seq. No. 170 Seq. ID OJ990203_07.9819.C31
Gene No. 394 Strand +
Start 13418 End 14176
Name OJ990203_07.9819.C31.o2.gp Method AAT/GAP
Start 13418 End 14176
GI 5816562 Score 618
Exons 13418..13442, 13764..14176
GI Descrip. 6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No. 170 Seq. ID OJ990203_07.9819.C31
Gene No. 395 Strand -
Start 1 End 5754
Name OJ990203_07.9819.C31.o1.np Method AAT/NAP
Start 1 End 2759

GI	4680179	Score	794
Exons	1..84, 846..1879, 2679..2759		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	395	Strand	-
Start	1	End	5754
Name	OJ990203_07.9819.C31.o1.gs	Method	GENSCAN
Start	780	End	5754
GI	none	Score	.71
Exons	780..1895, 4446..4547, 4601..4821, 5691..5754		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	395	Strand	-
Start	1	End	5754
Name	OJ990203_07.9819.C31.o1.gp	Method	AAT/GAP
Start	2453	End	4743
GI	61605_1.R1084	Score	636
Exons	2453..2722, 3854..3934, 4574..4743		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o3.tm	Method	TBLASTX:Maize
Start	1182	End	1496
GI	none	Score	44
Exons	1182..1268, 1233..1496, 1309..1473		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o5.tw	Method	TBLASTX:Wheat
Start	1377	End	1733
GI	none	Score	81
Exons	1377..1733, 1378..1518, 1386..1526, 1555..1731		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o3.np	Method	AAT/NAP
Start	6053	End	13717
GI	5922631	Score	4539
Exons	6053..6109, 9078..10162, 10769..11694, 11821..11971, 12014..12586, 12632..12831, 13090..13334, 13593..13717		
GI Descrip.	(AP000492) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] gi|6016864|dbj|BAA85207.1| (AP000570) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativ		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717

Name	OJ990203_07.9819.C31.o2.ts	Method	TBLASTX:Soybean
Start	9088	End	9476
GI	none	Score	114
Exons	9088..9336, 9090..9332, 9372..9476, 9382..9468		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o4.tw	Method	TBLASTX:Wheat
Start	9099	End	9467
GI	none	Score	200
Exons	9099..9467, 9121..9462		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o4.tm	Method	TBLASTX:Maize
Start	9141	End	9414
GI	none	Score	90
Exons	9141..9239, 9243..9413, 9244..9414		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o3.tw	Method	TBLASTX:Wheat
Start	9504	End	9936
GI	none	Score	91
Exons	9504..9932, 9724..9936		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o1.tm	Method	TBLASTX:Maize
Start	9591	End	10035
GI	none	Score	128
Exons	9591..9617, 9615..9758, 9777..10034, 9780..10034, 9781..10035		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o1.ts	Method	TBLASTX:Soybean
Start	9702	End	10133
GI	none	Score	41
Exons	9702..10133, 9736..9876, 9928..10086		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o2.tw	Method	TBLASTX:Wheat
Start	9978	End	10397
GI	none	Score	228
Exons	9978..10397, 9979..10371		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o2.tm	Method	TBLASTX:Maize

Start	10266	End	10622
GI	none	Score	181
Exons	10266..10622, 10276..10581		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o3.ts	Method	TBLASTX:Soybean
Start	10347	End	10712
GI	none	Score	129
Exons	10347..10481, 10488..10712		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o7.tw	Method	TBLASTX:Wheat
Start	10397	End	10631
GI	none	Score	134
Exons	10397..10558, 10398..10631, 10399..10629		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o1.tw	Method	TBLASTX:Wheat
Start	10632	End	11428
GI	none	Score	114
Exons	10632..10925, 10636..10797, 10972..11196, 10974..11195, 11252..11428		

Seq. No.	170	Seq. ID	OJ990203_07.9819.C31
Gene No.	396	Strand	-
Start	6053	End	13717
Name	OJ990203_07.9819.C31.o6.tw	Method	TBLASTX:Wheat
Start	12008	End	12410
GI	none	Score	108
Exons	12008..12409, 12102..12410		

Seq. No.	171	Seq. ID	OJ990203_07.9819.C33
Gene No.	397	Strand	
Start	99	End	327
Name	OJ990203_07.9819.C33.o1.tm	Method	TBLASTX:Maize
Start	99	End	327
GI	none	Score	77
Exons	99..326, 139..246, 280..327		

Seq. No.	171	Seq. ID	OJ990203_07.9819.C33
Gene No.	397	Strand	
Start	99	End	327
Name	OJ990203_07.9819.C33.o1.tw	Method	TBLASTX:Wheat
Start	99	End	326
GI	none	Score	233
Exons	99..326		

Seq. No.	172	Seq. ID	OJ990203_07.9819.C34
Gene No.	398	Strand	-
Start	269	End	709
Name	OJ990203_07.9819.C34.o1.np	Method	AAT/NAP

Start	269	End	709
GI	5902447	Score	302
Exons	269..709		
GI Descrip.	(AB030283) orf4 [Oryza sativa]		

Seq. No.	172	Seq. ID	OJ990203_07.9819.C34
Gene No.	398	Strand	-
Start	269	End	709
Name	OJ990203_07.9819.C34.o1.gs	Method	GENSCAN
Start	299	End	657
GI	none	Score	.96
Exons	299..657		

Seq. No.	173	Seq. ID	OJ990203_07.9819.C35
Gene No.	399	Strand	+
Start	383	End	628
Name	OJ990203_07.9819.C35.o1.tm	Method	TBLASTX:Maize
Start	377	End	628
GI	none	Score	258
Exons	377..628, 387..578, 424..627		

Seq. No.	173	Seq. ID	OJ990203_07.9819.C35
Gene No.	399	Strand	+
Start	383	End	628
Name	OJ990203_07.9819.C35.o1.gs	Method	GENSCAN
Start	383	End	589
GI	none	Score	.73
Exons	383..589		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o7.tm	Method	TBLASTX:Maize
Start	197	End	441
GI	none	Score	41
Exons	197..259, 229..441, 320..409		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o1.gs	Method	GENSCAN
Start	202	End	4776
GI	none	Score	.97
Exons	202..4776		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o1.np	Method	AAT/NAP
Start	205	End	4779
GI	4680179	Score	6656
Exons	205..4779		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779

Name	OJ990203_07.9819.C36.o6.tw	Method	TBLASTX:Wheat
Start	250	End	583
GI	none	Score	104
Exons	250..582, 314..583		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o1.tm	Method	TBLASTX:Maize
Start	442	End	1029
GI	none	Score	146
Exons	442..711, 443..703, 458..754, 772..870, 773..868, 802..870, 868..1029, 875..1021, 877..1023		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o1.tw	Method	TBLASTX:Wheat
Start	583	End	1209
GI	none	Score	351
Exons	583..1209, 584..1153		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o3.tm	Method	TBLASTX:Maize
Start	1078	End	1370
GI	none	Score	150
Exons	1078..1368, 1082..1267, 1087..1299, 1179..1370		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o2.ts	Method	TBLASTX:Soybean
Start	1168	End	1428
GI	none	Score	52
Exons	1168..1236, 1168..1428, 1322..1423		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o1.tc	Method	TBLASTX:Cress
Start	1192	End	1518
GI	none	Score	90
Exons	1192..1335, 1336..1518		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o3.tw	Method	TBLASTX:Wheat
Start	1216	End	1695
GI	none	Score	219
Exons	1216..1695, 1217..1600, 1222..1677		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779

Name	OJ990203_07.9819.C36.o2.tw	Method	TBLASTX:Wheat
Start	1699	End	2208
GI	none	Score	305
Exons	1699..2208, 1790..2176		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o2.tm	Method	TBLASTX:Maize
Start	1783	End	2136
GI	none	Score	137
Exons	1783..2136, 1798..2094, 1868..2134		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o3.ts	Method	TBLASTX:Soybean
Start	1957	End	2199
GI	none	Score	197
Exons	1957..2199		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o5.tm	Method	TBLASTX:Maize
Start	2137	End	2490
GI	none	Score	117
Exons	2137..2490, 2219..2479		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o5.tw	Method	TBLASTX:Wheat
Start	2209	End	2511
GI	none	Score	197
Exons	2209..2511, 2210..2473		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o1.ts	Method	TBLASTX:Soybean
Start	2224	End	2619
GI	none	Score	122
Exons	2224..2583, 2225..2467, 2442..2576, 2506..2580, 2587..2619, 2587..2619		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o4.tm	Method	TBLASTX:Maize
Start	2506	End	2977
GI	none	Score	100
Exons	2506..2973, 2539..2886, 2732..2977		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779

Name	OJ990203_07.9819.C36.o4.tw	Method	TBLASTX:Wheat
Start	2560	End	3046
GI	none	Score	313
Exons	2560..3042, 2603..3046		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o4.ts	Method	TBLASTX:Soybean
Start	2692	End	2973
GI	none	Score	66
Exons	2692..2973, 2693..2890		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o8.tw	Method	TBLASTX:Wheat
Start	3217	End	3571
GI	none	Score	79
Exons	3217..3570, 3253..3387, 3476..3571		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o6.tm	Method	TBLASTX:Maize
Start	3304	End	3624
GI	none	Score	209
Exons	3304..3624		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o8.tm	Method	TBLASTX:Maize
Start	3970	End	4267
GI	none	Score	64
Exons	3970..4266, 4060..4176, 4079..4267		

Seq. No.	174	Seq. ID	OJ990203_07.9819.C36
Gene No.	400	Strand	-
Start	202	End	4779
Name	OJ990203_07.9819.C36.o7.tw	Method	TBLASTX:Wheat
Start	4147	End	4510
GI	none	Score	84
Exons	4147..4506, 4148..4381, 4406..4510		

Seq. No.	175	Seq. ID	OJ990203_07.9819.C37
Gene No.	401	Strand	+
Start	428	End	623
Name	OJ990203_07.9819.C37.o1.gs	Method	GENSCAN
Start	428	End	623
GI	none	Score	.55
Exons	428..623		

Seq. No.	175	Seq. ID	OJ990203_07.9819.C37
Gene No.	402	Strand	+
Start	599	End	920
Name	OJ990203_07.9819.C37.o1.np	Method	AAT/NAP

Start	599	End	920
GI	5441880	Score	151
Exons	599..920		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	176	Seq. ID	OJ990203_07.9819.C38
Gene No.	403	Strand	+
Start	339	End	624
Name	OJ990203_07.9819.C38.o1.gs	Method	GENSCAN
Start	339	End	624
GI	none	Score	.49
Exons	339..624		

Seq. No.	177	Seq. ID	OJ990203_07.9819.C39
Gene No.	404	Strand	-
Start	1	End	760
Name	OJ990203_07.9819.C39.o1.np	Method	AAT/NAP
Start	1	End	760
GI	3786007	Score	265
Exons	1..112, 146..485, 702..760		
GI Descrip.	(AC005499) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	177	Seq. ID	OJ990203_07.9819.C39
Gene No.	404	Strand	-
Start	1	End	760
Name	OJ990203_07.9819.C39.o1.tm	Method	TBLASTX:Maize
Start	131	End	478
GI	none	Score	124
Exons	131..424, 150..377, 275..409, 416..478, 434..478		

Seq. No.	177	Seq. ID	OJ990203_07.9819.C39
Gene No.	404	Strand	-
Start	1	End	760
Name	OJ990203_07.9819.C39.o1.gs	Method	GENSCAN
Start	146	End	478
GI	none	Score	.58
Exons	146..478		

Seq. No.	177	Seq. ID	OJ990203_07.9819.C39
Gene No.	404	Strand	-
Start	1	End	760
Name	OJ990203_07.9819.C39.o1.tc	Method	TBLASTX:Cress
Start	146	End	478
GI	none	Score	150
Exons	146..283, 278..478		

Seq. No.	177	Seq. ID	OJ990203_07.9819.C39
Gene No.	404	Strand	-
Start	1	End	760
Name	OJ990203_07.9819.C39.o1.ts	Method	TBLASTX:Soybean
Start	188	End	488
GI	none	Score	71
Exons	188..481, 189..365, 200..481, 264..488		

Seq. No.	177	Seq. ID	OJ990203_07.9819.C39

Gene No.	404	Strand	-
Start	1	End	760
Name	OJ990203_07.9819.C39.o1.gp	Method	AAT/GAP
Start	412	End	500
GI	LIB3432-029-P1-K1-D2	Score	155
Exons	412..500		
GI Descrip.	'3786007 8.0e-31 (AC005499) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	178	Seq. ID	OJ990203_07.9819.C40
Gene No.	405	Strand	+
Start	279	End	858
Name	OJ990203_07.9819.C40.o1.np	Method	AAT/NAP
Start	279	End	858
GI	6907088	Score	538
Exons	279..416, 592..858		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	179	Seq. ID	OJ990203_07.9819.C41
Gene No.	406	Strand	+
Start	467	End	1275
Name	OJ990203_07.9819.C41.o1.gs	Method	GENSCAN
Start	467	End	1275
GI	none	Score	.77
Exons	467..512, 1121..1275		

Seq. No.	179	Seq. ID	OJ990203_07.9819.C41
Gene No.	407	Strand	-
Start	1	End	592
Name	OJ990203_07.9819.C41.o1.np	Method	AAT/NAP
Start	1	End	592
GI	6907086	Score	222
Exons	1..592		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	180	Seq. ID	OJ990203_07.9819.C42
Gene No.	408	Strand	+
Start	316	End	789
Name	OJ990203_07.9819.C42.o1.gs	Method	GENSCAN
Start	316	End	789
GI	none	Score	.41
Exons	316..789		

Seq. No.	181	Seq. ID	OJ990203_07.9819.C43
Gene No.	409	Strand	+
Start	778	End	1076
Name	OJ990203_07.9819.C43.o1.gp	Method	AAT/GAP
Start	778	End	1076
GI	7406_1.R1084	Score	435
Exons	778..1076		
GI Descrip.	'1122315/emb|CAA63901| 7.0e-10 (X94191) heat shock protein 17.0 [Pennisetum glaucum]'		

Seq. No.	182	Seq. ID	OJ990203_07.9819.C44
Gene No.	410	Strand	+
Start	1110	End	1235
Name	OJ990203_07.9819.C44.o1.gs	Method	GENSCAN

Start	1110	End	1235
GI	none	Score	.75
Exons	1110..1235		

Seq. No.	183	Seq. ID	OJ990203_07.9819.C46
Gene No.	411	Strand	+
Start	132	End	611
Name	OJ990203_07.9819.C46.o1.gs	Method	GENSCAN
Start	132	End	611
GI	none	Score	.71
Exons	132..373, 459..611		

Seq. No.	183	Seq. ID	OJ990203_07.9819.C46
Gene No.	412	Strand	-
Start	1172	End	1433
Name	OJ990203_07.9819.C46.o2.gs	Method	GENSCAN
Start	1172	End	1433
GI	none	Score	.93
Exons	1172..1324, 1399..1433		

Seq. No.	184	Seq. ID	OJ990203_07.9819.C47
Gene No.	413	Strand	-
Start	1860	End	3106
Name	OJ990203_07.9819.C47.o1.gs	Method	GENSCAN
Start	1860	End	3106
GI	none	Score	.5
Exons	1860..2416, 2599..3106		

Seq. No.	185	Seq. ID	OJ990203_07.9819.C48
Gene No.	414	Strand	+
Start	156	End	1341
Name	OJ990203_07.9819.C48.o1.gs	Method	GENSCAN
Start	156	End	1341
GI	none	Score	.83
Exons	156..251, 420..1341		

Seq. No.	186	Seq. ID	OJ990203_07.9819.C51
Gene No.	415	Strand	+
Start	446	End	641
Name	OJ990203_07.9819.C51.o1.gs	Method	GENSCAN
Start	446	End	641
GI	none	Score	.73
Exons	446..502, 592..641		

Seq. No.	187	Seq. ID	OJ990203_07.9819.C52
Gene No.	416	Strand	-
Start	115	End	679
Name	OJ990203_07.9819.C52.o1.gs	Method	GENSCAN
Start	115	End	679
GI	none	Score	.92
Exons	115..155, 589..679		

Seq. No.	188	Seq. ID	OJ990203_07.9819.C53
Gene No.	417	Strand	+
Start	1	End	931
Name	OJ990203_07.9819.C53.o1.np	Method	AAT/NAP
Start	1	End	931

GI	5042454	Score	93
Exons	1..43, 709..931		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	189	Seq. ID	OJ990203_07.9819.C54
Gene No.	418	Strand	+
Start	1109	End	1273
Name	OJ990203_07.9819.C54.o1.np	Method	AAT/NAP
Start	1109	End	1237
GI	6721543	Score	96
Exons	1109..1237		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa]		

Seq. No.	189	Seq. ID	OJ990203_07.9819.C54
Gene No.	418	Strand	+
Start	1109	End	1273
Name	OJ990203_07.9819.C54.o1.gp	Method	AAT/GAP
Start	1123	End	1273
GI	7406_1.R1084	Score	230
Exons	1123..1273		
GI Descrip.	'1122315/emb|CAA63901| 7.0e-10 (X94191) heat shock protein 17.0 [Pennisetum glaucum]'		

Seq. No.	190	Seq. ID	OJ990203_07.9819.C55
Gene No.	419	Strand	+
Start	1	End	1178
Name	OJ990203_07.9819.C55.o1.np	Method	AAT/NAP
Start	1	End	1178
GI	5441880	Score	1293
Exons	1..836, 1099..1178		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	190	Seq. ID	OJ990203_07.9819.C55
Gene No.	419	Strand	+
Start	1	End	1178
Name	OJ990203_07.9819.C55.o1.gs	Method	GENSCAN
Start	66	End	1100
GI	none	Score	.68
Exons	66..654, 735..790, 923..1100		

Seq. No.	190	Seq. ID	OJ990203_07.9819.C55
Gene No.	419	Strand	+
Start	1	End	1178
Name	OJ990203_07.9819.C55.o1.tm	Method	TBLASTX:Maize
Start	393	End	853
GI	none	Score	93
Exons	393..521, 401..499, 555..659, 572..655, 643..792, 653..844, 662..853		

Seq. No.	190	Seq. ID	OJ990203_07.9819.C55
Gene No.	419	Strand	+
Start	1	End	1178
Name	OJ990203_07.9819.C55.o1.gp	Method	AAT/GAP
Start	436	End	866
GI	5701669	Score	808

Exons	436..866		
GI Descrip.	5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		
Seq. No.	190	Seq. ID	OJ990203_07.9819.C55
Gene No.	419	Strand	+
Start	1	End	1178
Name	OJ990203_07.9819.C55.o1.tw	Method	TBLASTX:Wheat
Start	686	End	1066
GI	none	Score	192
Exons	686..880, 695..892, 886..1065, 890..1066		
Seq. No.	191	Seq. ID	OJ990203_07.9819.C56
Gene No.	420	Strand	+
Start	150	End	952
Name	OJ990203_07.9819.C56.o1.np	Method	AAT/NAP
Start	150	End	952
GI	5441880	Score	388
Exons	150..261, 506..603, 850..952		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		
Seq. No.	191	Seq. ID	OJ990203_07.9819.C56
Gene No.	420	Strand	+
Start	150	End	952
Name	OJ990203_07.9819.C56.o1.gs	Method	GENSCAN
Start	188	End	759
GI	none	Score	.65
Exons	188..261, 354..474, 506..603, 694..759		
Seq. No.	191	Seq. ID	OJ990203_07.9819.C56
Gene No.	421	Strand	-
Start	177	End	253
Name	OJ990203_07.9819.C56.o1.gp	Method	AAT/GAP
Start	177	End	253
GI	LIB3475-007-P1-K1-G8	Score	118
Exons	177..253		
GI Descrip.	'5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]'		
Seq. No.	192	Seq. ID	OJ990203_07.9819.C57
Gene No.	422	Strand	+
Start	263	End	421
Name	OJ990203_07.9819.C57.o1.gs	Method	GENSCAN
Start	263	End	421
GI	none	Score	.43
Exons	263..421		
Seq. No.	193	Seq. ID	OJ990203_07.9819.C58
Gene No.	423	Strand	+
Start	1	End	730
Name	OJ990203_07.9819.C58.o1.np	Method	AAT/NAP
Start	1	End	730
GI	5441880	Score	763

Exons	1..72, 130..428, 505..730		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	193	Seq. ID	OJ990203_07.9819.C58
Gene No.	423	Strand	+
Start	1	End	730
Name	OJ990203_07.9819.C58.o1.gs	Method	GENSCAN
Start	130	End	647
GI	none	Score	.82
Exons	130..428, 505..647		

Seq. No.	193	Seq. ID	OJ990203_07.9819.C58
Gene No.	423	Strand	+
Start	1	End	730
Name	OJ990203_07.9819.C58.o1.gp	Method	AAT/GAP
Start	256	End	730
GI	LIB3475-007-P1-K1-G8	Score	650
Exons	256..428, 505..730		
GI Descrip.	'5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]'		

Seq. No.	194	Seq. ID	OJ990203_07.9819.C59
Gene No.	424	Strand	+
Start	272	End	1251
Name	OJ990203_07.9819.C59.o1.gs	Method	GENSCAN
Start	272	End	1251
GI	none	Score	.47
Exons	272..326, 683..789, 949..1251		

Seq. No.	194	Seq. ID	OJ990203_07.9819.C59
Gene No.	425	Strand	-
Start	604	End	712
Name	OJ990203_07.9819.C59.o1.gp	Method	AAT/GAP
Start	604	End	712
GI	LIB3431-045-P1-N1-A10	Score	149
Exons	604..712		
GI Descrip.	'5441876/dbj|AP000367.1|AP000367 0.0e+00 Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)'		

Seq. No.	195	Seq. ID	OJ990203_07.9819.C60
Gene No.	426	Strand	-
Start	1	End	1034
Name	OJ990203_07.9819.C60.o1.np	Method	AAT/NAP
Start	1	End	1034
GI	4558666	Score	783
Exons	1..724, 822..1034		
GI Descrip.	(AC007063) putative Na/H antiporter [Arabidopsis thaliana]		

Seq. No.	195	Seq. ID	OJ990203_07.9819.C60
Gene No.	426	Strand	-
Start	1	End	1034
Name	OJ990203_07.9819.C60.o1.tm	Method	TBLASTX:Maize
Start	185	End	553
GI	none	Score	189

Exons	185..238, 273..449, 302..499, 500..553, 501..548		
Seq. No.	195	Seq. ID	OJ990203_07.9819.C60
Gene No.	426	Strand	-
Start	1	End	1034
Name	OJ990203_07.9819.C60.o1.tc	Method	TBLASTX:Cress
Start	356	End	860
GI	none	Score	53
Exons	356..442, 485..523, 512..721, 822..860		
Seq. No.	196	Seq. ID	OJ990203_07.9819.C61
Gene No.	427	Strand	+
Start	1073	End	1154
Name	OJ990203_07.9819.C61.o1.gs	Method	GENSCAN
Start	1073	End	1154
GI	none	Score	.79
Exons	1073..1154		
Seq. No.	196	Seq. ID	OJ990203_07.9819.C61
Gene No.	428	Strand	-
Start	241	End	515
Name	OJ990203_07.9819.C61.o1.gp	Method	AAT/GAP
Start	241	End	515
GI	61605_1.R1084	Score	449
Exons	241..515		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		
Seq. No.	196	Seq. ID	OJ990203_07.9819.C61
Gene No.	429	Strand	-
Start	886	End	1722
Name	OJ990203_07.9819.C61.o1.np	Method	AAT/NAP
Start	886	End	1722
GI	6063554	Score	173
Exons	886..1060, 1695..1722		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		
Seq. No.	197	Seq. ID	OJ990203_07.9819.C62
Gene No.	430	Strand	+
Start	140	End	348
Name	OJ990203_07.9819.C62.o1.gs	Method	GENSCAN
Start	140	End	348
GI	none	Score	.56
Exons	140..348		
Seq. No.	198	Seq. ID	OJ990203_07.9819.C64
Gene No.	431	Strand	+
Start	129	End	1484
Name	OJ990203_07.9819.C64.o1.gs	Method	GENSCAN
Start	129	End	1484
GI	none	Score	.97
Exons	129..1484		
Seq. No.	198	Seq. ID	OJ990203_07.9819.C64
Gene No.	432	Strand	-

Start	2029	End	2138
Name	OJ990203_07.9819.C64.o1.gp	Method	AAT/GAP
Start	2029	End	2138
GI	uC-osflcyp082b07a1	Score	159
Exons	2029..2138		
GI Descrip.	'218221/dbj|D10675|RICSINE1R6 3.0e-30 Oryza sativa p-SINE1-r6 gene, repeat sequence'		

Seq. No.	199	Seq. ID	OJ990203_07.9819.C65
Gene No.	433	Strand	-
Start	286	End	438
Name	OJ990203_07.9819.C65.o1.gs	Method	GENSCAN
Start	286	End	438
GI	none	Score	.92
Exons	286..438		

Seq. No.	200	Seq. ID	OJ990203_07.9819.C67
Gene No.	434	Strand	+
Start	352	End	1575
Name	OJ990203_07.9819.C67.o1.gs	Method	GENSCAN
Start	352	End	1575
GI	none	Score	.54
Exons	352..489, 830..1575		

Seq. No.	201	Seq. ID	OJ990203_07.9819.C68
Gene No.	435	Strand	+
Start	240	End	935
Name	OJ990203_07.9819.C68.o1.gs	Method	GENSCAN
Start	240	End	935
GI	none	Score	1
Exons	240..935		

Seq. No.	201	Seq. ID	OJ990203_07.9819.C68
Gene No.	436	Strand	-
Start	2314	End	3282
Name	OJ990203_07.9819.C68.o2.gs	Method	GENSCAN
Start	2314	End	3282
GI	none	Score	.49
Exons	2314..2392, 2694..3282		

Seq. No.	202	Seq. ID	OJ990203_07.9819.C69
Gene No.	437	Strand	+
Start	116	End	2446
Name	OJ990203_07.9819.C69.o1.gs	Method	GENSCAN
Start	116	End	2284
GI	none	Score	.79
Exons	116..274, 933..1138, 1271..2284		

Seq. No.	202	Seq. ID	OJ990203_07.9819.C69
Gene No.	437	Strand	+
Start	116	End	2446
Name	OJ990203_07.9819.C69.o1.np	Method	AAT/NAP
Start	1403	End	2446
GI	5441880	Score	1103
Exons	1403..2446		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein.		

(AC003981) [Oryza sativa]

Seq. No.	202	Seq. ID	OJ990203_07.9819.C69
Gene No.	437	Strand	+
Start	116	End	2446
Name	OJ990203_07.9819.C69.o1.tm	Method	TBLASTX:Maize
Start	1970	End	2335
GI	none	Score	270
Exons	1970..2335, 1975..2319		

Seq. No.	203	Seq. ID	OJ990203_07.9819.C71
Gene No.	438	Strand	-
Start	278	End	549
Name	OJ990203_07.9819.C71.o1.gs	Method	GENSCAN
Start	278	End	549
GI	none	Score	.83
Exons	278..376, 496..549		

Seq. No.	204	Seq. ID	OJ990203_07.9819.C72
Gene No.	439	Strand	-
Start	138	End	521
Name	OJ990203_07.9819.C72.o1.gs	Method	GENSCAN
Start	138	End	521
GI	none	Score	.8
Exons	138..521		

Seq. No.	204	Seq. ID	OJ990203_07.9819.C72
Gene No.	440	Strand	-
Start	1831	End	3744
Name	OJ990203_07.9819.C72.o2.gs	Method	GENSCAN
Start	1831	End	3060
GI	none	Score	.46
Exons	1831..1908, 2170..2263, 2748..2907, 3001..3060		

Seq. No.	204	Seq. ID	OJ990203_07.9819.C72
Gene No.	440	Strand	-
Start	1831	End	3744
Name	OJ990203_07.9819.C72.o1.np	Method	AAT/NAP
Start	2761	End	3744
GI	4538965	Score	244
Exons	2761..2907, 3001..3060, 3484..3744		
GI Descrip.	(AL049488) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	205	Seq. ID	OJ990203_07.9819.C75
Gene No.	441	Strand	+
Start	418	End	1024
Name	OJ990203_07.9819.C75.o1.gs	Method	GENSCAN
Start	418	End	1024
GI	none	Score	.59
Exons	418..615, 863..1024		

Seq. No.	206	Seq. ID	OJ990203_07.9819.C76
Gene No.	442	Strand	-
Start	1	End	1204
Name	OJ990203_07.9819.C76.o1.np	Method	AAT/NAP
Start	1	End	1204
GI	5441880	Score	589

Exons	1..236, 768..1204		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	206	Seq. ID	OJ990203_07.9819.C76
Gene No.	442	Strand	-
Start	1	End	1204
Name	OJ990203_07.9819.C76.o1.gs	Method	GENSCAN
Start	821	End	1044
GI	none	Score	.44
Exons	821..1044		

Seq. No.	207	Seq. ID	OJ990203_07.9819.C77
Gene No.	443	Strand	+
Start	33	End	706
Name	OJ990203_07.9819.C77.o1.np	Method	AAT/NAP
Start	33	End	706
GI	5441880	Score	434
Exons	33..706		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	207	Seq. ID	OJ990203_07.9819.C77
Gene No.	443	Strand	+
Start	33	End	706
Name	OJ990203_07.9819.C77.o1.gs	Method	GENSCAN
Start	202	End	621
GI	none	Score	.66
Exons	202..621		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	444	Strand	+
Start	29	End	595
Name	OJ990203_07.9819.C79.o1.gp	Method	AAT/GAP
Start	29	End	595
GI	36697_1.R1084	Score	1090
Exons	29..595		
GI Descrip.	'128592/sp|P29162|NTP3_TOBAC 2.0e-35 POLLEN-SPECIFIC PROTEIN NTP303 PRECURSOR >gi_82190_pir__S22495 pollen-specific protein precursor - common tobacco >gi_19902_emb_CAA43454_ (X61146) pollen specific protein [Nicotiana tabacum]'		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	445	Strand	-
Start	294	End	1557
Name	OJ990203_07.9819.C79.o1.tm	Method	TBLASTX:Maize
Start	286	End	1479
GI	none	Score	408
Exons	286..552, 297..596, 298..597, 1161..1478, 1162..1479		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	445	Strand	-
Start	294	End	1557
Name	OJ990203_07.9819.C79.o1.gs	Method	GENSCAN
Start	294	End	1448

GI	none	Score	.85
Exons	294..597, 1162..1448		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	445	Strand	-
Start	294	End	1557
Name	OJ990203_07.9819.C79.o1.np	Method	AAT/NAP
Start	303	End	1557
GI	6179398	Score	656
Exons	303..597, 1162..1557		
GI Descrip.	(AJ249211) BNH protein [Arabidopsis thaliana]		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	445	Strand	-
Start	294	End	1557
Name	OJ990203_07.9819.C79.o1.tc	Method	TBLASTX:Cress
Start	306	End	1479
GI	none	Score	242
Exons	306..590, 316..591, 1164..1478, 1165..1479		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	445	Strand	-
Start	294	End	1557
Name	OJ990203_07.9819.C79.o1.ts	Method	TBLASTX:Soybean
Start	306	End	1247
GI	none	Score	216
Exons	306..590, 313..603, 1164..1247, 1168..1242		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	445	Strand	-
Start	294	End	1557
Name	OJ990203_07.9819.C79.o1.tw	Method	TBLASTX:Wheat
Start	465	End	1428
GI	none	Score	178
Exons	465..596, 466..597, 1161..1427, 1162..1428		

Seq. No.	208	Seq. ID	OJ990203_07.9819.C79
Gene No.	445	Strand	-
Start	294	End	1557
Name	OJ990203_07.9819.C79.o2.ts	Method	TBLASTX:Soybean
Start	1282	End	1478
GI	none	Score	155
Exons	1282..1476, 1296..1478, 1320..1478		

Seq. No.	209	Seq. ID	OJ990203_07.9819.C80
Gene No.	446	Strand	+
Start	87	End	224
Name	OJ990203_07.9819.C80.o1.gs	Method	GENSCAN
Start	87	End	224
GI	none	Score	.7
Exons	87..224		

Seq. No.	210	Seq. ID	OJ990203_07.9819.C81
Gene No.	447	Strand	+
Start	717	End	1068
Name	OJ990203_07.9819.C81.o1.gs	Method	GENSCAN
Start	717	End	1068

GI	none	Score	.7
Exons	717..885, 995..1068		

Seq. No.	210	Seq. ID	OJ990203_07.9819.C81
Gene No.	448	Strand	-
Start	170	End	3285
Name	OJ990203_07.9819.C81.o1.np	Method	AAT/NAP
Start	170	End	2215
GI	2224810	Score	91
Exons	170..189, 1910..2215		
GI Descrip.	(Z97022) cysteine proteinase [Hordeum vulgare]		

Seq. No.	210	Seq. ID	OJ990203_07.9819.C81
Gene No.	448	Strand	-
Start	170	End	3285
Name	OJ990203_07.9819.C81.o2.gs	Method	GENSCAN
Start	1426	End	3285
GI	none	Score	.57
Exons	1426..1503, 1779..2353, 3216..3285		

Seq. No.	211	Seq. ID	OJ990203_07.9819.C82
Gene No.	449	Strand	+
Start	312	End	1753
Name	OJ990203_07.9819.C82.o1.gs	Method	GENSCAN
Start	312	End	1753
GI	none	Score	.76
Exons	312..434, 792..894, 1254..1549, 1747..1753		

Seq. No.	211	Seq. ID	OJ990203_07.9819.C82
Gene No.	449	Strand	+
Start	312	End	1753
Name	OJ990203_07.9819.C82.o1.gp	Method	AAT/GAP
Start	972	End	1549
GI	LIB3432-029-P1-K1-D2	Score	642
Exons	972..1031, 1254..1549		
GI Descrip.	'3786007 8.0e-31 (AC005499) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	211	Seq. ID	OJ990203_07.9819.C82
Gene No.	449	Strand	+
Start	312	End	1753
Name	OJ990203_07.9819.C82.o1.np	Method	AAT/NAP
Start	1294	End	1544
GI	3786007	Score	216
Exons	1294..1544		
GI Descrip.	(AC005499) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	211	Seq. ID	OJ990203_07.9819.C82
Gene No.	449	Strand	+
Start	312	End	1753
Name	OJ990203_07.9819.C82.o1.ts	Method	TBLASTX:Soybean
Start	1370	End	1570
GI	none	Score	202
Exons	1370..1570, 1374..1544		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+

Start	1	End	1285
Name	OJ990203_07.9819.C83.o1.np	Method	AAT/NAP
Start	1	End	1069
GI	3786007	Score	583
Exons	1..483, 788..1069		
GI Descrip.	(AC005499) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o2.tc	Method	TBLASTX:Cress
Start	1	End	366
GI	none	Score	51
Exons	1..60, 169..366, 195..323		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o1.tm	Method	TBLASTX:Maize
Start	1	End	495
GI	none	Score	77
Exons	1..144, 111..458, 148..495		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o2.ts	Method	TBLASTX:Soybean
Start	94	End	480
GI	none	Score	145
Exons	94..336, 171..323, 379..480		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o1.gs	Method	GENSCAN
Start	160	End	1285
GI	none	Score	.58
Exons	160..483, 791..1020, 1225..1285		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o2.tw	Method	TBLASTX:Wheat
Start	169	End	462
GI	none	Score	150
Exons	169..366, 222..344, 364..462		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o2.tm	Method	TBLASTX:Maize
Start	764	End	1074
GI	none	Score	246
Exons	764..1072, 778..1074		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+

Start	1	End	1285
Name	OJ990203_07.9819.C83.o1.ts	Method	TBLASTX:Soybean
Start	788	End	1072
GI	none	Score	223
Exons	788..1072, 793..984		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o1.tc	Method	TBLASTX:Cress
Start	830	End	1057
GI	none	Score	215
Exons	830..1057, 832..909, 955..1056		

Seq. No.	212	Seq. ID	OJ990203_07.9819.C83
Gene No.	450	Strand	+
Start	1	End	1285
Name	OJ990203_07.9819.C83.o1.tw	Method	TBLASTX:Wheat
Start	839	End	1069
GI	none	Score	188
Exons	839..1069, 895..1044		

Seq. No.	213	Seq. ID	OJ990203_07.9819.C89
Gene No.	451	Strand	+
Start	591	End	624
Name	OJ990203_07.9819.C89.o1.gs	Method	GENSCAN
Start	591	End	624
GI	none	Score	.84
Exons	591..624		

Seq. No.	213	Seq. ID	OJ990203_07.9819.C89
Gene No.	452	Strand	-
Start	107	End	192
Name	OJ990203_07.9819.C89.o1.gp	Method	AAT/GAP
Start	107	End	192
GI	LIB3477-003-P1-K1-E9	Score	98
Exons	107..192		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		

Seq. No.	214	Seq. ID	OJ990203_07.9819.C90
Gene No.	453	Strand	-
Start	614	End	842
Name	OJ990203_07.9819.C90.o1.gs	Method	GENSCAN
Start	614	End	842
GI	none	Score	.42
Exons	614..727, 768..842		

Seq. No.	215	Seq. ID	OJ990203_07.9819.C91
Gene No.	454	Strand	+
Start	122	End	231
Name	OJ990203_07.9819.C91.o1.gs	Method	GENSCAN
Start	122	End	231
GI	none	Score	.66
Exons	122..231		

Seq. No.	215	Seq. ID	OJ990203_07.9819.C91
Gene No.	455	Strand	-
Start	1	End	2948
Name	OJ990203_07.9819.C91.o2.np	Method	AAT/NAP
Start	1	End	2777
GI	5441880	Score	306
Exons	1..57, 2589..2777		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	215	Seq. ID	OJ990203_07.9819.C91
Gene No.	455	Strand	-
Start	1	End	2948
Name	OJ990203_07.9819.C91.o1.np	Method	AAT/NAP
Start	201	End	1645
GI	6907088	Score	1003
Exons	201..597, 1094..1332, 1508..1645		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	215	Seq. ID	OJ990203_07.9819.C91
Gene No.	455	Strand	-
Start	1	End	2948
Name	OJ990203_07.9819.C91.o2.gs	Method	GENSCAN
Start	2556	End	2948
GI	none	Score	.6
Exons	2556..2948		

Seq. No.	216	Seq. ID	OJ990203_07.9819.C92
Gene No.	456	Strand	-
Start	987	End	1894
Name	OJ990203_07.9819.C92.o1.gs	Method	GENSCAN
Start	987	End	1894
GI	none	Score	.54
Exons	987..1072, 1744..1894		

Seq. No.	217	Seq. ID	OJ990203_07.9819.C94
Gene No.	457	Strand	+
Start	361	End	513
Name	OJ990203_07.9819.C94.o1.gs	Method	GENSCAN
Start	361	End	513
GI	none	Score	.56
Exons	361..513		

Seq. No.	217	Seq. ID	OJ990203_07.9819.C94
Gene No.	458	Strand	-
Start	202	End	997
Name	OJ990203_07.9819.C94.o1.np	Method	AAT/NAP
Start	202	End	997
GI	6069646	Score	454
Exons	202..997		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	218	Seq. ID	OJ990203_07.9819.C96
Gene No.	459	Strand	+
Start	416	End	666
Name	OJ990203_07.9819.C96.o1.gp	Method	AAT/GAP
Start	416	End	666
GI	101153_1.R1084	Score	387
Exons	416..666		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-115 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	218	Seq. ID	OJ990203_07.9819.C96
Gene No.	460	Strand	-
Start	407	End	532
Name	OJ990203_07.9819.C96.o1.gs	Method	GENSCAN
Start	407	End	532
GI	none	Score	.91
Exons	407..532		

Seq. No.	219	Seq. ID	OJ990203_07.9819.C97
Gene No.	461	Strand	+
Start	146	End	262
Name	OJ990203_07.9819.C97.o1.gs	Method	GENSCAN
Start	146	End	262
GI	none	Score	.74
Exons	146..246, 252..262		

Seq. No.	219	Seq. ID	OJ990203_07.9819.C97
Gene No.	462	Strand	-
Start	814	End	1846
Name	OJ990203_07.9819.C97.o1.np	Method	AAT/NAP
Start	794	End	1846
GI	4558666	Score	664
Exons	794..889, 985..1846		
GI Descrip.	(AC007063) putative Na/H antiporter [Arabidopsis thaliana]		

Seq. No.	219	Seq. ID	OJ990203_07.9819.C97
Gene No.	462	Strand	-
Start	814	End	1846
Name	OJ990203_07.9819.C97.o2.gs	Method	GENSCAN
Start	814	End	1842
GI	none	Score	1
Exons	814..1842		

Seq. No.	219	Seq. ID	OJ990203_07.9819.C97
Gene No.	462	Strand	-
Start	814	End	1846
Name	OJ990203_07.9819.C97.o1.ts	Method	TBLASTX:Soybean
Start	1165	End	1585
GI	none	Score	61
Exons	1165..1272, 1384..1482, 1525..1584, 1529..1585		

Seq. No.	219	Seq. ID	OJ990203_07.9819.C97
Gene No.	462	Strand	-
Start	814	End	1846
Name	OJ990203_07.9819.C97.o1.tm	Method	TBLASTX:Maize
Start	1426	End	1783
GI	none	Score	196

Exons	1426..1479, 1525..1782, 1526..1783		
Seq. No.	219	Seq. ID	OJ990203_07.9819.C97
Gene No.	462	Strand	-
Start	814	End	1846
Name	OJ990203_07.9819.C97.o1.tc	Method	TBLASTX:Cress
Start	1450	End	1764
GI	none	Score	77
Exons	1450..1482, 1525..1764, 1529..1651		
Seq. No.	220	Seq. ID	OJ990203_07.9819.C98
Gene No.	463	Strand	-
Start	303	End	405
Name	OJ990203_07.9819.C98.o1.gs	Method	GENSCAN
Start	303	End	405
GI	none	Score	.48
Exons	303..405		
Seq. No.	221	Seq. ID	OJ990203_07.9819.C99
Gene No.	464	Strand	-
Start	1	End	479
Name	OJ990203_07.9819.C99.o1.np	Method	AAT/NAP
Start	1	End	479
GI	3786007	Score	233
Exons	1..28, 178..479		
GI Descrip.	(AC005499) hypothetical protein [Arabidopsis thaliana]		
Seq. No.	221	Seq. ID	OJ990203_07.9819.C99
Gene No.	464	Strand	-
Start	1	End	479
Name	OJ990203_07.9819.C99.o1.ts	Method	TBLASTX:Soybean
Start	157	End	357
GI	none	Score	145
Exons	157..357, 183..353		
Seq. No.	221	Seq. ID	OJ990203_07.9819.C99
Gene No.	464	Strand	-
Start	1	End	479
Name	OJ990203_07.9819.C99.o1.gp	Method	AAT/GAP
Start	178	End	438
GI	LIB3432-029-P1-K1-D2	Score	469
Exons	178..438		
GI Descrip.	'3786007 8.0e-31 (AC005499) hypothetical protein [Arabidopsis thaliana]'		
Seq. No.	221	Seq. ID	OJ990203_07.9819.C99
Gene No.	464	Strand	-
Start	1	End	479
Name	OJ990203_07.9819.C99.o1.gs	Method	GENSCAN
Start	178	End	353
GI	none	Score	.92
Exons	178..353		
Seq. No.	222	Seq. ID	OJ990223_01.9819.C1
Gene No.	465	Strand	-
Start	359	End	485
Name	OJ990223_01.9819.C1.o1.gs	Method	GENSCAN

Start	359	End	485
GI	none	Score	.42
Exons	359..485		

Seq. No.	223	Seq. ID	OJ990223_01.9819.C4
Gene No.	466	Strand	
Start	421	End	666
Name	OJ990223_01.9819.C4.o1.tw	Method	TBLASTX:Wheat
Start	421	End	666
GI	none	Score	172
Exons	421..666		

Seq. No.	223	Seq. ID	OJ990223_01.9819.C4
Gene No.	466	Strand	
Start	421	End	666
Name	OJ990223_01.9819.C4.o1.tm	Method	TBLASTX:Maize
Start	439	End	666
GI	none	Score	125
Exons	439..666, 443..571, 457..645		

Seq. No.	224	Seq. ID	OJ990223_01.9819.C5
Gene No.	467	Strand	+
Start	435	End	748
Name	OJ990223_01.9819.C5.o1.gp	Method	AAT/GAP
Start	435	End	748
GI	18281_1.R1084	Score	550
Exons	435..748		
GI Descrip.	'4741923/gb|AAD28757.1|AF130849_1 5.0e-14 (AF130849) PIT1 [Arabidopsis thaliana]'		

Seq. No.	225	Seq. ID	OJ990223_01.9819.C7
Gene No.	468	Strand	+
Start	363	End	489
Name	OJ990223_01.9819.C7.o1.gs	Method	GENSCAN
Start	363	End	489
GI	none	Score	.77
Exons	363..489		

Seq. No.	226	Seq. ID	OJ990223_01.9819.C8
Gene No.	469	Strand	+
Start	1	End	726
Name	OJ990223_01.9819.C8.o1.np	Method	AAT/NAP
Start	1	End	726
GI	4741923	Score	67
Exons	1..84, 179..258, 668..726		
GI Descrip.	(AF130849) PIT1 [Arabidopsis thaliana]		

Seq. No.	226	Seq. ID	OJ990223_01.9819.C8
Gene No.	469	Strand	+
Start	1	End	726
Name	OJ990223_01.9819.C8.o1.gp	Method	AAT/GAP
Start	185	End	726
GI	18281_1.R1084	Score	179
Exons	185..258, 668..726		
GI Descrip.	'4741923/gb|AAD28757.1|AF130849_1 5.0e-14 (AF130849) PIT1 [Arabidopsis thaliana]'		

Seq. No.	227	Seq. ID	OJ990223_01.9819.C9
Gene No.	470	Strand	+
Start	538	End	1184
Name	OJ990223_01.9819.C9.o1.gp	Method	AAT/GAP
Start	538	End	658
GI	18281_1.R1084	Score	157
Exons	538..658		
GI Descrip.	'4741923/gb|AAD28757.1|AF130849_1 5.0e-14 (AF130849) PIT1 [Arabidopsis thaliana]'		

Seq. No.	227	Seq. ID	OJ990223_01.9819.C9
Gene No.	470	Strand	+
Start	538	End	1184
Name	OJ990223_01.9819.C9.o1.gs	Method	GENSCAN
Start	541	End	1184
GI	none	Score	.78
Exons	541..658, 699..833, 907..1014, 1101..1184		

Seq. No.	227	Seq. ID	OJ990223_01.9819.C9
Gene No.	470	Strand	+
Start	538	End	1184
Name	OJ990223_01.9819.C9.o1.tm	Method	TBLASTX:Maize
Start	626	End	992
GI	none	Score	53
Exons	626..658, 738..830, 748..801, 749..826, 750..833, 888..992, 889..975, 894..983		

Seq. No.	228	Seq. ID	OJ990223_01.9819.C10
Gene No.	471	Strand	+
Start	975	End	1360
Name	OJ990223_01.9819.C10.o1.gp	Method	AAT/GAP
Start	975	End	1360
GI	LIB3434-053-P1-K1-D6	Score	743
Exons	975..1360		
GI Descrip.	'3426046 3.0e-14 (AC005168) similar to salt-inducible protein [Arabidopsis thaliana]'		

Seq. No.	228	Seq. ID	OJ990223_01.9819.C10
Gene No.	472	Strand	-
Start	310	End	1507
Name	OJ990223_01.9819.C10.o1.gs	Method	GENSCAN
Start	310	End	1470
GI	none	Score	.62
Exons	310..1470		

Seq. No.	228	Seq. ID	OJ990223_01.9819.C10
Gene No.	472	Strand	-
Start	310	End	1507
Name	OJ990223_01.9819.C10.o1.tm	Method	TBLASTX:Maize
Start	334	End	1173
GI	none	Score	547
Exons	334..744, 338..742, 667..861, 739..975, 832..1068, 937..1068, 937..1173		

Seq. No.	228	Seq. ID	OJ990223_01.9819.C10
Gene No.	472	Strand	-
Start	310	End	1507

Name	OJ990223_01.9819.C10.o1.ts	Method	TBLASTX:Soybean
Start	394	End	1155
GI	none	Score	235
Exons	394..696, 395..667, 676..876, 880..933	680..877, 700..1098, 805..1155,	

Seq. No.	228	Seq. ID	OJ990223_01.9819.C10
Gene No.	472	Strand	-
Start	310	End	1507
Name	OJ990223_01.9819.C10.o1.tc	Method	TBLASTX:Cress
Start	409	End	1245
GI	none	Score	77
Exons	409..645, 667..825, 679..1035, 688..906, 764..1036, 796..1182, 871..1077, 874..1245, 896..1228, 940..1245, 976..1221, 1087..1245		

Seq. No.	228	Seq. ID	OJ990223_01.9819.C10
Gene No.	472	Strand	-
Start	310	End	1507
Name	OJ990223_01.9819.C10.o2.tm	Method	TBLASTX:Maize
Start	1209	End	1507
GI	none	Score	82
Exons	1209..1274, 1209..1277, 1210..1278, 1210..1278, 1288..1344, 1289..1345, 1291..1506, 1294..1506, 1343..1507		

Seq. No.	229	Seq. ID	OJ990223_01.9819.C11
Gene No.	473	Strand	+
Start	219	End	2844
Name	OJ990223_01.9819.C11.o1.gs	Method	GENSCAN
Start	219	End	2844
GI	none	Score	.67
Exons	219..381, 2373..2567, 2750..2844		

Seq. No.	229	Seq. ID	OJ990223_01.9819.C11
Gene No.	474	Strand	-
Start	2090	End	3896
Name	OJ990223_01.9819.C11.o1.np	Method	AAT/NAP
Start	2090	End	3706
GI	99922	Score	680
Exons	2090..2232, 2861..3706		
GI Descrip.	hypothetical protein - soybean gi|930025|emb|CAA31883| (X13528) ORF (334 AA) [Glycine max]		

Seq. No.	229	Seq. ID	OJ990223_01.9819.C11
Gene No.	474	Strand	-
Start	2090	End	3896
Name	OJ990223_01.9819.C11.o1.tm	Method	TBLASTX:Maize
Start	2845	End	3269
GI	none	Score	92
Exons	2845..3015, 2865..3014, 3030..3260, 3037..3264, 3132..3269		

Seq. No.	229	Seq. ID	OJ990223_01.9819.C11
Gene No.	474	Strand	-
Start	2090	End	3896
Name	OJ990223_01.9819.C11.o1.tw	Method	TBLASTX:Wheat
Start	2854	End	3312
GI	none	Score	69

Exons	2854..3015, 2859..3014, 3058..3153, 3060..3155, 3162..3266, 3169..3267, 3256..3312		
Seq. No.	229	Seq. ID	OJ990223_01.9819.C11
Gene No.	474	Strand	-
Start	2090	End	3896
Name	OJ990223_01.9819.C11.o1.tc	Method	TBLASTX:Cress
Start	3108	End	3458
GI	none	Score	49
Exons	3108..3458, 3109..3183, 3205..3261, 3301..3450		
Seq. No.	229	Seq. ID	OJ990223_01.9819.C11
Gene No.	474	Strand	-
Start	2090	End	3896
Name	OJ990223_01.9819.C11.o2.gs	Method	GENSCAN
Start	3202	End	3896
GI	none	Score	.49
Exons	3202..3340, 3805..3896		
Seq. No.	229	Seq. ID	OJ990223_01.9819.C11
Gene No.	474	Strand	-
Start	2090	End	3896
Name	OJ990223_01.9819.C11.o1.ts	Method	TBLASTX:Soybean
Start	3475	End	3758
GI	none	Score	41
Exons	3475..3606, 3477..3614, 3587..3757, 3588..3758		
Seq. No.	230	Seq. ID	OJ990223_01.9819.C13
Gene No.	475	Strand	-
Start	655	End	723
Name	OJ990223_01.9819.C13.o1.gs	Method	GENSCAN
Start	655	End	723
GI	none	Score	.57
Exons	655..723		
Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	476	Strand	
Start	787	End	1151
Name	OJ990223_01.9819.C14.o4.tw	Method	TBLASTX:Wheat
Start	787	End	1151
GI	none	Score	105
Exons	787..900, 801..902, 911..1111, 1021..1083, 1091..1144, 1092..1151		
Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	477	Strand	
Start	1471	End	1720
Name	OJ990223_01.9819.C14.o5.tw	Method	TBLASTX:Wheat
Start	1471	End	1720
GI	none	Score	82
Exons	1471..1581, 1585..1671, 1586..1654, 1649..1720, 1650..1712		
Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	478	Strand	
Start	2043	End	3770
Name	OJ990223_01.9819.C14.o1.tm	Method	TBLASTX:Maize
Start	2043	End	3003

GI	none	Score	284
Exons	2043..2399, 2057..2329, 2375..2515, 2398..2505, 2515..3003, 2517..2663, 2730..2792, 2788..2883		

Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	478	Strand	
Start	2043	End	3770
Name	OJ990223_01.9819.C14.o1.tw	Method	TBLASTX:Wheat
Start	2090	End	2407
GI	none	Score	282
Exons	2090..2335, 2091..2372, 2375..2407		

Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	478	Strand	
Start	2043	End	3770
Name	OJ990223_01.9819.C14.o1.ts	Method	TBLASTX:Soybean
Start	2605	End	3177
GI	none	Score	55
Exons	2605..2664, 2734..2961, 2850..2960, 2950..3135, 3136..3177		

Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	478	Strand	
Start	2043	End	3770
Name	OJ990223_01.9819.C14.o3.tw	Method	TBLASTX:Wheat
Start	2758	End	3308
GI	none	Score	268
Exons	2758..3120, 2853..3023, 3210..3308		

Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	478	Strand	
Start	2043	End	3770
Name	OJ990223_01.9819.C14.o2.tm	Method	TBLASTX:Maize
Start	3207	End	3677
GI	none	Score	249
Exons	3207..3578, 3213..3407, 3588..3677		

Seq. No.	231	Seq. ID	OJ990223_01.9819.C14
Gene No.	478	Strand	
Start	2043	End	3770
Name	OJ990223_01.9819.C14.o2.tw	Method	TBLASTX:Wheat
Start	3408	End	3770
GI	none	Score	284
Exons	3408..3767, 3609..3770		

Seq. No.	232	Seq. ID	OJ990223_01.9819.C15
Gene No.	479	Strand	+
Start	419	End	944
Name	OJ990223_01.9819.C15.o1.gs	Method	GENSCAN
Start	419	End	944
GI	none	Score	.43
Exons	419..658, 833..944		

Seq. No.	232	Seq. ID	OJ990223_01.9819.C15
Gene No.	480	Strand	-
Start	2014	End	4595
Name	OJ990223_01.9819.C15.o2.gs	Method	GENSCAN
Start	2014	End	4595

GI	none	Score	.46
Exons	2014..2170, 2404..2483, 2605..2715, 2986..3214, 3804..3828, 4224..4337, 4535..4595		

Seq. No.	232	Seq. ID	OJ990223_01.9819.C15
Gene No.	480	Strand	-
Start	2014	End	4595
Name	OJ990223_01.9819.C15.o1.np	Method	AAT/NAP
Start	2113	End	3560
GI	4585884	Score	487
Exons	2113..2232, 2382..2715, 2814..3560		
GI Descrip.	(AC005850) Hypothetical protein [Arabidopsis thaliana]		

Seq. No.	232	Seq. ID	OJ990223_01.9819.C15
Gene No.	480	Strand	-
Start	2014	End	4595
Name	OJ990223_01.9819.C15.o1.tm	Method	TBLASTX:Maize
Start	2361	End	2722
GI	none	Score	128
Exons	2361..2600, 2379..2579, 2594..2722, 2604..2714		

Seq. No.	232	Seq. ID	OJ990223_01.9819.C15
Gene No.	480	Strand	-
Start	2014	End	4595
Name	OJ990223_01.9819.C15.o1.ts	Method	TBLASTX:Soybean
Start	2418	End	2741
GI	none	Score	107
Exons	2418..2600, 2627..2740, 2640..2741		

Seq. No.	232	Seq. ID	OJ990223_01.9819.C15
Gene No.	480	Strand	-
Start	2014	End	4595
Name	OJ990223_01.9819.C15.o1.tw	Method	TBLASTX:Wheat
Start	2809	End	3180
GI	none	Score	121
Exons	2809..3054, 2812..3096, 2813..3058, 3100..3180		

Seq. No.	232	Seq. ID	OJ990223_01.9819.C15
Gene No.	480	Strand	-
Start	2014	End	4595
Name	OJ990223_01.9819.C15.o2.tm	Method	TBLASTX:Maize
Start	2851	End	3297
GI	none	Score	94
Exons	2851..3114, 3118..3297		

Seq. No.	233	Seq. ID	OJ990223_01.9819.C16
Gene No.	481	Strand	-
Start	298	End	521
Name	OJ990223_01.9819.C16.o1.gs	Method	GENSCAN
Start	298	End	521
GI	none	Score	1
Exons	298..521		

Seq. No.	234	Seq. ID	OJ990223_01.9819.C18
Gene No.	482	Strand	+
Start	1369	End	1959
Name	OJ990223_01.9819.C18.o1.np	Method	AAT/NAP

Start	1369	End	1959
GI	6907092	Score	437
Exons	1369..1655, 1711..1752, 1822..1959		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	234	Seq. ID	OJ990223_01.9819.C18
Gene No.	483	Strand	-
Start	1278	End	5047
Name	OJ990223_01.9819.C18.o2.gs	Method	GENSCAN
Start	1278	End	4994
GI	none	Score	.54
Exons	1278..1505, 1522..1815, 2269..2345, 4547..4994		

Seq. No.	234	Seq. ID	OJ990223_01.9819.C18
Gene No.	483	Strand	-
Start	1278	End	5047
Name	OJ990223_01.9819.C18.o1.gp	Method	AAT/GAP
Start	3580	End	4014
GI	2428185	Score	656
Exons	3580..4014		
GI Descrip.	5852170/emb|AL117265.1|OST17804 1.0e-177 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804		

Seq. No.	234	Seq. ID	OJ990223_01.9819.C18
Gene No.	483	Strand	-
Start	1278	End	5047
Name	OJ990223_01.9819.C18.o2.np	Method	AAT/NAP
Start	4149	End	5047
GI	5852178	Score	495
Exons	4149..4244, 4607..4710, 4742..5047		
GI Descrip.	(AL117265) zhb0008.1 [Oryza sativa]		

Seq. No.	235	Seq. ID	OJ990223_01.9819.C22
Gene No.	484	Strand	+
Start	1	End	326
Name	OJ990223_01.9819.C22.o1.np	Method	AAT/NAP
Start	1	End	326
GI	6498441	Score	173
Exons	1..326		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	236	Seq. ID	OJ990223_01.9819.C25
Gene No.	485	Strand	+
Start	974	End	1098
Name	OJ990223_01.9819.C25.o1.gs	Method	GENSCAN
Start	974	End	1098
GI	none	Score	.83
Exons	974..1098		

Seq. No.	236	Seq. ID	OJ990223_01.9819.C25
Gene No.	486	Strand	+
Start	2802	End	2963
Name	OJ990223_01.9819.C25.o2.gs	Method	GENSCAN
Start	2802	End	2963
GI	none	Score	.48

Exons	2802..2963		
Seq. No.	237	Seq. ID	OJ990223_01.9819.C26
Gene No.	487	Strand	+
Start	62	End	202
Name	OJ990223_01.9819.C26.o1.gp	Method	AAT/GAP
Start	62	End	202
GI	30174_1.R1084	Score	224
Exons	62..202		
GI Descrip.	'2160182 2.0e-10 (AC000132) ESTs gb_ATTS1236,gb_T43334,gb_N97019,gb_AA395203 come from this gene. [Arabidopsis thaliana]'		
Seq. No.	237	Seq. ID	OJ990223_01.9819.C26
Gene No.	488	Strand	+
Start	734	End	1024
Name	OJ990223_01.9819.C26.o2.gp	Method	AAT/GAP
Start	734	End	1024
GI	15355_1.R1084	Score	528
Exons	734..1024		
GI Descrip.	'4586433/dbj|BAA76401.1| 7.0e-16 (AB016798) ribosomal protein L29/cell surface heparin binding protein HIP [Sus scrofa] >gi_4586439_dbj_BAA76404.1_ (AB017196) ribosomal protein L29/heparin/heparan sulfate interacting protein [Sus scrofa]'		
Seq. No.	238	Seq. ID	OJ990223_01.9819.C27
Gene No.	489	Strand	+
Start	336	End	553
Name	OJ990223_01.9819.C27.o1.gs	Method	GENSCAN
Start	336	End	553
GI	none	Score	.86
Exons	336..429, 450..553		
Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o2.np	Method	AAT/NAP
Start	861	End	3504
GI	4972718	Score	80
Exons	861..908, 2518..2814, 3172..3350, 3444..3504		
GI Descrip.	(AF132166) unknown [Drosophila melanogaster]		
Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o1.gs	Method	GENSCAN
Start	1285	End	3808
GI	none	Score	.91
Exons	1285..1528, 1742..3350, 3564..3808		
Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o3.ts	Method	TBLASTX:Soybean
Start	1298	End	1830
GI	none	Score	131
Exons	1298..1453, 1333..1452, 1477..1530, 1741..1830, 1742..1810		

Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o1.ts	Method	TBLASTX:Soybean
Start	1838	End	2485
GI	none	Score	114
Exons	1838..2008, 1840..2268, 1840..2484, 2204..2437, 2309..2485, 2314..2481		

Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o2.tm	Method	TBLASTX:Maize
Start	1840	End	2244
GI	none	Score	63
Exons	1840..1920, 1841..1921, 1903..2151, 1907..2134, 2158..2226, 2176..2244		

Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o1.tm	Method	TBLASTX:Maize
Start	2305	End	2847
GI	none	Score	154
Exons	2305..2706, 2306..2449, 2306..2722, 2314..2670, 2504..2707, 2694..2834, 2695..2847, 2699..2797, 2713..2829		

Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o1.np	Method	AAT/NAP
Start	2510	End	3504
GI	4972718	Score	80
Exons	2510..2814, 3172..3350, 3444..3504		
GI Descrip.	(AF132166) unknown [Drosophila melanogaster]		

Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o2.ts	Method	TBLASTX:Soybean
Start	2546	End	2829
GI	none	Score	139
Exons	2546..2704, 2548..2703, 2683..2829, 2699..2800		

Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o1.gp	Method	AAT/GAP
Start	2611	End	3069
GI	3761423	Score	872
Exons	2611..3069		

Seq. No.	239	Seq. ID	OJ990223_01.9819.C28
Gene No.	490	Strand	-
Start	1285	End	3808
Name	OJ990223_01.9819.C28.o1.tc	Method	TBLASTX:Cress

Start	3160	End	3627
GI	none	Score	179
Exons	3160..3351, 3173..3352, 3186..3353, 3401..3505, 3428..3499, 3442..3504, 3574..3627		

Seq. No.	240	Seq. ID	OJ990223_01.9819.C29
Gene No.	491	Strand	-
Start	264	End	1082
Name	OJ990223_01.9819.C29.o1.tm	Method	TBLASTX:Maize
Start	244	End	681
GI	none	Score	141
Exons	244..423, 248..451, 265..417, 613..657, 613..681		

Seq. No.	240	Seq. ID	OJ990223_01.9819.C29
Gene No.	491	Strand	-
Start	264	End	1082
Name	OJ990223_01.9819.C29.o1.gs	Method	GENSCAN
Start	264	End	1082
GI	none	Score	.82
Exons	264..417, 613..735, 976..1082		

Seq. No.	241	Seq. ID	OJ990223_01.9819.C30
Gene No.	492	Strand	+
Start	1	End	1487
Name	OJ990223_01.9819.C30.o1.np	Method	AAT/NAP
Start	1	End	1487
GI	4582447	Score	442
Exons	1..80, 408..1487		
GI Descrip.	(AC007071) putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	241	Seq. ID	OJ990223_01.9819.C30
Gene No.	492	Strand	+
Start	1	End	1487
Name	OJ990223_01.9819.C30.o1.tm	Method	TBLASTX:Maize
Start	976	End	1482
GI	none	Score	393
Exons	976..1482, 978..1244, 1057..1299, 1341..1400		

Seq. No.	241	Seq. ID	OJ990223_01.9819.C30
Gene No.	492	Strand	+
Start	1	End	1487
Name	OJ990223_01.9819.C30.o1.tw	Method	TBLASTX:Wheat
Start	1024	End	1338
GI	none	Score	235
Exons	1024..1338, 1050..1244		

Seq. No.	242	Seq. ID	OJ990223_01.9819.C31
Gene No.	493	Strand	+
Start	1	End	1812
Name	OJ990223_01.9819.C31.o1.np	Method	AAT/NAP
Start	1	End	1812
GI	2244915	Score	147
Exons	1..371, 1750..1812		
GI Descrip.	(Z97339) reverse transcriptase like protein [Arabidopsis thaliana]		

Seq. No.	242	Seq. ID	OJ990223_01.9819.C31
Gene No.	493	Strand	+
Start	1	End	1812
Name	OJ990223_01.9819.C31.o1.tw	Method	TBLASTX:Wheat
Start	1	End	499
GI	none	Score	261
Exons	1..150, 14..391, 169..252, 368..499		

Seq. No.	242	Seq. ID	OJ990223_01.9819.C31
Gene No.	493	Strand	+
Start	1	End	1812
Name	OJ990223_01.9819.C31.o1.ts	Method	TBLASTX:Soybean
Start	131	End	511
GI	none	Score	153
Exons	131..412, 169..261, 449..511		

Seq. No.	242	Seq. ID	OJ990223_01.9819.C31
Gene No.	493	Strand	+
Start	1	End	1812
Name	OJ990223_01.9819.C31.o1.tm	Method	TBLASTX:Maize
Start	137	End	505
GI	none	Score	160
Exons	137..322, 145..261, 155..313, 386..505		

Seq. No.	242	Seq. ID	OJ990223_01.9819.C31
Gene No.	493	Strand	+
Start	1	End	1812
Name	OJ990223_01.9819.C31.o1.gs	Method	GENSCAN
Start	221	End	1322
GI	none	Score	.56
Exons	221..371, 498..685, 1215..1322		

Seq. No.	243	Seq. ID	OJ990223_01.9819.C32
Gene No.	494	Strand	-
Start	427	End	523
Name	OJ990223_01.9819.C32.o1.gs	Method	GENSCAN
Start	427	End	523
GI	none	Score	.66
Exons	427..523		

Seq. No.	244	Seq. ID	OJ990223_01.9819.C36
Gene No.	495	Strand	+
Start	446	End	520
Name	OJ990223_01.9819.C36.o1.gs	Method	GENSCAN
Start	446	End	520
GI	none	Score	.48
Exons	446..520		

Seq. No.	245	Seq. ID	OJ990223_01.9819.C38
Gene No.	496	Strand	-
Start	1	End	729
Name	OJ990223_01.9819.C38.o1.np	Method	AAT/NAP
Start	1	End	729
GI	1495804	Score	193
Exons	1..68, 503..729		
GI Descrip.	(X96406) 13-lipoxygenase [Solanum tuberosum]		

Seq. No.	245	Seq. ID	OJ990223_01.9819.C38
Gene No.	496	Strand	-
Start	1	End	729
Name	OJ990223_01.9819.C38.o1.gs	Method	GENSCAN
Start	138	End	680
GI	none	Score	.64
Exons	138..680		

Seq. No.	245	Seq. ID	OJ990223_01.9819.C38
Gene No.	496	Strand	-
Start	1	End	729
Name	OJ990223_01.9819.C38.o1.ts	Method	TBLASTX:Soybean
Start	510	End	726
GI	none	Score	88
Exons	510..671, 667..726		

Seq. No.	245	Seq. ID	OJ990223_01.9819.C38
Gene No.	496	Strand	-
Start	1	End	729
Name	OJ990223_01.9819.C38.o1.tm	Method	TBLASTX:Maize
Start	543	End	729
GI	none	Score	83
Exons	543..671, 561..638, 652..729, 667..729		

Seq. No.	246	Seq. ID	OJ990223_01.9819.C41
Gene No.	497	Strand	+
Start	57	End	447
Name	OJ990223_01.9819.C41.o1.gs	Method	GENSCAN
Start	57	End	447
GI	none	Score	.79
Exons	57..110, 115..204, 253..447		

Seq. No.	247	Seq. ID	OJ990223_01.9819.C42
Gene No.	498	Strand	-
Start	1	End	5376
Name	OJ990223_01.9819.C42.o1.np	Method	AAT/NAP
Start	1	End	5376
GI	6678834	Score	132
Exons	1..24, 3276..3377, 3984..4064, 4301..4438, 4591..4689, 5255..5376		
GI Descrip.	meiotic check point regulator gi|1717793|sp|P53995|TS24_MOUSE PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) gi|1083553|pir||A55117 tsg24 protein - mouse gi|642252|emb|CAA56450| (X80169) tsg24 [Mus musculus]		

Seq. No.	247	Seq. ID	OJ990223_01.9819.C42
Gene No.	498	Strand	-
Start	1	End	5376
Name	OJ990223_01.9819.C42.o1.gs	Method	GENSCAN
Start	711	End	4441
GI	none	Score	.73
Exons	711..854, 881..997, 3306..3377, 3984..4064, 4301..4441		

Seq. No.	248	Seq. ID	OJ990223_01.9819.C43
Gene No.	499	Strand	+
Start	526	End	3265
Name	OJ990223_01.9819.C43.o1.np	Method	AAT/NAP

Start	526	End	3265
GI	5042463	Score	135
Exons	526..735, 1402..1582, 1628..1688, 3234..3265		
GI Descrip.	(AC007789) unknown protein [Oryza sativa]		

Seq. No.	249	Seq. ID	OJ990223_01.9819.C46
Gene No.	500	Strand	+
Start	1148	End	1553
Name	OJ990223_01.9819.C46.o1.np	Method	AAT/NAP
Start	1148	End	1553
GI	6539571	Score	63
Exons	1148..1290, 1490..1553		
GI Descrip.	(AP000836) hypothetical protein [Oryza sativa]		

Seq. No.	250	Seq. ID	OJ990223_01.9819.C47
Gene No.	501	Strand	+
Start	388	End	1937
Name	OJ990223_01.9819.C47.o1.np	Method	AAT/NAP
Start	388	End	1937
GI	6598934	Score	150
Exons	388..412, 1710..1937		
GI Descrip.	(AC018721) unknown protein [Arabidopsis thaliana]		

Seq. No.	250	Seq. ID	OJ990223_01.9819.C47
Gene No.	502	Strand	-
Start	254	End	612
Name	OJ990223_01.9819.C47.o1.gs	Method	GENSCAN
Start	254	End	612
GI	none	Score	.56
Exons	254..335, 487..612		

Seq. No.	250	Seq. ID	OJ990223_01.9819.C47
Gene No.	503	Strand	
Start	1712	End	1892
Name	OJ990223_01.9819.C47.o1.tm	Method	TBLASTX:Maize
Start	1712	End	1890
GI	none	Score	211
Exons	1712..1882, 1715..1882, 1716..1883, 1717..1890		

Seq. No.	250	Seq. ID	OJ990223_01.9819.C47
Gene No.	503	Strand	
Start	1712	End	1892
Name	OJ990223_01.9819.C47.o1.tw	Method	TBLASTX:Wheat
Start	1712	End	1892
GI	none	Score	204
Exons	1712..1882, 1721..1882, 1728..1892		

Seq. No.	251	Seq. ID	OJ990223_01.9819.C51
Gene No.	504	Strand	+
Start	526	End	597
Name	OJ990223_01.9819.C51.o1.gs	Method	GENSCAN
Start	526	End	597
GI	none	Score	.7
Exons	526..597		

Seq. No.	252	Seq. ID	OJ990223_01.9819.C52
Gene No.	505	Strand	+

Start	409	End	5236
Name	OJ990223_01.9819.C52.o1.np	Method	AAT/NAP
Start	409	End	5236
GI	6678834	Score	178
Exons	409..596, 1487..1576, 1665..1757, 1892..2022, 2155..2211, 5204..5236		
GI Descrip.	meiotic check point regulator gi|1717793|sp|P53995|TS24_MOUSE PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) gi|1083553|pir||A55117 tsg24 protein - mouse gi|642252|emb|CAA56450| (X80169) tsg24 [Mus musculus]		

Seq. No.	252	Seq. ID	OJ990223_01.9819.C52
Gene No.	505	Strand	+
Start	409	End	5236
Name	OJ990223_01.9819.C52.o1.gp	Method	AAT/GAP
Start	421	End	1746
GI	2800538	Score	650
Exons	421..596, 1487..1550, 1624..1746		
GI Descrip.	1717793/sp|P53995|TS24_MOUSE 4.0e-20 PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi_1083553_pir__A55117 tsg24 protein - mouse >gi_642252_emb_CAA56450_ (X80169) tsg24 [Mus musculus]		

Seq. No.	252	Seq. ID	OJ990223_01.9819.C52
Gene No.	505	Strand	+
Start	409	End	5236
Name	OJ990223_01.9819.C52.o1.gs	Method	GENSCAN
Start	423	End	3290
GI	none	Score	.95
Exons	423..596, 1487..1550, 1624..1763, 1856..1933, 2300..2398, 2895..3290		

Seq. No.	252	Seq. ID	OJ990223_01.9819.C52
Gene No.	506	Strand	-
Start	4732	End	4897
Name	OJ990223_01.9819.C52.o2.tm	Method	TBLASTX:Maize
Start	462	End	1710
GI	none	Score	139
Exons	462..596, 463..594, 465..599, 1474..1554, 1487..1549, 1622..1705, 1622..1708, 1623..1709, 1627..1710		

Seq. No.	252	Seq. ID	OJ990223_01.9819.C52
Gene No.	506	Strand	-
Start	4732	End	4897
Name	OJ990223_01.9819.C52.o1.tm	Method	TBLASTX:Maize
Start	1853	End	3257
GI	none	Score	98
Exons	1853..1999, 1854..2000, 1855..2004, 1855..2004, 1856..2005, 2125..2211, 2129..2227, 2129..2215, 2287..2355, 2288..2359, 2305..2400, 2877..3248, 2886..3164, 2905..3252, 3225..3257		

Seq. No.	252	Seq. ID	OJ990223_01.9819.C52
Gene No.	506	Strand	-
Start	4732	End	4897
Name	OJ990223_01.9819.C52.o2.gs	Method	GENSCAN
Start	4732	End	4897
GI	none	Score	.62
Exons	4732..4897		

Seq. No.	253	Seq. ID	OJ990223_01.9819.C53
Gene No.	507	Strand	-
Start	717	End	813
Name	OJ990223_01.9819.C53.o1.gs	Method	GENSCAN
Start	717	End	813
GI	none	Score	.61
Exons	717..813		

Seq. No.	254	Seq. ID	OJ990223_01.9819.C54
Gene No.	508	Strand	-
Start	1200	End	1528
Name	OJ990223_01.9819.C54.o1.gs	Method	GENSCAN
Start	1200	End	1528
GI	none	Score	.79
Exons	1200..1316, 1436..1528		

Seq. No.	255	Seq. ID	OJ990223_01.9819.C59
Gene No.	509	Strand	-
Start	1376	End	3081
Name	OJ990223_01.9819.C59.o1.gs	Method	GENSCAN
Start	1376	End	3081
GI	none	Score	.56
Exons	1376..1434, 1865..2017, 2099..2204, 2884..3081		

Seq. No.	256	Seq. ID	OJ990223_01.9819.C60
Gene No.	510	Strand	-
Start	1	End	630
Name	OJ990223_01.9819.C60.o1.np	Method	AAT/NAP
Start	1	End	629
GI	6598934	Score	364
Exons	1..201, 451..629		
GI Descrip.	(AC018721) unknown protein [Arabidopsis thaliana]		

Seq. No.	256	Seq. ID	OJ990223_01.9819.C60
Gene No.	510	Strand	-
Start	1	End	630
Name	OJ990223_01.9819.C60.o1.gp	Method	AAT/GAP
Start	56	End	587
GI	15876_1.R1084	Score	436
Exons	56..201, 451..587		
GI Descrip.	'1717793/sp|P53995|TS24_MOUSE 4.0e-20 PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi_1083553_pir__A55117 tsg24 protein - mouse >gi_642252_emb_CAA56450_ (X80169) tsg24 [Mus musculus]'		

Seq. No.	256	Seq. ID	OJ990223_01.9819.C60
Gene No.	510	Strand	-
Start	1	End	630
Name	OJ990223_01.9819.C60.o1.tm	Method	TBLASTX:Maize
Start	56	End	630
GI	none	Score	49
Exons	56..85, 58..87, 86..205, 88..204, 97..207, 450..626, 450..626, 451..627, 451..630		

Seq. No.	256	Seq. ID	OJ990223_01.9819.C60
Gene No.	510	Strand	-
Start	1	End	630

Name	OJ990223_01.9819.C60.o1.tw	Method	TBLASTX:Wheat
Start	56	End	630
GI	none	Score	189
Exons	56..205, 58..207, 58..201, 451..621, 454..630		

Seq. No.	256	Seq. ID	OJ990223_01.9819.C60
Gene No.	510	Strand	-
Start	1	End	630
Name	OJ990223_01.9819.C60.o1.ts	Method	TBLASTX:Soybean
Start	56	End	630
GI	none	Score	150
Exons	56..202, 58..201, 66..203, 433..630, 461..577, 514..612		

Seq. No.	256	Seq. ID	OJ990223_01.9819.C60
Gene No.	510	Strand	-
Start	1	End	630
Name	OJ990223_01.9819.C60.o1.tc	Method	TBLASTX:Cress
Start	58	End	193
GI	none	Score	141
Exons	58..192, 59..193		

Seq. No.	256	Seq. ID	OJ990223_01.9819.C60
Gene No.	510	Strand	-
Start	1	End	630
Name	OJ990223_01.9819.C60.o1.gs	Method	GENSCAN
Start	451	End	622
GI	none	Score	.48
Exons	451..622		

Seq. No.	257	Seq. ID	OJ990223_01.9819.C61
Gene No.	511	Strand	+
Start	1978	End	3479
Name	OJ990223_01.9819.C61.o1.gs	Method	GENSCAN
Start	1978	End	3479
GI	none	Score	.56
Exons	1978..2170, 2305..2378, 2423..3479		

Seq. No.	257	Seq. ID	OJ990223_01.9819.C61
Gene No.	512	Strand	-
Start	1	End	3597
Name	OJ990223_01.9819.C61.o1.np	Method	AAT/NAP
Start	1	End	3597
GI	6721512	Score	94
Exons	1..55, 2242..2356, 3561..3597		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	258	Seq. ID	OJ990223_01.9819.C62
Gene No.	513	Strand	+
Start	1	End	1531
Name	OJ990223_01.9819.C62.o2.np	Method	AAT/NAP
Start	1	End	1366
GI	5902444	Score	701
Exons	1..1366		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	258	Seq. ID	OJ990223_01.9819.C62
Gene No.	513	Strand	+

Start	1	End	1531
Name	OJ990223_01.9819.C62.o1.gs	Method	GENSCAN
Start	164	End	1531
GI	none	Score	.48
Exons	164..1255, 1424..1531		

Seq. No.	258	Seq. ID	OJ990223_01.9819.C62
Gene No.	513	Strand	+
Start	1	End	1531
Name	OJ990223_01.9819.C62.o1.tw	Method	TBLASTX:Wheat
Start	731	End	1498
GI	none	Score	147
Exons	731..913, 742..912, 950..1186, 952..1176, 1333..1497, 1334..1498		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o1.np	Method	AAT/NAP
Start	1	End	2923
GI	5902445	Score	2727
Exons	1..1639, 1679..2923		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o3.tm	Method	TBLASTX:Maize
Start	56	End	235
GI	none	Score	217
Exons	56..235, 58..234		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o1.tw	Method	TBLASTX:Wheat
Start	104	End	523
GI	none	Score	470
Exons	104..523, 119..244, 178..264, 299..490, 430..522		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o2.tm	Method	TBLASTX:Maize
Start	263	End	646
GI	none	Score	332
Exons	263..646, 430..645		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o1.ts	Method	TBLASTX:Soybean
Start	374	End	799
GI	none	Score	308
Exons	374..799, 433..549		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+

Start	1	End	2923
Name	OJ990223_01.9819.C63.o4.tw	Method	TBLASTX:Wheat
Start	572	End	949
GI	none	Score	193
Exons	572..811, 572..679, 804..938, 820..939, 821..949, 824..943		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o2.ts	Method	TBLASTX:Soybean
Start	1016	End	1396
GI	none	Score	77
Exons	1016..1138, 1145..1396, 1276..1374		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o5.tw	Method	TBLASTX:Wheat
Start	1016	End	1429
GI	none	Score	125
Exons	1016..1117, 1021..1125, 1160..1429, 1160..1297, 1276..1383		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o1.tm	Method	TBLASTX:Maize
Start	1799	End	2104
GI	none	Score	344
Exons	1799..2104, 1837..2103		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o3.tw	Method	TBLASTX:Wheat
Start	1799	End	2182
GI	none	Score	371
Exons	1799..2182, 1807..2181		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o2.tw	Method	TBLASTX:Wheat
Start	2306	End	2914
GI	none	Score	338
Exons	2306..2758, 2320..2409, 2455..2562, 2783..2914, 2788..2913		

Seq. No.	259	Seq. ID	OJ990223_01.9819.C63
Gene No.	514	Strand	+
Start	1	End	2923
Name	OJ990223_01.9819.C63.o4.tm	Method	TBLASTX:Maize
Start	2612	End	2878
GI	none	Score	140
Exons	2612..2794, 2795..2878		

Seq. No.	260	Seq. ID	OJ990223_01.9819.C64
Gene No.	515	Strand	+
Start	168	End	458

Name	OJ990223_01.9819.C64.o1.gs	Method	GENSCAN
Start	168	End	458
GI	none	Score	.45
Exons	168..458		

Seq. No.	260	Seq. ID	OJ990223_01.9819.C64
Gene No.	516	Strand	-
Start	653	End	4523
Name	OJ990223_01.9819.C64.o2.gs	Method	GENSCAN
Start	653	End	4523
GI	none	Score	.77
Exons	653..1077, 1269..1414, 1669..2000, 2010..2298, 2366..2424, 2495..2677, 2745..2869, 3079..3197, 3319..3501, 3659..3809, 4175..4267, 4363..4449, 4505..4523		

Seq. No.	260	Seq. ID	OJ990223_01.9819.C64
Gene No.	516	Strand	-
Start	653	End	4523
Name	OJ990223_01.9819.C64.o1.np	Method	AAT/NAP
Start	1536	End	3145
GI	6721561	Score	1050
Exons	1536..2298, 2366..2424, 2495..2711, 3110..3145		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	260	Seq. ID	OJ990223_01.9819.C64
Gene No.	516	Strand	-
Start	653	End	4523
Name	OJ990223_01.9819.C64.o2.np	Method	AAT/NAP
Start	2098	End	3758
GI	6721558	Score	248
Exons	2098..2298, 2741..2869, 3659..3758		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa] gi|6815083|dbj|BAA90369.1| (AP001081) hypothetical protein [Oryza sativa]		

Seq. No.	261	Seq. ID	OJ990223_01.9819.C65
Gene No.	517	Strand	+
Start	1	End	3160
Name	OJ990223_01.9819.C65.o2.np	Method	AAT/NAP
Start	1	End	3160
GI	6069646	Score	510
Exons	1..82, 1516..1873, 2156..3160		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	261	Seq. ID	OJ990223_01.9819.C65
Gene No.	517	Strand	+
Start	1	End	3160
Name	OJ990223_01.9819.C65.o1.gs	Method	GENSCAN
Start	150	End	2889

GI	none	Score	.54
Exons	150..223, 268..412, 547..639, 1550..1689, 2002..2229, 2467..2640, 2815..2889		

Seq. No.	261	Seq. ID	OJ990223_01.9819.C65
Gene No.	518	Strand	-
Start	1	End	2169
Name	OJ990223_01.9819.C65.o1.np	Method	AAT/NAP
Start	1	End	1793
GI	6721512	Score	87
Exons	1..218, 1753..1793		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	261	Seq. ID	OJ990223_01.9819.C65
Gene No.	518	Strand	-
Start	1	End	2169
Name	OJ990223_01.9819.C65.o1.tm	Method	TBLASTX:Maize
Start	1515	End	2082
GI	none	Score	303
Exons	1515..1676, 1516..2082		

Seq. No.	261	Seq. ID	OJ990223_01.9819.C65
Gene No.	518	Strand	-
Start	1	End	2169
Name	OJ990223_01.9819.C65.o1.tw	Method	TBLASTX:Wheat
Start	1729	End	2169
GI	none	Score	220
Exons	1729..2025, 1764..1994, 2011..2169, 2076..2168		

Seq. No.	261	Seq. ID	OJ990223_01.9819.C65
Gene No.	519	Strand	
Start	2404	End	2721
Name	OJ990223_01.9819.C65.o2.tw	Method	TBLASTX:Wheat
Start	2404	End	2721
GI	none	Score	67
Exons	2404..2481, 2413..2550, 2577..2717, 2578..2721		

Seq. No.	261	Seq. ID	OJ990223_01.9819.C65
Gene No.	520	Strand	
Start	2673	End	2957
Name	OJ990223_01.9819.C65.o2.tm	Method	TBLASTX:Maize
Start	2673	End	2957
GI	none	Score	302
Exons	2673..2957, 2680..2952		

Seq. No.	262	Seq. ID	OJ990223_01.9819.C66
Gene No.	521	Strand	+
Start	586	End	654
Name	OJ990223_01.9819.C66.o1.gs	Method	GENSCAN
Start	586	End	654
GI	none	Score	.95
Exons	586..654		

Seq. No.	263	Seq. ID	OJ990223_01.9819.C67
Gene No.	522	Strand	+
Start	1	End	1435
Name	OJ990223_01.9819.C67.o1.np	Method	AAT/NAP

Start	1	End	1435
GI	6678834	Score	148
Exons	1..191, 295..416, 522..691, 1414..1435		
GI Descrip.	meiotic check point regulator gi|1717793|sp|P53995|TS24_MOUSE PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) gi|1083553|pir||A55117 tsg24 protein - mouse gi|642252|emb|CAA56450| (X80169) tsg24 [Mus musculus]		

Seq. No.	263	Seq. ID	OJ990223_01.9819.C67
Gene No.	522	Strand	+
Start	1	End	1435
Name	OJ990223_01.9819.C67.o1.gs	Method	GENSCAN
Start	114	End	682
GI	none	Score	.83
Exons	114..191, 295..416, 522..682		

Seq. No.	264	Seq. ID	OJ990223_01.9819.C69
Gene No.	523	Strand	+
Start	1911	End	2032
Name	OJ990223_01.9819.C69.o1.gs	Method	GENSCAN
Start	1911	End	2032
GI	none	Score	.93
Exons	1911..2032		

Seq. No.	264	Seq. ID	OJ990223_01.9819.C69
Gene No.	524	Strand	-
Start	4247	End	4368
Name	OJ990223_01.9819.C69.o2.gs	Method	GENSCAN
Start	4247	End	4368
GI	none	Score	.56
Exons	4247..4368		

Seq. No.	265	Seq. ID	OJ990223_01.9819.C72
Gene No.	525	Strand	+
Start	285	End	351
Name	OJ990223_01.9819.C72.o1.gs	Method	GENSCAN
Start	285	End	351
GI	none	Score	.96
Exons	285..351		

Seq. No.	266	Seq. ID	OJ990223_01.9819.C75
Gene No.	526	Strand	-
Start	332	End	630
Name	OJ990223_01.9819.C75.o1.gs	Method	GENSCAN
Start	332	End	630
GI	none	Score	.96
Exons	332..450, 570..630		

Seq. No.	267	Seq. ID	OJ990223_01.9819.C76
Gene No.	527	Strand	+
Start	870	End	1077
Name	OJ990223_01.9819.C76.o1.gs	Method	GENSCAN
Start	870	End	1077
GI	none	Score	.92
Exons	870..1077		

Seq. No.	268	Seq. ID	OJ990223_01.9819.C77

Gene No.	528	Strand	+
Start	1	End	1170
Name	OJ990223_01.9819.C77.o1.np	Method	AAT/NAP
Start	1	End	1170
GI	5777617	Score	60
Exons	1..26, 1070..1170		
GI Descrip.	(AJ245900) CAA30375.1 protein [Oryza sativa]		

Seq. No.	268	Seq. ID	OJ990223_01.9819.C77
Gene No.	528	Strand	+
Start	1	End	1170
Name	OJ990223_01.9819.C77.o1.gs	Method	GENSCAN
Start	79	End	333
GI	none	Score	.49
Exons	79..333		

Seq. No.	268	Seq. ID	OJ990223_01.9819.C77
Gene No.	529	Strand	-
Start	1156	End	1398
Name	OJ990223_01.9819.C77.o2.gs	Method	GENSCAN
Start	1156	End	1398
GI	none	Score	.48
Exons	1156..1398		

Seq. No.	269	Seq. ID	OJ990223_01.9819.C79
Gene No.	530	Strand	+
Start	340	End	712
Name	OJ990223_01.9819.C79.o1.gs	Method	GENSCAN
Start	340	End	712
GI	none	Score	.96
Exons	340..381, 587..712		

Seq. No.	270	Seq. ID	OJ990223_01.9819.C80
Gene No.	531	Strand	+
Start	2617	End	2963
Name	OJ990223_01.9819.C80.o2.gs	Method	GENSCAN
Start	2617	End	2963
GI	none	Score	.74
Exons	2617..2638, 2866..2963		

Seq. No.	270	Seq. ID	OJ990223_01.9819.C80
Gene No.	532	Strand	-
Start	811	End	1387
Name	OJ990223_01.9819.C80.o1.gs	Method	GENSCAN
Start	811	End	1385
GI	none	Score	.96
Exons	811..894, 937..1040, 1313..1385		

Seq. No.	270	Seq. ID	OJ990223_01.9819.C80
Gene No.	532	Strand	-
Start	811	End	1387
Name	OJ990223_01.9819.C80.o1.gp	Method	AAT/GAP
Start	933	End	1387
GI	LIB3434-013-P1-K1-F3	Score	271
Exons	933..1040, 1313..1387		
GI Descrip.	'126411/sp|P24095|LOXX_SOYBN 2.0e-32 SEED LIPOXYGENASE >gi_99932_pir__S13381 lipoxygenase (EC 1.13.11.12) - soybean		

>gi_18746_emb_CAA39604_ (X56139) lipoxygenase [Glycine max]'

Seq. No.	271	Seq. ID	OJ990223_01.9819.C81
Gene No.	533	Strand	+
Start	1	End	621
Name	OJ990223_01.9819.C81.o1.gp	Method	AAT/GAP
Start	1	End	537
GI	15355_1.R1084	Score	303
Exons	1..20, 233..290, 401..537		
GI Descrip.	'4586433/dbj|BAA76401.1| 7.0e-16 (AB016798) ribosomal protein L29/cell surface heparin binding protein HIP [Sus scrofa] >gi_4586439_dbj_BAA76404.1_ (AB017196) ribosomal protein L29/heparin/heparan sulfate interacting protein [Sus scrofa]'		

Seq. No.	271	Seq. ID	OJ990223_01.9819.C81
Gene No.	533	Strand	+
Start	1	End	621
Name	OJ990223_01.9819.C81.o1.gs	Method	GENSCAN
Start	244	End	533
GI	none	Score	.99
Exons	244..290, 401..533		

Seq. No.	271	Seq. ID	OJ990223_01.9819.C81
Gene No.	533	Strand	+
Start	1	End	621
Name	OJ990223_01.9819.C81.o1.tm	Method	TBLASTX:Maize
Start	430	End	545
GI	none	Score	195
Exons	430..534, 432..545		

Seq. No.	271	Seq. ID	OJ990223_01.9819.C81
Gene No.	533	Strand	+
Start	1	End	621
Name	OJ990223_01.9819.C81.o1.ts	Method	TBLASTX:Soybean
Start	430	End	549
GI	none	Score	180
Exons	430..549, 432..536		

Seq. No.	271	Seq. ID	OJ990223_01.9819.C81
Gene No.	533	Strand	+
Start	1	End	621
Name	OJ990223_01.9819.C81.o1.np	Method	AAT/NAP
Start	432	End	621
GI	6321147	Score	129
Exons	432..621		
GI Descrip.	Ribosomal protein L29 (YL43); Rpl29p gi|1710563|sp|P05747|RL29_YEAST 60S RIBOSOMAL PROTEIN L29 (YL43) gi|2119153|pir||S71066 ribosomal protein L29.e, cytosolic - yeast (Saccharomyces cerevisiae)		

Seq. No.	272	Seq. ID	OJ990223_01.9819.C82
Gene No.	534	Strand	+
Start	177	End	343
Name	OJ990223_01.9819.C82.o1.gs	Method	GENSCAN
Start	177	End	343
GI	none	Score	.6
Exons	177..343		

Seq. No.	273	Seq. ID	OJ990223_01.9819.C85
Gene No.	535	Strand	-
Start	468	End	697
Name	OJ990223_01.9819.C85.o1.gs	Method	GENSCAN
Start	468	End	697
GI	none	Score	.92
Exons	468..551, 638..697		

Seq. No.	274	Seq. ID	OJ990203_02.9819.C2
Gene No.	536	Strand	+
Start	581	End	716
Name	OJ990203_02.9819.C2.o1.gs	Method	GENSCAN
Start	581	End	716
GI	none	Score	.58
Exons	581..716		

Seq. No.	275	Seq. ID	OJ990203_02.9819.C3
Gene No.	537	Strand	+
Start	198	End	895
Name	OJ990203_02.9819.C3.o1.gs	Method	GENSCAN
Start	198	End	895
GI	none	Score	.76
Exons	198..490, 839..895		

Seq. No.	276	Seq. ID	OJ990203_02.9819.C4
Gene No.	538	Strand	+
Start	36	End	615
Name	OJ990203_02.9819.C4.o1.gs	Method	GENSCAN
Start	36	End	615
GI	none	Score	.4
Exons	36..204, 465..615		

Seq. No.	277	Seq. ID	OJ990203_02.9819.C5
Gene No.	539	Strand	-
Start	98	End	491
Name	OJ990203_02.9819.C5.o1.gp	Method	AAT/GAP
Start	98	End	459
GI	none	Score	566
Exons	98..459		

Seq. No.	277	Seq. ID	OJ990203_02.9819.C5
Gene No.	539	Strand	-
Start	98	End	491
Name	OJ990203_02.9819.C5.o1.gs	Method	GENSCAN
Start	354	End	491
GI	none	Score	.77
Exons	354..491		

Seq. No.	278	Seq. ID	OJ990203_02.9819.C8
Gene No.	540	Strand	-
Start	1	End	633
Name	OJ990203_02.9819.C8.o1.np	Method	AAT/NAP
Start	1	End	633
GI	1708424	Score	151
Exons	1..45, 102..314, 582..633		
GI Descrip.	ISOFLAVONE REDUCTASE HOMOLOG gi|1230614 (U48590) isoflavone		

reductase-like protein [Lupinus albus]

Seq. No.	278	Seq. ID	OJ990203_02.9819.C8
Gene No.	540	Strand	-
Start	1	End	633
Name	OJ990203_02.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	103	End	309
GI	none	Score	133
Exons	103..267, 107..301, 109..309		

Seq. No.	278	Seq. ID	OJ990203_02.9819.C8
Gene No.	540	Strand	-
Start	1	End	633
Name	OJ990203_02.9819.C8.o1.gs	Method	GENSCAN
Start	111	End	186
GI	none	Score	.71
Exons	111..186		

Seq. No.	278	Seq. ID	OJ990203_02.9819.C8
Gene No.	540	Strand	-
Start	1	End	633
Name	OJ990203_02.9819.C8.o1.tc	Method	TBLASTX:Cress
Start	112	End	353
GI	none	Score	106
Exons	112..324, 122..316, 161..346, 291..353		

Seq. No.	278	Seq. ID	OJ990203_02.9819.C8
Gene No.	540	Strand	-
Start	1	End	633
Name	OJ990203_02.9819.C8.o1.ts	Method	TBLASTX:Soybean
Start	112	End	323
GI	none	Score	111
Exons	112..309, 162..323, 164..310, 216..311		

Seq. No.	279	Seq. ID	OJ990203_02.9819.C14
Gene No.	541	Strand	+
Start	92	End	520
Name	OJ990203_02.9819.C14.o1.gs	Method	GENSCAN
Start	92	End	514
GI	none	Score	.82
Exons	92..248, 504..514		

Seq. No.	279	Seq. ID	OJ990203_02.9819.C14
Gene No.	541	Strand	+
Start	92	End	520
Name	OJ990203_02.9819.C14.o1.gp	Method	AAT/GAP
Start	406	End	520
GI	none	Score	140
Exons	406..520		

Seq. No.	280	Seq. ID	OJ990203_02.9819.C15
Gene No.	542	Strand	-
Start	406	End	509
Name	OJ990203_02.9819.C15.o1.gs	Method	GENSCAN
Start	406	End	509
GI	none	Score	.79
Exons	406..509		

Seq. No.	281	Seq. ID	OJ990203_02.9819.C17
Gene No.	543	Strand	-
Start	495	End	553
Name	OJ990203_02.9819.C17.o1.gs	Method	GENSCAN
Start	495	End	553
GI	none	Score	.89
Exons	495..553		

Seq. No.	282	Seq. ID	OJ990203_02.9819.C18
Gene No.	544	Strand	+
Start	1	End	611
Name	OJ990203_02.9819.C18.o1.np	Method	AAT/NAP
Start	1	End	611
GI	2499819	Score	172
Exons	1..132, 326..424, 527..611		
GI Descrip.	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR gi|2130068|pir||S66516 aspartic proteinase 1 precursor - rice gi|1030715|dbj|BAA06876.1| (D32165) aspartic protease [Oryza sativa] gi|1711289|dbj|BAA06875| (D32144) aspartic protease [Oryza sativa]		

Seq. No.	282	Seq. ID	OJ990203_02.9819.C18
Gene No.	544	Strand	+
Start	1	End	611
Name	OJ990203_02.9819.C18.o1.tm	Method	TBLASTX:Maize
Start	328	End	609
GI	none	Score	144
Exons	328..432, 329..424, 519..560, 561..608, 562..609, 565..609	525..554, 526..561, 561..608,	

Seq. No.	282	Seq. ID	OJ990203_02.9819.C18
Gene No.	544	Strand	+
Start	1	End	611
Name	OJ990203_02.9819.C18.o1.gs	Method	GENSCAN
Start	330	End	424
GI	none	Score	.99
Exons	330..424		

Seq. No.	283	Seq. ID	OJ990203_02.9819.C20
Gene No.	545	Strand	-
Start	95	End	235
Name	OJ990203_02.9819.C20.o1.gs	Method	GENSCAN
Start	95	End	235
GI	none	Score	.95
Exons	95..235		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	546	Strand	+
Start	1	End	2155
Name	OJ990203_02.9819.C22.o1.np	Method	AAT/NAP
Start	1	End	1954
GI	4455190	Score	267
Exons	1..42, 592..678, 764..836, 959..1012, 1726..1954		
GI Descrip.	(AL035440) putative protein [Arabidopsis thaliana]		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22

Gene No.	546	Strand	+
Start	1	End	2155
Name	OJ990203_02.9819.C22.o1.gs	Method	GENSCAN
Start	536	End	1650
GI	none	Score	.62
Exons	536..678, 764..836, 959..1012, 1583..1650		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	546	Strand	+
Start	1	End	2155
Name	OJ990203_02.9819.C22.o1.gp	Method	AAT/GAP
Start	1717	End	2155
GI	LIB3433-011-Q6-K1-G7	Score	833
Exons	1717..2155		
GI Descrip.	'4455190/emb|CAB36513.1| 8.0e-09 (AL035440) putative protein [Arabidopsis thaliana]'		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	547	Strand	+
Start	7838	End	13818
Name	OJ990203_02.9819.C22.o4.gs	Method	GENSCAN
Start	7838	End	13818
GI	none	Score	.47
Exons	7838..7984, 8577..8765, 8879..8954, 8978..9100, 9122..9225, 9290..9384, 9792..9841, 10100..10312, 11489..11576, 12034..12288, 13371..13818		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	547	Strand	+
Start	7838	End	13818
Name	OJ990203_02.9819.C22.o2.np	Method	AAT/NAP
Start	9063	End	13706
GI	6069646	Score	379
Exons	9063..9131, 13305..13706		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	548	Strand	+
Start	19639	End	22789
Name	OJ990203_02.9819.C22.o3.gp	Method	AAT/GAP
Start	19639	End	20264
GI	2310235	Score	295
Exons	19639..19676, 20125..20264		
GI Descrip.	5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	548	Strand	+
Start	19639	End	22789
Name	OJ990203_02.9819.C22.o4.gp	Method	AAT/GAP
Start	20129	End	22789
GI	342_1.R1084	Score	4544
Exons	20129..22789		

GI Descrip. '4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	548	Strand	+
Start	19639	End	22789
Name	OJ990203_02.9819.C22.o3.np	Method	AAT/NAP
Start	20938	End	22789
GI	6742729	Score	2933
Exons	20938..22789		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	549	Strand	-
Start	1922	End	5135
Name	OJ990203_02.9819.C22.o2.gs	Method	GENSCAN
Start	1922	End	5135
GI	none	Score	.49
Exons	1922..2071, 2651..2853, 3989..4157, 4962..5135		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	550	Strand	-
Start	6531	End	7090
Name	OJ990203_02.9819.C22.o2.tm	Method	TBLASTX:Maize
Start	536	End	2043
GI	none	Score	49
Exons	536..562, 612..677, 612..677, 613..726, 613..681, 763..837, 764..838, 961..1014, 963..1013, 1713..1937, 1721..1936, 1723..1938, 1996..2043		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	550	Strand	-
Start	6531	End	7090
Name	OJ990203_02.9819.C22.o3.gs	Method	GENSCAN
Start	6531	End	7090
GI	none	Score	.73
Exons	6531..6634, 6771..6855, 7025..7090		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	551	Strand	
Start	20431	End	20827
Name	OJ990203_02.9819.C22.o4.tw	Method	TBLASTX:Wheat
Start	20431	End	20827
GI	none	Score	99
Exons	20431..20583, 20450..20569, 20566..20817, 20574..20816, 20577..20819, 20579..20827		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	552	Strand	
Start	20748	End	21621
Name	OJ990203_02.9819.C22.o1.ts	Method	TBLASTX:Soybean
Start	20748	End	21177
GI	none	Score	103
Exons	20748..20831, 20749..20823, 20824..20886, 20881..21177, 20935..21159		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22

Gene No.	552	Strand	
Start	20748	End	21621
Name	OJ990203_02.9819.C22.o1.tc	Method	TBLASTX:Cress
Start	20910	End	21258
GI	none	Score	301
Exons	20910..21062, 20917..21258, 21102..21239		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	552	Strand	
Start	20748	End	21621
Name	OJ990203_02.9819.C22.o2.tw	Method	TBLASTX:Wheat
Start	21046	End	21515
GI	none	Score	72
Exons	21046..21099, 21054..21098, 21100..21204, 21111..21200, 21208..21306, 21213..21305, 21286..21510, 21306..21515, 21307..21510, 21309..21515		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	552	Strand	
Start	20748	End	21621
Name	OJ990203_02.9819.C22.o1.tm	Method	TBLASTX:Maize
Start	21091	End	21549
GI	none	Score	247
Exons	21091..21345, 21103..21345, 21355..21549		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	552	Strand	
Start	20748	End	21621
Name	OJ990203_02.9819.C22.o2.ts	Method	TBLASTX:Soybean
Start	21379	End	21621
GI	none	Score	207
Exons	21379..21621		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	553	Strand	
Start	21610	End	22050
Name	OJ990203_02.9819.C22.o3.tw	Method	TBLASTX:Wheat
Start	21610	End	22050
GI	none	Score	102
Exons	21610..21732, 21621..21755, 21729..21908, 21730..21969, 21742..21924, 21895..22041, 21967..22050, 21975..22049		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	554	Strand	
Start	22065	End	22787
Name	OJ990203_02.9819.C22.o1.tw	Method	TBLASTX:Wheat
Start	22065	End	22787
GI	none	Score	439
Exons	22065..22412, 22066..22401, 22392..22508, 22393..22764, 22403..22777, 22548..22787, 22649..22774		

Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	554	Strand	
Start	22065	End	22787
Name	OJ990203_02.9819.C22.o3.tm	Method	TBLASTX:Maize
Start	22108	End	22401
GI	none	Score	291

Exons	22108..22401, 22119..22394, 22198..22401		
Seq. No.	284	Seq. ID	OJ990203_02.9819.C22
Gene No.	554	Strand	
Start	22065	End	22787
Name	OJ990203_02.9819.C22.o2.tc	Method	TBLASTX:Cress
Start	22353	End	22787
GI	none	Score	56
Exons	22353..22412, 22357..22401, 22393..22764, 22403..22777, 22548..22787, 22649..22774		
Seq. No.	285	Seq. ID	OJ990203_02.9819.C23
Gene No.	555	Strand	+
Start	1	End	1462
Name	OJ990203_02.9819.C23.o1.np	Method	AAT/NAP
Start	1	End	687
GI	4680203	Score	352
Exons	1..687		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		
Seq. No.	285	Seq. ID	OJ990203_02.9819.C23
Gene No.	555	Strand	+
Start	1	End	1462
Name	OJ990203_02.9819.C23.o1.gp	Method	AAT/GAP
Start	302	End	1462
GI	342_1.R1084	Score	1743
Exons	302..779, 920..1462		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		
Seq. No.	285	Seq. ID	OJ990203_02.9819.C23
Gene No.	556	Strand	+
Start	2453	End	2749
Name	OJ990203_02.9819.C23.o2.gp	Method	AAT/GAP
Start	2453	End	2749
GI	38782_1.R1084	Score	488
Exons	2453..2749		
GI Descrip.	'6069643/dbj|AP000616.1|AP000616 0.0e+00 Oryza sativa genomic DNA, chromosome 6, clone:P0514G12'		
Seq. No.	285	Seq. ID	OJ990203_02.9819.C23
Gene No.	557	Strand	-
Start	2000	End	2749
Name	OJ990203_02.9819.C23.o1.tw	Method	TBLASTX:Wheat
Start	304	End	633
GI	none	Score	43
Exons	304..339, 318..458, 319..459, 472..552, 541..633, 567..632		
Seq. No.	285	Seq. ID	OJ990203_02.9819.C23
Gene No.	557	Strand	-
Start	2000	End	2749
Name	OJ990203_02.9819.C23.o2.np	Method	AAT/NAP
Start	2000	End	2749
GI	6907086	Score	115
Exons	2000..2273, 2694..2749		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	558	Strand	+
Start	89	End	12127
Name	OJ990203_02.9819.C24.o1.gs	Method	GENSCAN
Start	89	End	12127
GI	none	Score	.59
Exons	89..184, 1071..1306, 1418..1804, 2048..2327, 2373..2492, 2588..2729, 2855..3021, 3314..3487, 3547..3692, 3777..3849, 4700..4808, 5054..5211, 5716..5792, 7062..7114, 9106..9395, 10710..10883, 11900..12127		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	558	Strand	+
Start	89	End	12127
Name	OJ990203_02.9819.C24.o1.np	Method	AAT/NAP
Start	1056	End	5436
GI	4680204	Score	882
Exons	1056..2492, 2588..3095, 4700..4758, 5376..5436		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	558	Strand	+
Start	89	End	12127
Name	OJ990203_02.9819.C24.o1.gp	Method	AAT/GAP
Start	3962	End	4269
GI	LIB3432-059-P1-K1-D8	Score	534
Exons	3962..4269		
GI Descrip.	'5734616/dbj|AP000391.1|AP000391 0.0e+00 Oryza sativa genomic DNA, chromosome 6, clone:P0538C01'		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	558	Strand	+
Start	89	End	12127
Name	OJ990203_02.9819.C24.o2.np	Method	AAT/NAP
Start	5035	End	6186
GI	4322486	Score	138
Exons	5035..5211, 5716..5792, 6123..6186		
GI Descrip.	(AF086907) root gravitropism control protein [Arabidopsis thaliana]		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	559	Strand	-
Start	9940	End	13095
Name	OJ990203_02.9819.C24.o3.np	Method	AAT/NAP
Start	9940	End	13095
GI	6539570	Score	150
Exons	9940..9966, 11809..11882, 11933..12094, 13056..13095		
GI Descrip.	(AP000836) hypothetical protein [Oryza sativa]		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	560	Strand	-
Start	14196	End	15151
Name	OJ990203_02.9819.C24.o1.tw	Method	TBLASTX:Wheat
Start	1699	End	2102
GI	none	Score	65
Exons	1699..1839, 1699..1815, 1701..1937, 1701..1880, 1802..1942, 2007..2102, 2027..2101		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	560	Strand	-
Start	14196	End	15151
Name	OJ990203_02.9819.C24.o2.gs	Method	GENSCAN
Start	14196	End	15137
GI	none	Score	.86
Exons	14196..15137		

Seq. No.	286	Seq. ID	OJ990203_02.9819.C24
Gene No.	560	Strand	-
Start	14196	End	15151
Name	OJ990203_02.9819.C24.o4.np	Method	AAT/NAP
Start	14364	End	15151
GI	3941460	Score	137
Exons	14364..14457, 14992..15151		
GI Descrip.	(AF062884) putative transcription factor [Arabidopsis thaliana]		

Seq. No.	287	Seq. ID	OJ990203_02.9819.C27
Gene No.	561	Strand	-
Start	138	End	798
Name	OJ990203_02.9819.C27.o1.np	Method	AAT/NAP
Start	138	End	798
GI	418604	Score	1130
Exons	138..798		
GI Descrip.	HYPOTHETICAL 35.6 KD PROTEIN IN RPME-TDK INTERGENIC REGION (ORFP)		

Seq. No.	288	Seq. ID	OJ990203_02.9819.C28
Gene No.	562	Strand	+
Start	296	End	621
Name	OJ990203_02.9819.C28.o1.tc	Method	TBLASTX:Cress
Start	189	End	336
GI	none	Score	224
Exons	189..335, 190..336		

Seq. No.	288	Seq. ID	OJ990203_02.9819.C28
Gene No.	562	Strand	+
Start	296	End	621
Name	OJ990203_02.9819.C28.o1.gs	Method	GENSCAN
Start	296	End	491
GI	none	Score	.44
Exons	296..491		

Seq. No.	288	Seq. ID	OJ990203_02.9819.C28
Gene No.	562	Strand	+
Start	296	End	621
Name	OJ990203_02.9819.C28.o1.np	Method	AAT/NAP
Start	296	End	621
GI	2126090	Score	547
Exons	296..621		
GI Descrip.	transposase (insertion sequence IS10) - Escherichia coli gi|455676|bbs|140379 (S67119) transposase [Escherichia coli, LBB84, plasmid pXT107, IS10L/R-1, Peptide PlasmidTransposonInsertionMutant, 402 aa] [Escherichia coli] gi|6634720|gb|AAF19728.1|AC012463_2 (AC012463) T2E6.2 [Arabidopsis thaliana]		

Seq. No.	289	Seq. ID	OJ990203_02.9819.C29
Gene No.	563	Strand	-
Start	164	End	426
Name	OJ990203_02.9819.C29.o1.gs	Method	GENSCAN
Start	164	End	426
GI	none	Score	.83
Exons	164..190, 369..426		

Seq. No.	290	Seq. ID	OJ990203_02.9819.C42
Gene No.	564	Strand	-
Start	414	End	546
Name	OJ990203_02.9819.C42.o1.gs	Method	GENSCAN
Start	414	End	546
GI	none	Score	.51
Exons	414..546		

Seq. No.	291	Seq. ID	OJ990203_02.9819.C43
Gene No.	565	Strand	+
Start	74	End	403
Name	OJ990203_02.9819.C43.o1.gs	Method	GENSCAN
Start	74	End	403
GI	none	Score	.4
Exons	74..122, 222..403		

Seq. No.	292	Seq. ID	OJ990203_02.9819.C47
Gene No.	566	Strand	-
Start	516	End	647
Name	OJ990203_02.9819.C47.o1.gs	Method	GENSCAN
Start	516	End	647
GI	none	Score	.93
Exons	516..647		

Seq. No.	293	Seq. ID	OJ990203_02.9819.C48
Gene No.	567	Strand	+
Start	121	End	613
Name	OJ990203_02.9819.C48.o1.gs	Method	GENSCAN
Start	121	End	613
GI	none	Score	.64
Exons	121..204, 410..482, 525..613		

Seq. No.	294	Seq. ID	OJ990203_02.9819.C52
Gene No.	568	Strand	-
Start	522	End	657
Name	OJ990203_02.9819.C52.o1.gs	Method	GENSCAN
Start	522	End	657
GI	none	Score	.43
Exons	522..657		

Seq. No.	295	Seq. ID	OJ990203_02.9819.C58
Gene No.	569	Strand	+
Start	250	End	517
Name	OJ990203_02.9819.C58.o1.gs	Method	GENSCAN
Start	250	End	517
GI	none	Score	.71
Exons	250..360, 445..517		

Seq. No.	296	Seq. ID	OJ990203_02.9819.C59
Gene No.	570	Strand	-
Start	348	End	475
Name	OJ990203_02.9819.C59.o1.gs	Method	GENSCAN
Start	348	End	475
GI	none	Score	.42
Exons	348..475		

Seq. No.	297	Seq. ID	OJ990203_02.9819.C61
Gene No.	571	Strand	+
Start	515	End	618
Name	OJ990203_02.9819.C61.o1.gs	Method	GENSCAN
Start	515	End	618
GI	none	Score	.79
Exons	515..618		

Seq. No.	298	Seq. ID	OJ990203_03.9819.C2
Gene No.	572	Strand	-
Start	48	End	628
Name	OJ990203_03.9819.C2.o1.gs	Method	GENSCAN
Start	48	End	544
GI	none	Score	.46
Exons	48..544		

Seq. No.	298	Seq. ID	OJ990203_03.9819.C2
Gene No.	572	Strand	-
Start	48	End	628
Name	OJ990203_03.9819.C2.o1.np	Method	AAT/NAP
Start	51	End	628
GI	418604	Score	996
Exons	51..628		
GI Descrip.	HYPOTHETICAL 35.6 KD PROTEIN IN RPME-TDK INTERGENIC REGION (ORFP)		

Seq. No.	299	Seq. ID	OJ990203_03.9819.C3
Gene No.	573	Strand	-
Start	1	End	466
Name	OJ990203_03.9819.C3.o1.np	Method	AAT/NAP
Start	1	End	466
GI	5103193	Score	798
Exons	1..466		
GI Descrip.	(AP000342) transposase of Tn10 [Plasmid R100] gi|5738084|gb|AAD50242.1|AF162223_1 (AF162223) IS10-left transposase [Shigella flexneri]		

Seq. No.	299	Seq. ID	OJ990203_03.9819.C3
Gene No.	573	Strand	-
Start	1	End	466
Name	OJ990203_03.9819.C3.o1.gs	Method	GENSCAN
Start	13	End	466
GI	none	Score	.99
Exons	13..466		

Seq. No.	299	Seq. ID	OJ990203_03.9819.C3
Gene No.	574	Strand	
Start	426	End	573
Name	OJ990203_03.9819.C3.o1.tc	Method	TBLASTX:Cress

Start	426	End	573
GI	none	Score	216
Exons	426..572, 427..573, 427..573		

Seq. No.	300	Seq. ID	OJ990203_03.9819.C4
Gene No.	575	Strand	-
Start	264	End	631
Name	OJ990203_03.9819.C4.o1.gs	Method	GENSCAN
Start	264	End	631
GI	none	Score	.49
Exons	264..433, 482..631		

Seq. No.	301	Seq. ID	OJ990203_03.9819.C5
Gene No.	576	Strand	-
Start	388	End	543
Name	OJ990203_03.9819.C5.o1.gs	Method	GENSCAN
Start	388	End	543
GI	none	Score	.68
Exons	388..543		

Seq. No.	302	Seq. ID	OJ990203_03.9819.C7
Gene No.	577	Strand	-
Start	388	End	1135
Name	OJ990203_03.9819.C7.o1.np	Method	AAT/NAP
Start	388	End	1135
GI	6587862	Score	137
Exons	388..489, 854..1135		
GI Descrip.	(AC012680) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	302	Seq. ID	OJ990203_03.9819.C7
Gene No.	577	Strand	-
Start	388	End	1135
Name	OJ990203_03.9819.C7.o1.gs	Method	GENSCAN
Start	854	End	974
GI	none	Score	.92
Exons	854..974		

Seq. No.	303	Seq. ID	OJ990203_03.9819.C8
Gene No.	578	Strand	+
Start	27	End	8205
Name	OJ990203_03.9819.C8.o1.np	Method	AAT/NAP
Start	27	End	3005
GI	6587862	Score	577
Exons	27..442, 809..890, 1417..1499, 1809..1920, 2524..2631, 2868..3005		
GI Descrip.	(AC012680) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	303	Seq. ID	OJ990203_03.9819.C8
Gene No.	578	Strand	+
Start	27	End	8205
Name	OJ990203_03.9819.C8.o1.gs	Method	GENSCAN
Start	296	End	8205
GI	none	Score	.45
Exons	296..442, 1809..1920, 2524..2631, 4543..4600, 4649..4703, 5878..6123, 6250..6462, 7123..7222, 7329..7415, 8008..8205		

Seq. No.	303	Seq. ID	OJ990203_03.9819.C8

Gene No.	578	Strand	+
Start	27	End	8205
Name	OJ990203_03.9819.C8.o1.gp	Method	AAT/GAP
Start	1403	End	2615
GI	LIB3432-024-P1-K1-E6	Score	731
Exons	1403..1607, 1809..1920, 2524..2615		
GI Descrip.	'3402713 2.0e-23 (AC004261) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	303	Seq. ID	OJ990203_03.9819.C8
Gene No.	578	Strand	+
Start	27	End	8205
Name	OJ990203_03.9819.C8.o1.tm	Method	TBLASTX:Maize
Start	1410	End	1572
GI	none	Score	189
Exons	1410..1571, 1414..1572		

Seq. No.	303	Seq. ID	OJ990203_03.9819.C8
Gene No.	578	Strand	+
Start	27	End	8205
Name	OJ990203_03.9819.C8.o1.ts	Method	TBLASTX:Soybean
Start	1410	End	2583
GI	none	Score	196
Exons	1410..1571, 1417..1596, 1420..1596, 1813..1923, 1815..1922, 2434..2583		

Seq. No.	303	Seq. ID	OJ990203_03.9819.C8
Gene No.	578	Strand	+
Start	27	End	8205
Name	OJ990203_03.9819.C8.o1.tw	Method	TBLASTX:Wheat
Start	7302	End	7424
GI	none	Score	181
Exons	7302..7424, 7303..7416, 7304..7420		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	579	Strand	+
Start	1	End	1575
Name	OJ990203_03.9819.C9.o1.np	Method	AAT/NAP
Start	1	End	1454
GI	5306265	Score	138
Exons	1..94, 189..242, 355..444, 940..1008, 1167..1454		
GI Descrip.	(AC006233) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	579	Strand	+
Start	1	End	1575
Name	OJ990203_03.9819.C9.o1.gs	Method	GENSCAN
Start	130	End	1575
GI	none	Score	.7
Exons	130..242, 355..529, 567..643, 1159..1511, 1551..1575		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	580	Strand	+
Start	21555	End	22817
Name	OJ990203_03.9819.C9.o6.gs	Method	GENSCAN
Start	21555	End	22817
GI	none	Score	.98

Exons	21555..22817		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	581	Strand	+
Start	24530	End	31071
Name	OJ990203_03.9819.C9.o7.gs	Method	GENSCAN
Start	24530	End	31050
GI	none	Score	.55
Exons	24530..24919, 25266..25344, 25413..25517, 25668..25848, 25968..26115, 26394..26519, 26608..26682, 26755..27124, 27326..27370, 27750..28153, 28798..28909, 29134..29418, 29488..29697, 29852..29901, 30260..30304, 30343..31050		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	581	Strand	+
Start	24530	End	31071
Name	OJ990203_03.9819.C9.o5.np	Method	AAT/NAP
Start	25712	End	31071
GI	6069646	Score	1119
Exons	25712..25764, 29036..29811, 30098..31071		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	582	Strand	+
Start	35141	End	41723
Name	OJ990203_03.9819.C9.o9.gs	Method	GENSCAN
Start	35141	End	41723
GI	none	Score	.46
Exons	35141..35170, 35323..35507, 35919..36273, 36958..37307, 37385..37521, 37994..38215, 40093..40149, 41332..41423, 41595..41723		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	582	Strand	+
Start	35141	End	41723
Name	OJ990203_03.9819.C9.o7.np	Method	AAT/NAP
Start	35865	End	36085
GI	4558556	Score	53
Exons	35865..36085		
GI Descrip.	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	583	Strand	+
Start	47301	End	47375
Name	OJ990203_03.9819.C9.o4.gp	Method	AAT/GAP
Start	47301	End	47375
GI	72424_1.R1084	Score	62
Exons	47301..47375		
GI Descrip.	'2842493/emb|CAA16890.1| 8.0e-32 (AL021749) predicted protein [Arabidopsis thaliana]'		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9

Gene No.	584	Strand	-
Start	10998	End	20574
Name	OJ990203_03.9819.C9.o4.gs	Method	GENSCAN
Start	10998	End	18522
GI	none	Score	.59
Exons	10998..11095, 11173..11846, 12454..12662, 13487..13580, 14973..15143, 15324..15404, 16119..16244, 17301..17708, 17795..18522		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	584	Strand	-
Start	10998	End	20574
Name	OJ990203_03.9819.C9.o1.gp	Method	AAT/GAP
Start	17020	End	17903
GI	23445_1.R1084	Score	1516
Exons	17020..17708, 17795..17903		
GI Descrip.	'2464901/emb|CAB16804.1| 1.0e-24 (Z99708) putative protein [Arabidopsis thaliana]'		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	584	Strand	-
Start	10998	End	20574
Name	OJ990203_03.9819.C9.o2.np	Method	AAT/NAP
Start	17288	End	19265
GI	6587861	Score	1295
Exons	17288..17708, 17795..18522, 18978..19265		
GI Descrip.	(AC012680) putative transporter [Arabidopsis thaliana]		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	584	Strand	-
Start	10998	End	20574
Name	OJ990203_03.9819.C9.o2.gp	Method	AAT/GAP
Start	17970	End	18173
GI	none	Score	323
Exons	17970..18173		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	584	Strand	-
Start	10998	End	20574
Name	OJ990203_03.9819.C9.o5.gs	Method	GENSCAN
Start	18903	End	20574
GI	none	Score	.6
Exons	18903..19409, 20419..20574		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	584	Strand	-
Start	10998	End	20574
Name	OJ990203_03.9819.C9.o3.gp	Method	AAT/GAP
Start	19115	End	19314
GI	568367	Score	323
Exons	19115..19314		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	585	Strand	-
Start	31774	End	34251
Name	OJ990203_03.9819.C9.o8.gs	Method	GENSCAN
Start	31774	End	34251

GI	none	Score	.89
Exons	31774..32263, 32659..32752, 32990..33404, 33961..34251		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	585	Strand	-
Start	31774	End	34251
Name	OJ990203_03.9819.C9.o6.np	Method	AAT/NAP
Start	31840	End	34248
GI	6587861	Score	1495
Exons	31840..32263, 32659..33404, 33961..34248		
GI Descrip.	(AC012680) putative transporter [Arabidopsis thaliana]		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	586	Strand	-
Start	43020	End	44887
Name	OJ990203_03.9819.C9.o10.gs	Method	GENSCAN
Start	43020	End	44887
GI	none	Score	.58
Exons	43020..43043, 44675..44887		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o3.tc	Method	TBLASTX:Cress
Start	17333	End	32196
GI	none	Score	115
Exons	17333..17566, 17334..17549, 17540..17641, 31882..32103, 31898..32035, 32113..32196, 32123..32194		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o5.tm	Method	TBLASTX:Maize
Start	17387	End	32154
GI	none	Score	121
Exons	17387..17566, 17403..17561, 17552..17599, 31885..32154, 31886..32038, 31891..32148, 31893..32153		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o1.tc	Method	TBLASTX:Cress
Start	17795	End	33152
GI	none	Score	178
Exons	17795..18151, 17797..18174, 32659..32829, 32661..33089, 32926..33078, 33108..33152		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o2.tc	Method	TBLASTX:Cress
Start	18383	End	34227
GI	none	Score	108
Exons	18383..18520, 18385..18525, 18966..19271, 18967..19050, 19108..19176, 19179..19241, 33265..33414, 33267..33413, 33958..34227, 33959..34021		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o7.tm	Method	TBLASTX:Maize
Start	18981	End	34227
GI	none	Score	66
Exons	18981..19145, 18982..19050, 19108..19143, 19149..19271, 19179..19244, 33967..34125, 34132..34227		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o1.ts	Method	TBLASTX:Soybean
Start	18993	End	34231
GI	none	Score	127
Exons	18993..19247, 18994..19248, 33976..34023, 33977..34231, 34087..34227		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o2.tm	Method	TBLASTX:Maize
Start	22076	End	22355
GI	none	Score	58
Exons	22076..22150, 22077..22121, 22138..22353, 22139..22348, 22142..22354, 22146..22355		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o9.tm	Method	TBLASTX:Maize
Start	27962	End	28201
GI	none	Score	138
Exons	27962..28099, 28103..28201		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o4.tm	Method	TBLASTX:Maize
Start	28420	End	28761
GI	none	Score	291
Exons	28420..28761, 28455..28502, 28615..28743		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o6.tm	Method	TBLASTX:Maize
Start	28891	End	29339
GI	none	Score	37
Exons	28891..28923, 29037..29249, 29238..29339		

Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o2.tw	Method	TBLASTX:Wheat
Start	29229	End	29534
GI	none	Score	190

Exons	29229..29534, 29267..29533		
Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o1.tm	Method	TBLASTX:Maize
Start	29340	End	30026
GI	none	Score	483
Exons	29340..30026, 29375..29548, 29789..30025		
Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o1.tw	Method	TBLASTX:Wheat
Start	29667	End	30107
GI	none	Score	247
Exons	29667..29972, 29669..29968, 29979..30086, 30018..30107		
Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o8.tm	Method	TBLASTX:Maize
Start	30096	End	30381
GI	none	Score	183
Exons	30096..30266, 30097..30267, 30274..30381		
Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o3.tm	Method	TBLASTX:Maize
Start	30469	End	30999
GI	none	Score	92
Exons	30469..30573, 30598..30834, 30600..30827, 30808..30999		
Seq. No.	304	Seq. ID	OJ990203_03.9819.C9
Gene No.	587	Strand	-
Start	46909	End	50461
Name	OJ990203_03.9819.C9.o11.gs	Method	GENSCAN
Start	46909	End	50461
GI	none	Score	.57
Exons	46909..47051, 47861..47934, 50415..50461		
Seq. No.	305	Seq. ID	OJ990203_03.9819.C10
Gene No.	588	Strand	-
Start	6370	End	7269
Name	OJ990203_03.9819.C10.o2.gs	Method	GENSCAN
Start	6370	End	7269
GI	none	Score	.74
Exons	6370..6570, 7195..7269		
Seq. No.	305	Seq. ID	OJ990203_03.9819.C10
Gene No.	589	Strand	-
Start	16257	End	19693
Name	OJ990203_03.9819.C10.o4.gs	Method	GENSCAN
Start	16257	End	19693
GI	none	Score	.74
Exons	16257..16299, 16662..16739, 18379..18386, 18638..18933,		

19269..19374, 19562..19693

Seq. No.	306	Seq. ID	OJ990203_03.9819.C11
Gene No.	590	Strand	+
Start	134	End	226
Name	OJ990203_03.9819.C11.o1.gs	Method	GENSCAN
Start	134	End	226
GI	none	Score	.65
Exons	134..226		

Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	591	Strand	+
Start	165	End	1999
Name	OJ990203_03.9819.C12.o1.gs	Method	GENSCAN
Start	165	End	1999
GI	none	Score	.57
Exons	165..222, 1917..1999		

Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	592	Strand	-
Start	2315	End	4604
Name	OJ990203_03.9819.C12.o1.gp	Method	AAT/GAP
Start	2249	End	4037
GI	9025_1.R1084	Score	1166
Exons	2249..2380, 3202..3365, 3491..3560, 3763..4037		
GI Descrip.	'2944180 2.0e-45 (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]'		

Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	592	Strand	-
Start	2315	End	4604
Name	OJ990203_03.9819.C12.o1.tm	Method	TBLASTX:Maize
Start	2283	End	4543
GI	none	Score	110
Exons	2283..2381, 2288..2383, 3174..3287, 3188..3289, 3196..3366, 3197..3367, 3489..3560, 3490..3561, 3490..3576, 3497..3577, 3760..3843, 3760..3843, 4104..4205, 4105..4206, 4109..4207, 4338..4388, 4338..4388, 4339..4389, 4339..4389, 4486..4542, 4487..4543		

Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	592	Strand	-
Start	2315	End	4604
Name	OJ990203_03.9819.C12.o2.gs	Method	GENSCAN
Start	2315	End	4538
GI	none	Score	.74
Exons	2315..2380, 3202..3457, 3660..3691, 3763..3840, 4104..4205, 4341..4449, 4486..4538		

Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	592	Strand	-
Start	2315	End	4604
Name	OJ990203_03.9819.C12.o1.np	Method	AAT/NAP
Start	2327	End	4604
GI	4567205	Score	503
Exons	2327..2380, 3202..3365, 3491..3560, 3763..3840, 4104..4205, 4341..4387, 4482..4604		

GI Descrip.	(AC007168) putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]		
Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	592	Strand	-
Start	2315	End	4604
Name	OJ990203_03.9819.C12.o1.tw	Method	TBLASTX:Wheat
Start	2327	End	3843
GI	none	Score	213
Exons	2327..2383, 3188..3283, 3196..3366, 3197..3370, 3489..3560, 3490..3567, 3493..3561, 3494..3577, 3760..3843, 3760..3843		
Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	592	Strand	-
Start	2315	End	4604
Name	OJ990203_03.9819.C12.o1.tc	Method	TBLASTX:Cress
Start	3194	End	4542
GI	none	Score	165
Exons	3194..3367, 3199..3366, 3489..3560, 3490..3564, 3760..3837, 4085..4159, 4104..4193, 4105..4218, 4338..4385, 4474..4542		
Seq. No.	307	Seq. ID	OJ990203_03.9819.C12
Gene No.	592	Strand	-
Start	2315	End	4604
Name	OJ990203_03.9819.C12.o1.ts	Method	TBLASTX:Soybean
Start	3196	End	3564
GI	5677912	Score	163
Exons	3196..3366, 3197..3370, 3489..3560, 3490..3564		
GI Descrip.	4567205/gb_AAD23621.1_AC007168_12 3.0e-42 (AC007168) putative trehalose-6-phosphate phosphatase [Arabidopsis thaliana]		
Seq. No.	308	Seq. ID	OJ990203_03.9819.C13
Gene No.	593	Strand	+
Start	98	End	751
Name	OJ990203_03.9819.C13.o1.gs	Method	GENSCAN
Start	98	End	751
GI	none	Score	.51
Exons	98..219, 571..751		
Seq. No.	309	Seq. ID	OJ990203_03.9819.C14
Gene No.	594	Strand	+
Start	3968	End	4989
Name	OJ990203_03.9819.C14.o3.gs	Method	GENSCAN
Start	3968	End	4989
GI	none	Score	.46
Exons	3968..4162, 4694..4795, 4900..4989		
Seq. No.	309	Seq. ID	OJ990203_03.9819.C14
Gene No.	595	Strand	-
Start	2817	End	3052
Name	OJ990203_03.9819.C14.o1.np	Method	AAT/NAP
Start	2817	End	3052
GI	6650373	Score	53
Exons	2817..3052		
GI Descrip.	(AF095718) RRM-type RNA-binding protein PTB [Mus musculus]		
Seq. No.	309	Seq. ID	OJ990203_03.9819.C14

Gene No.	596	Strand	-
Start	5368	End	8110
Name	OJ990203_03.9819.C14.o4.gs	Method	GENSCAN
Start	5368	End	8110
GI	none	Score	.85
Exons	5368..5594, 7300..7436, 8109..8110		

Seq. No.	310	Seq. ID	OJ990203_03.9819.C15
Gene No.	597	Strand	+
Start	312	End	425
Name	OJ990203_03.9819.C15.o1.gs	Method	GENSCAN
Start	312	End	425
GI	none	Score	.92
Exons	312..425		

Seq. No.	311	Seq. ID	OJ990203_03.9819.C16
Gene No.	598	Strand	-
Start	239	End	276
Name	OJ990203_03.9819.C16.o1.gs	Method	GENSCAN
Start	239	End	276
GI	none	Score	.98
Exons	239..276		

Seq. No.	312	Seq. ID	OJ990203_03.9819.C21
Gene No.	599	Strand	+
Start	211	End	522
Name	OJ990203_03.9819.C21.o1.gs	Method	GENSCAN
Start	211	End	522
GI	none	Score	.95
Exons	211..522		

Seq. No.	313	Seq. ID	OJ990203_03.9819.C22
Gene No.	600	Strand	-
Start	1	End	390
Name	OJ990203_03.9819.C22.o1.np	Method	AAT/NAP
Start	1	End	390
GI	4768976	Score	110
Exons	1..136, 295..390		
GI Descrip.	(AF140488) hypothetical protein [Oryza sativa]		

Seq. No.	313	Seq. ID	OJ990203_03.9819.C22
Gene No.	600	Strand	-
Start	1	End	390
Name	OJ990203_03.9819.C22.o1.gp	Method	AAT/GAP
Start	137	End	228
GI	9025_1.R1084	Score	122
Exons	137..228		
GI Descrip.	'2944180 2.0e-45 (AF007779) trehalose-6-phosphate phosphatase [Arabidopsis thaliana]'		

Seq. No.	313	Seq. ID	OJ990203_03.9819.C22
Gene No.	601	Strand	-
Start	295	End	398
Name	OJ990203_03.9819.C22.o1.gs	Method	GENSCAN
Start	295	End	396
GI	none	Score	.83
Exons	295..396		

Seq. No.	313	Seq. ID	OJ990203_03.9819.C22
Gene No.	601	Strand	-
Start	295	End	398
Name	OJ990203_03.9819.C22.o1.tm	Method	TBLASTX:Maize
Start	295	End	398
GI	none	Score	174
Exons	295..396, 296..397, 300..398		

Seq. No.	314	Seq. ID	OJ990203_03.9819.C24
Gene No.	602	Strand	-
Start	106	End	249
Name	OJ990203_03.9819.C24.o1.gs	Method	GENSCAN
Start	106	End	249
GI	none	Score	.94
Exons	106..249		

Seq. No.	315	Seq. ID	OJ990113_04.9819.C1
Gene No.	603	Strand	-
Start	519	End	689
Name	OJ990113_04.9819.C1.o1.gs	Method	GENSCAN
Start	519	End	689
GI	none	Score	.47
Exons	519..689		

Seq. No.	316	Seq. ID	OJ990113_04.9819.C4
Gene No.	604	Strand	+
Start	989	End	1755
Name	OJ990113_04.9819.C4.o1.gs	Method	GENSCAN
Start	989	End	1755
GI	none	Score	.64
Exons	989..1095, 1645..1755		

Seq. No.	317	Seq. ID	OJ990113_04.9819.C5
Gene No.	605	Strand	-
Start	1	End	1936
Name	OJ990113_04.9819.C5.o1.np	Method	AAT/NAP
Start	1	End	1936
GI	6815097	Score	759
Exons	1..33, 140..1807, 1905..1936		
GI Descrip.	(AP001081) Similar to putative copia polyprotein (AC006248) [Oryza sativa]		

Seq. No.	317	Seq. ID	OJ990113_04.9819.C5
Gene No.	605	Strand	-
Start	1	End	1936
Name	OJ990113_04.9819.C5.o1.tc	Method	TBLASTX:Cress
Start	450	End	710
GI	none	Score	101
Exons	450..710, 451..708		

Seq. No.	318	Seq. ID	OJ990113_04.9819.C6
Gene No.	606	Strand	+
Start	215	End	299
Name	OJ990113_04.9819.C6.o1.gs	Method	GENSCAN
Start	215	End	299
GI	none	Score	.7

Exons	215..299		
Seq. No.	319	Seq. ID	OJ990113_04.9819.C7
Gene No.	607	Strand	+
Start	997	End	1126
Name	OJ990113_04.9819.C7.o1.gs	Method	GENSCAN
Start	997	End	1126
GI	none	Score	.96
Exons	997..1126		
Seq. No.	320	Seq. ID	OJ990113_04.9819.C10
Gene No.	608	Strand	-
Start	243	End	338
Name	OJ990113_04.9819.C10.o1.gp	Method	AAT/GAP
Start	243	End	338
GI	none	Score	129
Exons	243..338		
Seq. No.	320	Seq. ID	OJ990113_04.9819.C10
Gene No.	609	Strand	-
Start	263	End	960
Name	OJ990113_04.9819.C10.o1.np	Method	AAT/NAP
Start	263	End	960
GI	3037018	Score	313
Exons	263..600, 646..960		
GI Descrip.	(AF041330) NADH dehydrogenase subunit 5 [Bodo saltans]		
Seq. No.	320	Seq. ID	OJ990113_04.9819.C10
Gene No.	609	Strand	-
Start	263	End	960
Name	OJ990113_04.9819.C10.o2.gp	Method	AAT/GAP
Start	446	End	601
GI	jC-osleLIB3474037g11a1	Score	267
Exons	446..601		
GI Descrip.	'5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]'		
Seq. No.	321	Seq. ID	OJ990113_04.9819.C13
Gene No.	610	Strand	+
Start	1	End	1092
Name	OJ990113_04.9819.C13.o1.np	Method	AAT/NAP
Start	1	End	1092
GI	137616	Score	1459
Exons	1..1092		
GI Descrip.	TERMINASE LARGE SUBUNIT (DNA PACKAGING PROTEIN A) (GPA) gi|76025|pir||JVBPAL DNA-packaging protein A - phage lambda gi|215106 (J02459) A (DNA packaging;641) [Bacteriophage lambda]		
Seq. No.	321	Seq. ID	OJ990113_04.9819.C13
Gene No.	610	Strand	+
Start	1	End	1092
Name	OJ990113_04.9819.C13.o1.gs	Method	GENSCAN
Start	63	End	800
GI	none	Score	.89
Exons	63..800		
Seq. No.	322	Seq. ID	OJ990113_04.9819.C14

Gene No.	611	Strand	+
Start	1	End	607
Name	OJ990113_04.9819.C14.o1.np	Method	AAT/NAP
Start	1	End	607
GI	3192691	Score	725
Exons	1..607		
GI Descrip.	(AF064539) gp8 [Bacteriophage N15]		

Seq. No.	322	Seq. ID	OJ990113_04.9819.C14
Gene No.	611	Strand	+
Start	1	End	607
Name	OJ990113_04.9819.C14.o1.gs	Method	GENSCAN
Start	70	End	473
GI	none	Score	.55
Exons	70..473		

Seq. No.	323	Seq. ID	OJ990113_04.9819.C15
Gene No.	612	Strand	-
Start	401	End	514
Name	OJ990113_04.9819.C15.o1.gs	Method	GENSCAN
Start	401	End	514
GI	none	Score	.78
Exons	401..514		

Seq. No.	324	Seq. ID	OJ990113_04.9819.C17
Gene No.	613	Strand	-
Start	59	End	193
Name	OJ990113_04.9819.C17.o1.gs	Method	GENSCAN
Start	59	End	193
GI	none	Score	.72
Exons	59..193		

Seq. No.	325	Seq. ID	OJ990113_04.9819.C18
Gene No.	614	Strand	+
Start	120	End	295
Name	OJ990113_04.9819.C18.o1.gs	Method	GENSCAN
Start	120	End	295
GI	none	Score	.83
Exons	120..295		

Seq. No.	326	Seq. ID	OJ990113_04.9819.C23
Gene No.	615	Strand	-
Start	995	End	1105
Name	OJ990113_04.9819.C23.o1.gs	Method	GENSCAN
Start	995	End	1105
GI	none	Score	.48
Exons	995..1105		

Seq. No.	327	Seq. ID	OJ990113_04.9819.C27
Gene No.	616	Strand	-
Start	137	End	196
Name	OJ990113_04.9819.C27.o1.gs	Method	GENSCAN
Start	137	End	196
GI	none	Score	.47
Exons	137..196		

Seq. No.	328	Seq. ID	OJ990113_04.9819.C28

Gene No.	617	Strand	-
Start	926	End	1737
Name	OJ990113_04.9819.C28.o1.gs	Method	GENSCAN
Start	926	End	1737
GI	none	Score	.74
Exons	926..1005, 1616..1737		

Seq. No.	329	Seq. ID	OJ990113_04.9819.C29
Gene No.	618	Strand	+
Start	1	End	1215
Name	OJ990113_04.9819.C29.o1.np	Method	AAT/NAP
Start	1	End	1215
GI	6815097	Score	86
Exons	1..150, 1197..1215		
GI Descrip.	(AP001081) Similar to putative copia polyprotein (AC006248) [Oryza sativa]		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	619	Strand	+
Start	417	End	800
Name	OJ990113_04.9819.C32.o1.gp	Method	AAT/GAP
Start	417	End	800
GI	uC-osflcyp033a04b1	Score	669
Exons	417..800		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	620	Strand	+
Start	1744	End	3712
Name	OJ990113_04.9819.C32.o1.gs	Method	GENSCAN
Start	1744	End	3712
GI	none	Score	.84
Exons	1744..2008, 2234..2336, 2667..2852, 3000..3110, 3196..3274, 3357..3449, 3527..3712		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	621	Strand	+
Start	12052	End	16965
Name	OJ990113_04.9819.C32.o4.gs	Method	GENSCAN
Start	12052	End	13126
GI	none	Score	.74
Exons	12052..12522, 12578..13126		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	621	Strand	+
Start	12052	End	16965
Name	OJ990113_04.9819.C32.o2.np	Method	AAT/NAP
Start	12127	End	16794
GI	6815097	Score	3367
Exons	12127..12988, 13493..14109, 14224..15887, 16029..16794		
GI Descrip.	(AP001081) Similar to putative copia polyprotein (AC006248) [Oryza sativa]		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	621	Strand	+
Start	12052	End	16965

Name	OJ990113_04.9819.C32.o5.gs	Method	GENSCAN
Start	13586	End	16965
GI	none	Score	.46
Exons	13586..13827, 14028..14148, 14437..15519, 15664..15756, 15790..16965		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	622	Strand	+
Start	22545	End	28864
Name	OJ990113_04.9819.C32.o3.np	Method	AAT/NAP
Start	22545	End	28864
GI	5852180	Score	465
Exons	22545..22570, 26117..26170, 27153..27271, 27323..27717, 28811..28864		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	623	Strand	-
Start	350	End	12519
Name	OJ990113_04.9819.C32.o1.np	Method	AAT/NAP
Start	350	End	12519
GI	4680186	Score	227
Exons	350..550, 12492..12519		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	623	Strand	-
Start	350	End	12519
Name	OJ990113_04.9819.C32.o2.gs	Method	GENSCAN
Start	4010	End	4314
GI	none	Score	.65
Exons	4010..4218, 4278..4314		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	624	Strand	-
Start	20055	End	23675
Name	OJ990113_04.9819.C32.o6.gs	Method	GENSCAN
Start	20055	End	23675
GI	none	Score	.49
Exons	20055..20128, 22197..22409, 22432..22565, 23608..23675		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	625	Strand	-
Start	26019	End	26400
Name	OJ990113_04.9819.C32.o1.tc	Method	TBLASTX:Cress
Start	12145	End	12465
GI	none	Score	190
Exons	12145..12465		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	625	Strand	-
Start	26019	End	26400
Name	OJ990113_04.9819.C32.o1.ts	Method	TBLASTX:Soybean
Start	15415	End	15860
GI	5509260	Score	129
Exons	15415..15600, 15418..15621, 15667..15753, 15780..15860, 15781..15852		

GI Descrip. -

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	625	Strand	-
Start	26019	End	26400
Name	OJ990113_04.9819.C32.o3.tm	Method	TBLASTX:Maize
Start	15517	End	15951
GI	none	Score	124
Exons	15517..15741, 15781..15951		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	625	Strand	-
Start	26019	End	26400
Name	OJ990113_04.9819.C32.o2.ts	Method	TBLASTX:Soybean
Start	16281	End	16869
GI	none	Score	212
Exons	16281..16388, 16285..16647, 16443..16562, 16753..16869		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	625	Strand	-
Start	26019	End	26400
Name	OJ990113_04.9819.C32.o1.tm	Method	TBLASTX:Maize
Start	16303	End	16626
GI	none	Score	373
Exons	16303..16626, 16314..16625, 16435..16626		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	625	Strand	-
Start	26019	End	26400
Name	OJ990113_04.9819.C32.o2.tm	Method	TBLASTX:Maize
Start	16626	End	17015
GI	none	Score	89
Exons	16626..16691, 16627..16689, 16746..16973, 16750..16971, 16980..17015		

Seq. No.	330	Seq. ID	OJ990113_04.9819.C32
Gene No.	625	Strand	-
Start	26019	End	26400
Name	OJ990113_04.9819.C32.o3.gp	Method	AAT/GAP
Start	26019	End	26400
GI	uC-osf1cyp033a04b1	Score	627
Exons	26019..26400		

GI Descrip. '6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'

Seq. No.	331	Seq. ID	OJ990113_04.9819.C33
Gene No.	626	Strand	+
Start	281	End	2551
Name	OJ990113_04.9819.C33.o1.gs	Method	GENSCAN
Start	281	End	2516
GI	none	Score	.49
Exons	281..653, 880..2516		

Seq. No.	331	Seq. ID	OJ990113_04.9819.C33
Gene No.	626	Strand	+
Start	281	End	2551
Name	OJ990113_04.9819.C33.o1.np	Method	AAT/NAP

Start	2268	End	2551
GI	4680339	Score	105
Exons	2268..2551		
GI Descrip.	(AF128457) hypothetical protein [Oryza sativa subsp. indica]		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	627	Strand	+
Start	465	End	1631
Name	OJ990113_04.9819.C34.o1.gs	Method	GENSCAN
Start	465	End	1631
GI	none	Score	.6
Exons	465..831, 844..1192, 1475..1631		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	628	Strand	+
Start	5914	End	10310
Name	OJ990113_04.9819.C34.o3.gs	Method	GENSCAN
Start	5914	End	10310
GI	none	Score	.4
Exons	5914..6038, 6383..6578, 6594..6679, 6981..7525, 7693..7817, 7930..8070, 8456..8581, 8608..9041, 9169..9314, 9460..9727, 9826..9953, 10255..10310		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	628	Strand	+
Start	5914	End	10310
Name	OJ990113_04.9819.C34.o1.np	Method	AAT/NAP
Start	7426	End	9042
GI	6721561	Score	885
Exons	7426..7496, 7886..8070, 8141..8199, 8281..9042		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	629	Strand	+
Start	12591	End	26951
Name	OJ990113_04.9819.C34.o4.np	Method	AAT/NAP
Start	12591	End	17710
GI	2429362	Score	191
Exons	12591..12771, 17133..17710		
GI Descrip.	(AF020261) proline rich protein [Santalum album]		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	629	Strand	+
Start	12591	End	26951
Name	OJ990113_04.9819.C34.o3.np	Method	AAT/NAP
Start	13313	End	16624
GI	4680203	Score	2053
Exons	13313..14887, 14930..15022, 15176..15406, 15683..16624		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	629	Strand	+
Start	12591	End	26951

Name	OJ990113_04.9819.C34.o5.gs	Method	GENSCAN
Start	13313	End	26951
GI	none	Score	.66
Exons	13313..16568, 16947..17043, 17129..17614, 17685..17801, 20729..20776, 20874..21462, 21541..22002, 22084..22916, 22999..23169, 23336..23507, 23946..23985, 24249..24321, 25013..25809, 25957..26951		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	629	Strand	+
Start	12591	End	26951
Name	OJ990113_04.9819.C34.o1.gp	Method	AAT/GAP
Start	15278	End	16739
GI	5002953	Score	1281
Exons	15278..15409, 15668..16077, 16557..16739		
GI Descrip.	4680203/gb|AAD27566.1|AF114171_7 1.0e-39 (AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	629	Strand	+
Start	12591	End	26951
Name	OJ990113_04.9819.C34.o2.gp	Method	AAT/GAP
Start	23325	End	23845
GI	LIB3431-001-P1-N1-B5	Score	766
Exons	23325..23507, 23613..23845		
GI Descrip.	'4680203/gb|AAD27566.1|AF114171_7 1.0e-39 (AF114171) TNP2-like protein [Sorghum bicolor]'		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	630	Strand	+
Start	30281	End	32235
Name	OJ990113_04.9819.C34.o6.np	Method	AAT/NAP
Start	30281	End	32235
GI	4680186	Score	194
Exons	30281..30312, 32007..32235		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	631	Strand	-
Start	4095	End	4486
Name	OJ990113_04.9819.C34.o2.gs	Method	GENSCAN
Start	4095	End	4486
GI	none	Score	.53
Exons	4095..4341, 4347..4486		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	632	Strand	-
Start	10443	End	14568
Name	OJ990113_04.9819.C34.o2.np	Method	AAT/NAP
Start	10443	End	14568
GI	5902445	Score	597
Exons	10443..11124, 14548..14568		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718

Name	OJ990113_04.9819.C34.o2.tw	Method	TBLASTX:Wheat
Start	10452	End	11030
GI	none	Score	61
Exons	10452..10580, 10453..10578, 10608..11030, 10804..10911		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o3.tm	Method	TBLASTX:Maize
Start	10575	End	10838
GI	none	Score	193
Exons	10575..10838		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o4.tw	Method	TBLASTX:Wheat
Start	13667	End	14218
GI	none	Score	217
Exons	13667..14065, 13765..13788, 13906..14067, 14113..14208, 14114..14218		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o1.ts	Method	TBLASTX:Soybean
Start	13946	End	14365
GI	none	Score	126
Exons	13946..14065, 13948..14067, 14116..14361, 14117..14365		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o1.tc	Method	TBLASTX:Cress
Start	14113	End	14443
GI	none	Score	312
Exons	14113..14250, 14114..14443, 14287..14346, 14368..14442		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o3.tw	Method	TBLASTX:Wheat
Start	14231	End	14697
GI	none	Score	54
Exons	14231..14284, 14239..14274, 14285..14389, 14296..14382, 14381..14491, 14390..14506, 14394..14492, 14398..14568, 14509..14697, 14537..14692		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o1.tm	Method	TBLASTX:Maize
Start	14288	End	14731
GI	none	Score	229
Exons	14288..14533, 14338..14529, 14537..14731		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34

Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o2.ts	Method	TBLASTX:Soybean
Start	14566	End	14800
GI	none	Score	250
Exons	14566..14721, 14567..14800		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o5.tw	Method	TBLASTX:Wheat
Start	14939	End	15289
GI	none	Score	183
Exons	14939..15169, 14968..15168, 15205..15288, 15206..15289		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o4.tm	Method	TBLASTX:Maize
Start	14945	End	15160
GI	none	Score	166
Exons	14945..15091, 14974..15081, 15098..15160		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o2.tm	Method	TBLASTX:Maize
Start	15197	End	15682
GI	none	Score	299
Exons	15197..15682, 15214..15390, 15526..15675		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o1.tw	Method	TBLASTX:Wheat
Start	15293	End	16513
GI	none	Score	491
Exons	15293..15835, 15337..15783, 15854..16015, 15871..16011, 16019..16210, 16054..16194, 16199..16246, 16250..16291, 16253..16291, 16321..16392, 16322..16420, 16421..16513		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o2.tc	Method	TBLASTX:Cress
Start	15580	End	16006
GI	none	Score	209
Exons	15580..15783, 15584..15835, 15854..16006, 15871..15993		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o6.gs	Method	GENSCAN
Start	28045	End	33686
GI	none	Score	.43
Exons	28045..28073, 28141..28225, 28775..28975, 29289..29395, 30419..30995, 31961..32088, 32651..32732, 33174..33686		

Seq. No.	332	Seq. ID	OJ990113_04.9819.C34
Gene No.	633	Strand	-
Start	28045	End	33718
Name	OJ990113_04.9819.C34.o7.np	Method	AAT/NAP
Start	32631	End	33718
GI	6907087	Score	353
Exons	32631..32732, 33284..33718		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	333	Seq. ID	OJ990113_04.9819.C35
Gene No.	634	Strand	-
Start	1069	End	6504
Name	OJ990113_04.9819.C35.o1.gs	Method	GENSCAN
Start	1069	End	6504
GI	none	Score	.42
Exons	1069..1148, 1383..1509, 2208..2548, 2747..2901, 3072..3214, 3249..3383, 3547..3584, 3589..3656, 3946..4066, 4228..4356, 4564..4633, 6444..6504		

Seq. No.	334	Seq. ID	OJ990113_04.9819.C36
Gene No.	635	Strand	+
Start	1	End	8376
Name	OJ990113_04.9819.C36.o1.np	Method	AAT/NAP
Start	1	End	8376
GI	99755	Score	417
Exons	1..69, 7862..8376		
GI Descrip.	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi|16356|emb|CAA37917| (X53973) reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	334	Seq. ID	OJ990113_04.9819.C36
Gene No.	635	Strand	+
Start	1	End	8376
Name	OJ990113_04.9819.C36.o2.gs	Method	GENSCAN
Start	4644	End	8257
GI	none	Score	.44
Exons	4644..4799, 4805..4924, 6781..6862, 7198..7250, 7862..8002, 8042..8257		

Seq. No.	334	Seq. ID	OJ990113_04.9819.C36
Gene No.	635	Strand	+
Start	1	End	8376
Name	OJ990113_04.9819.C36.o1.tw	Method	TBLASTX:Wheat
Start	7888	End	8251
GI	none	Score	174
Exons	7888..8109, 7919..8122, 7973..8125, 8141..8251, 8152..8217		

Seq. No.	334	Seq. ID	OJ990113_04.9819.C36
Gene No.	635	Strand	+
Start	1	End	8376
Name	OJ990113_04.9819.C36.o1.tm	Method	TBLASTX:Maize
Start	7946	End	8367
GI	none	Score	413
Exons	7946..8257, 7947..8222, 7963..8223, 7973..8245, 8254..8367,		

8256..8363

Seq. No.	334	Seq. ID	OJ990113_04.9819.C36
Gene No.	635	Strand	+
Start	1	End	8376
Name	OJ990113_04.9819.C36.o1.ts	Method	TBLASTX:Soybean
Start	7967	End	8364
GI	none	Score	301
Exons	7967..8242, 7969..8220, 7976..8239, 8259..8360, 8260..8364		

Seq. No.	335	Seq. ID	OJ990113_04.9819.C37
Gene No.	636	Strand	+
Start	1026	End	3807
Name	OJ990113_04.9819.C37.o1.np	Method	AAT/NAP
Start	1026	End	3807
GI	2252851	Score	123
Exons	1026..1194, 1417..1605, 3754..3807		
GI Descrip.	(AF013294) No definition line found [Arabidopsis thaliana]		

Seq. No.	335	Seq. ID	OJ990113_04.9819.C37
Gene No.	637	Strand	-
Start	2393	End	3874
Name	OJ990113_04.9819.C37.o2.np	Method	AAT/NAP
Start	2393	End	3874
GI	4680339	Score	110
Exons	2393..2437, 2884..3136, 3827..3874		
GI Descrip.	(AF128457) hypothetical protein [Oryza sativa subsp. indica]		

Seq. No.	336	Seq. ID	OJ990113_04.9819.C38
Gene No.	638	Strand	-
Start	237	End	609
Name	OJ990113_04.9819.C38.o1.gs	Method	GENSCAN
Start	237	End	609
GI	none	Score	.9
Exons	237..609		

Seq. No.	337	Seq. ID	OJ990113_04.9819.C39
Gene No.	639	Strand	-
Start	737	End	1840
Name	OJ990113_04.9819.C39.o1.gs	Method	GENSCAN
Start	737	End	1840
GI	none	Score	.44
Exons	737..871, 1811..1840		

Seq. No.	338	Seq. ID	OJ990113_04.9819.C40
Gene No.	640	Strand	-
Start	805	End	938
Name	OJ990113_04.9819.C40.o1.gs	Method	GENSCAN
Start	805	End	938
GI	none	Score	.57
Exons	805..938		

Seq. No.	339	Seq. ID	OJ990113_04.9819.C41
Gene No.	641	Strand	-
Start	132	End	310
Name	OJ990113_04.9819.C41.o1.gs	Method	GENSCAN
Start	132	End	310

GI	none	Score	.69
Exons	132..310		

Seq. No.	340	Seq. ID	OJ990113_01.9819.C2
Gene No.	642	Strand	-
Start	21	End	723
Name	OJ990113_01.9819.C2.o1.gs	Method	GENSCAN
Start	21	End	455
GI	none	Score	.64
Exons	21..66, 165..199, 285..455		

Seq. No.	340	Seq. ID	OJ990113_01.9819.C2
Gene No.	642	Strand	-
Start	21	End	723
Name	OJ990113_01.9819.C2.o1.np	Method	AAT/NAP
Start	285	End	723
GI	6498436	Score	154
Exons	285..409, 509..723		
GI Descrip.	(AP000815) hypothetical protein [Oryza sativa]		

Seq. No.	341	Seq. ID	OJ990113_01.9819.C3
Gene No.	643	Strand	-
Start	86	End	335
Name	OJ990113_01.9819.C3.o1.gs	Method	GENSCAN
Start	86	End	335
GI	none	Score	.52
Exons	86..203, 312..335		

Seq. No.	342	Seq. ID	OJ990113_02.9819.C3
Gene No.	644	Strand	-
Start	211	End	1304
Name	OJ990113_02.9819.C3.o1.np	Method	AAT/NAP
Start	211	End	1304
GI	6907087	Score	109
Exons	211..312, 1276..1304		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	342	Seq. ID	OJ990113_02.9819.C3
Gene No.	644	Strand	-
Start	211	End	1304
Name	OJ990113_02.9819.C3.o1.gs	Method	GENSCAN
Start	231	End	1169
GI	none	Score	.82
Exons	231..312, 1095..1169		

Seq. No.	343	Seq. ID	OJ990113_02.9819.C6
Gene No.	645	Strand	-
Start	25	End	1735
Name	OJ990113_02.9819.C6.o1.gs	Method	GENSCAN
Start	25	End	1558
GI	none	Score	.59
Exons	25..218, 1159..1320, 1372..1558		

Seq. No.	343	Seq. ID	OJ990113_02.9819.C6
Gene No.	645	Strand	-

Start	25	End	1735
Name	OJ990113_02.9819.C6.o1.np	Method	AAT/NAP
Start	983	End	1312
GI	3192690	Score	301
Exons	983..1312		
GI Descrip.	(AF064539) gp7 [Bacteriophage N15]		

Seq. No.	343	Seq. ID	OJ990113_02.9819.C6
Gene No.	645	Strand	-
Start	25	End	1735
Name	OJ990113_02.9819.C6.o2.np	Method	AAT/NAP
Start	1325	End	1735
GI	3192689	Score	470
Exons	1325..1735		
GI Descrip.	(AF064539) gp6 [Bacteriophage N15]		

Seq. No.	344	Seq. ID	OJ990113_02.9819.C7
Gene No.	646	Strand	+
Start	122	End	1168
Name	OJ990113_02.9819.C7.o1.tc	Method	TBLASTX:Cress
Start	29	End	162
GI	none	Score	201
Exons	29..160, 29..160, 31..162, 34..162		

Seq. No.	344	Seq. ID	OJ990113_02.9819.C7
Gene No.	646	Strand	+
Start	122	End	1168
Name	OJ990113_02.9819.C7.o1.np	Method	AAT/NAP
Start	122	End	1168
GI	1196998	Score	1262
Exons	122..1168		
GI Descrip.	(J01829) unknown protein [Transposon Tn10] gi|5103202|dbj|BAA78838.1| (AP000342) transposase of Tn10 [Plasmid R100] gi|5706382|dbj|BAA83097.1| (AB026428) transposase [Methylomonas aminofaciens] gi|5738092|gb|AAD50250.1|AF162223_9 (AF162223) IS10-right transposase [Shigella flexneri] gi|6721110|gb|AAF26764.1|AC007396_13 (AC007396) T4O12.21 [Arabidopsis thaliana]		

Seq. No.	344	Seq. ID	OJ990113_02.9819.C7
Gene No.	646	Strand	+
Start	122	End	1168
Name	OJ990113_02.9819.C7.o1.gs	Method	GENSCAN
Start	122	End	1117
GI	none	Score	.42
Exons	122..473, 516..647, 995..1117		

Seq. No.	345	Seq. ID	OJ990113_02.9819.C10
Gene No.	647	Strand	+
Start	449	End	597
Name	OJ990113_02.9819.C10.o1.gp	Method	AAT/GAP
Start	449	End	597
GI	none	Score	222
Exons	449..597		

Seq. No.	346	Seq. ID	OJ990113_02.9819.C11
Gene No.	648	Strand	-

Start	1	End	810
Name	OJ990113_02.9819.C11.o1.np	Method	AAT/NAP
Start	1	End	810
GI	3192691	Score	1038
Exons	1..810		
GI Descrip.	(AF064539) gp8 [Bacteriophage N15]		

Seq. No.	346	Seq. ID	OJ990113_02.9819.C11
Gene No.	648	Strand	-
Start	1	End	810
Name	OJ990113_02.9819.C11.o1.gs	Method	GENSCAN
Start	88	End	810
GI	none	Score	.48
Exons	88..810		

Seq. No.	346	Seq. ID	OJ990113_02.9819.C11
Gene No.	649	Strand	-
Start	881	End	1197
Name	OJ990113_02.9819.C11.o2.np	Method	AAT/NAP
Start	881	End	1197
GI	3192690	Score	457
Exons	881..1197		
GI Descrip.	(AF064539) gp7 [Bacteriophage N15]		

Seq. No.	347	Seq. ID	OJ990113_02.9819.C12
Gene No.	650	Strand	-
Start	57	End	175
Name	OJ990113_02.9819.C12.o1.gp	Method	AAT/GAP
Start	57	End	175
GI	LIB3477-003-P1-K1-E9	Score	145
Exons	57..175		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		

Seq. No.	348	Seq. ID	OJ990113_02.9819.C13
Gene No.	651	Strand	+
Start	1	End	1205
Name	OJ990113_02.9819.C13.o1.np	Method	AAT/NAP
Start	1	End	1205
GI	2121177	Score	1656
Exons	1..1205		
GI Descrip.	hypothetical protein (transposon Tn1000) - Escherichia coli gi|43087|emb|CAA42758| (X60200) ORF [Escherichia coli] gi|303568|dbj|BAA03916| (D16449) ORF [Escherichia coli]		

Seq. No.	349	Seq. ID	OJ990423_06.9819.C2
Gene No.	652	Strand	+
Start	144	End	2346
Name	OJ990423_06.9819.C2.o1.np	Method	AAT/NAP
Start	144	End	891
GI	6742729	Score	1036
Exons	144..891		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	349	Seq. ID	OJ990423_06.9819.C2
Gene No.	652	Strand	+

Start	144	End	2346
Name	OJ990423_06.9819.C2.o2.gp	Method	AAT/GAP
Start	198	End	2346
GI	342_1.R1084	Score	3298
Exons	198..1495, 1531..1550, 1633..1730, 1840..2346		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	349	Seq. ID	OJ990423_06.9819.C2
Gene No.	652	Strand	+
Start	144	End	2346
Name	OJ990423_06.9819.C2.o1.gs	Method	GENSCAN
Start	392	End	1423
GI	none	Score	.53
Exons	392..1423		

Seq. No.	349	Seq. ID	OJ990423_06.9819.C2
Gene No.	653	Strand	-
Start	1069	End	1486
Name	OJ990423_06.9819.C2.o1.tm	Method	TBLASTX:Maize
Start	197	End	415
GI	none	Score	207
Exons	197..415, 199..387, 206..415		

Seq. No.	349	Seq. ID	OJ990423_06.9819.C2
Gene No.	653	Strand	-
Start	1069	End	1486
Name	OJ990423_06.9819.C2.o1.tw	Method	TBLASTX:Wheat
Start	197	End	1375
GI	none	Score	691
Exons	197..976, 197..547, 199..960, 971..1015, 971..1015, 1018..1113, 1022..1081, 1060..1200, 1061..1201, 1129..1209, 1214..1294, 1283..1375		

Seq. No.	349	Seq. ID	OJ990423_06.9819.C2
Gene No.	653	Strand	-
Start	1069	End	1486
Name	OJ990423_06.9819.C2.o1.tc	Method	TBLASTX:Cress
Start	342	End	793
GI	none	Score	175
Exons	342..524, 346..783, 346..789, 350..793, 644..793		

Seq. No.	349	Seq. ID	OJ990423_06.9819.C2
Gene No.	653	Strand	-
Start	1069	End	1486
Name	OJ990423_06.9819.C2.o1.gp	Method	AAT/GAP
Start	1069	End	1486
GI	LIB3431-028-P1-N1-A10	Score	828
Exons	1069..1486		
GI Descrip.	'4680203/gb|AAD27566.1|AF114171_7 3.0e-33 (AF114171) TNP2-like protein [Sorghum bicolor]'		

Seq. No.	350	Seq. ID	OJ990423_06.9819.C3
Gene No.	654	Strand	+
Start	49	End	127
Name	OJ990423_06.9819.C3.o1.gp	Method	AAT/GAP
Start	49	End	127

GI	LIB3477-003-P1-K1-E9	Score	116
Exons	49..127		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		

Seq. No.	350	Seq. ID	OJ990423_06.9819.C3
Gene No.	655	Strand	+
Start	1008	End	3806
Name	OJ990423_06.9819.C3.o1.np	Method	AAT/NAP
Start	1008	End	3806
GI	4680204	Score	970
Exons	1008..2444, 2519..3806		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	350	Seq. ID	OJ990423_06.9819.C3
Gene No.	655	Strand	+
Start	1008	End	3806
Name	OJ990423_06.9819.C3.o1.tw	Method	TBLASTX:Wheat
Start	1651	End	2054
GI	none	Score	62
Exons	1651..1791, 1651..1761, 1653..1889, 1653..1802, 1754..1921, 1884..2054, 1959..2054		

Seq. No.	351	Seq. ID	OJ990423_06.9819.C4
Gene No.	656	Strand	+
Start	126	End	735
Name	OJ990423_06.9819.C4.o1.gs	Method	GENSCAN
Start	126	End	735
GI	none	Score	.57
Exons	126..735		

Seq. No.	351	Seq. ID	OJ990423_06.9819.C4
Gene No.	656	Strand	+
Start	126	End	735
Name	OJ990423_06.9819.C4.o1.tm	Method	TBLASTX:Maize
Start	156	End	695
GI	none	Score	84
Exons	156..269, 261..365, 384..428, 471..695		

Seq. No.	352	Seq. ID	OJ990423_06.9819.C5
Gene No.	657	Strand	+
Start	1	End	653
Name	OJ990423_06.9819.C5.o1.np	Method	AAT/NAP
Start	1	End	653
GI	2281115	Score	234
Exons	1..171, 257..337, 416..653		
GI Descrip.	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]		

Seq. No.	352	Seq. ID	OJ990423_06.9819.C5
Gene No.	657	Strand	+
Start	1	End	653
Name	OJ990423_06.9819.C5.o1.tm	Method	TBLASTX:Maize
Start	72	End	478
GI	none	Score	89
Exons	72..173, 74..172, 79..174, 79..174, 215..322, 235..333, 254..334, 415..477, 416..478		

Seq. No.	352	Seq. ID	OJ990423_06.9819.C5
Gene No.	657	Strand	+
Start	1	End	653
Name	OJ990423_06.9819.C5.o1.ts	Method	TBLASTX:Soybean
Start	72	End	478
GI	none	Score	60
Exons	72..173, 72..173, 76..174, 77..193, 79..174, 235..336, 252..335, 254..337, 415..477, 416..478		

Seq. No.	352	Seq. ID	OJ990423_06.9819.C5
Gene No.	657	Strand	+
Start	1	End	653
Name	OJ990423_06.9819.C5.o1.tc	Method	TBLASTX:Cress
Start	79	End	475
GI	none	Score	139
Exons	79..174, 80..178, 81..173, 235..336, 254..337, 415..471, 416..475		

Seq. No.	352	Seq. ID	OJ990423_06.9819.C5
Gene No.	657	Strand	+
Start	1	End	653
Name	OJ990423_06.9819.C5.o1.gs	Method	GENSCAN
Start	149	End	478
GI	none	Score	.55
Exons	149..337, 416..478		

Seq. No.	353	Seq. ID	OJ990423_06.9819.C6
Gene No.	658	Strand	-
Start	638	End	1169
Name	OJ990423_06.9819.C6.o1.gs	Method	GENSCAN
Start	638	End	1103
GI	none	Score	.99
Exons	638..1103		

Seq. No.	353	Seq. ID	OJ990423_06.9819.C6
Gene No.	658	Strand	-
Start	638	End	1169
Name	OJ990423_06.9819.C6.o1.np	Method	AAT/NAP
Start	923	End	1169
GI	3249106	Score	131
Exons	923..1169		
GI Descrip.	(AC003114) T12M4.16 [Arabidopsis thaliana]		

Seq. No.	354	Seq. ID	OJ990423_06.9819.C8
Gene No.	659	Strand	+
Start	563	End	743
Name	OJ990423_06.9819.C8.o1.gs	Method	GENSCAN
Start	563	End	743
GI	none	Score	.9
Exons	563..743		

Seq. No.	355	Seq. ID	OJ990423_06.9819.C9
Gene No.	660	Strand	+
Start	113	End	1549
Name	OJ990423_06.9819.C9.o1.gs	Method	GENSCAN
Start	113	End	1549

GI	none	Score	.98
Exons	113..444, 554..727, 824..934, 1019..1091, 1186..1284, 1364..1549		

Seq. No.	355	Seq. ID	OJ990423_06.9819.C9
Gene No.	661	Strand	-
Start	1883	End	2027
Name	OJ990423_06.9819.C9.o1.gp	Method	AAT/GAP
Start	1883	End	2027
GI	21474_1.R1084	Score	236
Exons	1883..2027		
GI Descrip.	'3894159 2.0e-10 (AC005312) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	355	Seq. ID	OJ990423_06.9819.C9
Gene No.	662	Strand	-
Start	9256	End	10659
Name	OJ990423_06.9819.C9.o3.np	Method	AAT/NAP
Start	9256	End	10659
GI	6721512	Score	44
Exons	9256..9282, 10538..10659		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	355	Seq. ID	OJ990423_06.9819.C9
Gene No.	663	Strand	-
Start	12324	End	14636
Name	OJ990423_06.9819.C9.o1.tw	Method	TBLASTX:Wheat
Start	371	End	893
GI	none	Score	60
Exons	371..451, 540..722, 590..715, 822..893		

Seq. No.	355	Seq. ID	OJ990423_06.9819.C9
Gene No.	663	Strand	-
Start	12324	End	14636
Name	OJ990423_06.9819.C9.o1.tc	Method	TBLASTX:Cress
Start	2172	End	2396
GI	none	Score	108
Exons	2172..2396, 2173..2370		

Seq. No.	355	Seq. ID	OJ990423_06.9819.C9
Gene No.	663	Strand	-
Start	12324	End	14636
Name	OJ990423_06.9819.C9.o1.tm	Method	TBLASTX:Maize
Start	2175	End	2396
GI	none	Score	99
Exons	2175..2396, 2176..2370		

Seq. No.	355	Seq. ID	OJ990423_06.9819.C9
Gene No.	663	Strand	-
Start	12324	End	14636
Name	OJ990423_06.9819.C9.o4.np	Method	AAT/NAP
Start	12324	End	14636
GI	5042454	Score	187
Exons	12324..12384, 12730..12906, 14527..14636		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	664	Strand	+

Start	4098	End	10145
Name	OJ990423_06.9819.C10.o1.np	Method	AAT/NAP
Start	4076	End	10145
GI	6437558	Score	3558
Exons	4076..4295, 4780..4890, 5031..5134, 5656..5768, 5888..5985, 6082..6261, 6348..6569, 6701..6835, 6927..7209, 7293..7366, 7572..7792, 7878..7965, 8049..8148, 8226..8414, 8482..8513, 8590..8669, 8743..8832, 8936..9014, 9183..9225, 9318..9376, 9470..9635, 9785..10145		
GI Descrip.	(AC011623) putative ATPase (ISW2-like) [Arabidopsis thaliana]		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	664	Strand	+
Start	4098	End	10145
Name	OJ990423_06.9819.C10.o3.gs	Method	GENSCAN
Start	4098	End	9963
GI	none	Score	.89
Exons	4098..4433, 4768..4890, 5031..5134, 5656..5768, 5888..5985, 6082..6261, 6348..6569, 6701..6835, 6927..7209, 7293..7366, 7572..7792, 7878..7965, 8049..8142, 8226..8414, 8482..8513, 8548..8669, 8743..8832, 8936..9005, 9183..9225, 9318..9376, 9470..9635, 9785..9963		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	664	Strand	+
Start	4098	End	10145
Name	OJ990423_06.9819.C10.o1.gp	Method	AAT/GAP
Start	8346	End	8775
GI	LIB3434-057-P1-K1-B10	Score	330
Exons	8346..8414, 8482..8513, 8593..8669, 8743..8775		
GI Descrip.	'6041757/gb|AC011806.1|AC011806 1.0e-19 Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence'		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	665	Strand	-
Start	393	End	1815
Name	OJ990423_06.9819.C10.o1.gs	Method	GENSCAN
Start	393	End	1815
GI	none	Score	.67
Exons	393..947, 961..1815		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	665	Strand	-
Start	393	End	1815
Name	OJ990423_06.9819.C10.o2.tm	Method	TBLASTX:Maize
Start	522	End	1371
GI	none	Score	188
Exons	522..662, 610..939, 687..950, 952..1053, 983..1078, 1099..1368, 1175..1285, 1177..1371		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	665	Strand	-
Start	393	End	1815
Name	OJ990423_06.9819.C10.o5.tc	Method	TBLASTX:Cress
Start	522	End	894
GI	none	Score	85

Exons	522..641, 684..893, 691..825, 847..894		
Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	665	Strand	-
Start	393	End	1815
Name	OJ990423_06.9819.C10.o4.ts	Method	TBLASTX:Soybean
Start	540	End	999
GI	none	Score	75
Exons	540..638, 681..947, 685..825, 859..954, 952..999		
Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	665	Strand	-
Start	393	End	1815
Name	OJ990423_06.9819.C10.o8.tc	Method	TBLASTX:Cress
Start	985	End	1287
GI	none	Score	183
Exons	985..1146, 1096..1287		
Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	665	Strand	-
Start	393	End	1815
Name	OJ990423_06.9819.C10.o2.ts	Method	TBLASTX:Soybean
Start	1003	End	1785
GI	none	Score	67
Exons	1003..1074, 1099..1356, 1229..1300, 1417..1524, 1418..1525, 1528..1617, 1529..1663, 1627..1707, 1666..1785		
Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	665	Strand	-
Start	393	End	1815
Name	OJ990423_06.9819.C10.o3.tm	Method	TBLASTX:Maize
Start	1390	End	1785
GI	none	Score	308
Exons	1390..1782, 1391..1693, 1396..1785		
Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	666	Strand	
Start	4771	End	9005
Name	OJ990423_06.9819.C10.o1.tm	Method	TBLASTX:Maize
Start	4771	End	8823
GI	none	Score	45
Exons	4771..4809, 4790..4888, 5030..5134, 5031..5135, 5031..5135, 5032..5136, 5653..5769, 5654..5770, 5655..5774, 5889..5984, 5890..5985, 5893..5985, 6081..6257, 6081..6257, 6082..6261, 6082..6261, 6083..6268, 6345..6578, 6347..6508, 6348..6578, 6349..6594, 6554..6598, 6695..6838, 6699..6836, 6924..7211, 6926..7210, 7288..7371, 7290..7370, 7291..7377, 7564..7731, 7568..7795, 7569..7793, 7876..7962, 7877..7960, 7879..7965, 8028..8144, 8046..8147, 8048..8158, 8223..8411, 8225..8413, 8228..8416, 8476..8514, 8484..8513, 8569..8640, 8578..8673, 8591..8671, 8741..8821, 8743..8823, 8745..8822, 8749..8823		
Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	666	Strand	
Start	4771	End	9005
Name	OJ990423_06.9819.C10.o1.ts	Method	TBLASTX:Soybean
Start	5030	End	9005

GI	none	Score	67
Exons	5030..5110, 5030..5101, 5031..5123, 5654..5680, 5732..5770, 5889..5984, 5890..5985, 6082..6261, 6117..6260, 6345..6593, 6353..6508, 6382..6597, 6384..6599, 6695..6838, 6695..6799, 6699..6851, 6924..7211, 6924..7211, 6926..7213, 7276..7377, 7296..7373, 7564..7725, 7564..7725, 7568..7795, 7569..7793, 7867..7962, 7874..7957, 7878..7964, 7879..7965, 8038..8142, 8046..8147, 8046..8147, 8048..8167, 8227..8337, 8228..8416, 8231..8416, 8232..8417, 8476..8514, 8484..8513, 8569..8640, 8741..8809, 8780..8833, 8782..8841, 8926..8991, 8937..9005, 8938..8991		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	666	Strand	
Start	4771	End	9005
Name	OJ990423_06.9819.C10.o7.tc	Method	TBLASTX:Cress
Start	6429	End	6851
GI	none	Score	132
Exons	6429..6563, 6719..6838, 6719..6796, 6724..6801, 6771..6851		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	666	Strand	
Start	4771	End	9005
Name	OJ990423_06.9819.C10.o2.tc	Method	TBLASTX:Cress
Start	6959	End	7213
GI	none	Score	428
Exons	6959..7213, 6960..7211		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	666	Strand	
Start	4771	End	9005
Name	OJ990423_06.9819.C10.o1.tc	Method	TBLASTX:Cress
Start	7276	End	8280
GI	none	Score	370
Exons	7276..7377, 7569..7793, 7571..7795, 7866..7964, 7878..7961, 7879..7965, 8028..8147, 8054..8167, 8055..8147, 8223..8276, 8226..8276, 8227..8280, 8228..8278		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	666	Strand	
Start	4771	End	9005
Name	OJ990423_06.9819.C10.o3.tc	Method	TBLASTX:Cress
Start	8481	End	9005
GI	none	Score	39
Exons	8481..8510, 8590..8637, 8590..8643, 8719..8841, 8732..8842, 8741..8842, 8937..9005, 8943..9005		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	667	Strand	
Start	8926	End	9987
Name	OJ990423_06.9819.C10.o4.tm	Method	TBLASTX:Maize
Start	8926	End	9987
GI	none	Score	89
Exons	8926..9003, 8935..9009, 8937..9005, 8937..9023, 9171..9224, 9182..9226, 9312..9335, 9469..9633, 9469..9633, 9470..9634, 9784..9975, 9784..9987		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	667	Strand	
Start	8926	End	9987
Name	OJ990423_06.9819.C10.o3.ts	Method	TBLASTX:Soybean
Start	9467	End	9975
GI	none	Score	251
Exons	9467..9628, 9469..9630, 9470..9634, 9525..9635, 9784..9975, 9831..9968		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	667	Strand	
Start	8926	End	9987
Name	OJ990423_06.9819.C10.o6.tc	Method	TBLASTX:Cress
Start	9468	End	9619
GI	none	Score	118
Exons	9468..9614, 9469..9609, 9470..9619		

Seq. No.	356	Seq. ID	OJ990423_06.9819.C10
Gene No.	667	Strand	
Start	8926	End	9987
Name	OJ990423_06.9819.C10.o4.tc	Method	TBLASTX:Cress
Start	9816	End	9975
GI	none	Score	91
Exons	9816..9968, 9817..9975, 9837..9974		

Seq. No.	357	Seq. ID	OJ990423_06.9819.C11
Gene No.	668	Strand	-
Start	1	End	999
Name	OJ990423_06.9819.C11.o1.np	Method	AAT/NAP
Start	1	End	999
GI	6437558	Score	862
Exons	1..90, 183..317, 449..670, 757..999		
GI Descrip.	(AC011623) putative ATPase (ISW2-like) [Arabidopsis thaliana]		

Seq. No.	357	Seq. ID	OJ990423_06.9819.C11
Gene No.	668	Strand	-
Start	1	End	999
Name	OJ990423_06.9819.C11.o1.tc	Method	TBLASTX:Cress
Start	1	End	589
GI	none	Score	91
Exons	1..99, 2..91, 180..299, 180..299, 447..566, 455..589, 467..586		

Seq. No.	357	Seq. ID	OJ990423_06.9819.C11
Gene No.	668	Strand	-
Start	1	End	999
Name	OJ990423_06.9819.C11.o1.tm	Method	TBLASTX:Maize
Start	1	End	937
GI	none	Score	102
Exons	1..99, 2..91, 180..329, 180..323, 420..464, 424..669, 440..670, 440..673, 510..671, 750..935, 757..936, 757..936, 761..937, 761..937		

Seq. No.	357	Seq. ID	OJ990423_06.9819.C11
Gene No.	668	Strand	-
Start	1	End	999
Name	OJ990423_06.9819.C11.o1.ts	Method	TBLASTX:Soybean
Start	1	End	936

GI	none	Score	100
Exons	1..99, 2..91, 180..323, 192..323, 419..634, 421..636, 425..673, 510..665, 757..936, 758..901		

Seq. No.	357	Seq. ID	OJ990423_06.9819.C11
Gene No.	668	Strand	-
Start	1	End	999
Name	OJ990423_06.9819.C11.o1.gs	Method	GENSCAN
Start	183	End	861
GI	none	Score	.9
Exons	183..317, 449..670, 757..861		

Seq. No.	358	Seq. ID	OJ990423_06.9819.C13
Gene No.	669	Strand	+
Start	403	End	809
Name	OJ990423_06.9819.C13.o1.np	Method	AAT/NAP
Start	403	End	809
GI	5305335	Score	95
Exons	403..809		
GI Descrip.	(AF071081) proline-rich mucin homolog [Mycobacterium tuberculosis]		

Seq. No.	359	Seq. ID	OJ990423_06.9819.C14
Gene No.	670	Strand	-
Start	1	End	1245
Name	OJ990423_06.9819.C14.o1.np	Method	AAT/NAP
Start	1	End	1245
GI	6056404	Score	261
Exons	1..55, 166..241, 321..401, 503..592, 707..784, 859..1062, 1162..1245		
GI Descrip.	(AC009525) Similar to cullin proteins [Arabidopsis thaliana]		

Seq. No.	359	Seq. ID	OJ990423_06.9819.C14
Gene No.	670	Strand	-
Start	1	End	1245
Name	OJ990423_06.9819.C14.o1.ts	Method	TBLASTX:Soybean
Start	209	End	1062
GI	none	Score	48
Exons	209..244, 210..266, 321..398, 325..420, 500..610, 708..785, 712..786, 713..784, 851..1018, 859..1047, 859..1062		

Seq. No.	359	Seq. ID	OJ990423_06.9819.C14
Gene No.	670	Strand	-
Start	1	End	1245
Name	OJ990423_06.9819.C14.o1.tm	Method	TBLASTX:Maize
Start	339	End	1062
GI	none	Score	67
Exons	339..398, 343..420, 499..564, 500..610, 708..785, 713..784, 851..1018, 859..1023, 859..1062		

Seq. No.	359	Seq. ID	OJ990423_06.9819.C14
Gene No.	670	Strand	-
Start	1	End	1245
Name	OJ990423_06.9819.C14.o1.gs	Method	GENSCAN
Start	488	End	1146
GI	none	Score	.88
Exons	488..592, 859..1062, 1144..1146		

Seq. No.	359	Seq. ID	OJ990423_06.9819.C14
Gene No.	670	Strand	-
Start	1	End	1245
Name	OJ990423_06.9819.C14.o1.tc	Method	TBLASTX:Cress
Start	708	End	1062
GI	none	Score	65
Exons	708..788, 713..784, 859..1062, 865..1005		

Seq. No.	360	Seq. ID	OJ990423_06.9819.C16
Gene No.	671	Strand	-
Start	1	End	726
Name	OJ990423_06.9819.C16.o1.np	Method	AAT/NAP
Start	1	End	726
GI	6742169	Score	309
Exons	1..235, 378..430, 514..726		
GI Descrip.	(AF207621) potassium transporter KUP3p [Arabidopsis thaliana]		

Seq. No.	360	Seq. ID	OJ990423_06.9819.C16
Gene No.	671	Strand	-
Start	1	End	726
Name	OJ990423_06.9819.C16.o1.gs	Method	GENSCAN
Start	118	End	235
GI	none	Score	.99
Exons	118..235		

Seq. No.	360	Seq. ID	OJ990423_06.9819.C16
Gene No.	671	Strand	-
Start	1	End	726
Name	OJ990423_06.9819.C16.o1.tm	Method	TBLASTX:Maize
Start	161	End	697
GI	none	Score	69
Exons	161..238, 168..257, 375..431, 437..697, 498..692		

Seq. No.	360	Seq. ID	OJ990423_06.9819.C16
Gene No.	671	Strand	-
Start	1	End	726
Name	OJ990423_06.9819.C16.o1.tc	Method	TBLASTX:Cress
Start	164	End	698
GI	none	Score	60
Exons	164..238, 165..236, 360..431, 437..697, 498..698		

Seq. No.	360	Seq. ID	OJ990423_06.9819.C16
Gene No.	671	Strand	-
Start	1	End	726
Name	OJ990423_06.9819.C16.o1.ts	Method	TBLASTX:Soybean
Start	488	End	701
GI	none	Score	49
Exons	488..700, 501..563, 588..701		

Seq. No.	361	Seq. ID	OJ990423_06.9819.C18
Gene No.	672	Strand	-
Start	302	End	377
Name	OJ990423_06.9819.C18.o1.gs	Method	GENSCAN
Start	302	End	377
GI	none	Score	.95
Exons	302..377		

Seq. No.	362	Seq. ID	OJ990423_06.9819.C19
Gene No.	673	Strand	+
Start	139	End	272
Name	OJ990423_06.9819.C19.o1.gs	Method	GENSCAN
Start	139	End	272
GI	none	Score	.47
Exons	139..272		

Seq. No.	363	Seq. ID	OJ990423_06.9819.C21
Gene No.	674	Strand	+
Start	925	End	1616
Name	OJ990423_06.9819.C21.o1.gs	Method	GENSCAN
Start	925	End	1616
GI	none	Score	.49
Exons	925..994, 1474..1616		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o1.gp	Method	AAT/GAP
Start	1	End	1236
GI	342_1.R1084	Score	2159
Exons	1..1236		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o1.np	Method	AAT/NAP
Start	1	End	1236
GI	6742729	Score	1897
Exons	1..1236		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o1.gs	Method	GENSCAN
Start	48	End	1172
GI	none	Score	.56
Exons	48..1172		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o2.tw	Method	TBLASTX:Wheat
Start	64	End	522
GI	none	Score	111
Exons	64..198, 75..203, 75..197, 76..201, 125..202, 231..458, 231..458, 271..459, 459..521, 472..522		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o1.ts	Method	TBLASTX:Soybean

Start	555	End	797
GI	none	Score	67
Exons	555..797, 613..711		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o1.tm	Method	TBLASTX:Maize
Start	627	End	1085
GI	none	Score	103
Exons	627..821, 831..1085, 831..1073		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o1.tw	Method	TBLASTX:Wheat
Start	661	End	1130
GI	none	Score	173
Exons	661..867, 661..870, 666..890, 870..968, 871..963, 972..1076, 976..1065, 1077..1130, 1078..1122		

Seq. No.	364	Seq. ID	OJ990423_06.9819.C23
Gene No.	675	Strand	-
Start	1	End	1236
Name	OJ990423_06.9819.C23.o1.tc	Method	TBLASTX:Cress
Start	918	End	1205
GI	none	Score	88
Exons	918..1205, 937..1074, 1114..1167		

Seq. No.	365	Seq. ID	OJ990423_06.9819.C26
Gene No.	676	Strand	-
Start	1	End	958
Name	OJ990423_06.9819.C26.o1.np	Method	AAT/NAP
Start	1	End	958
GI	6437558	Score	878
Exons	1..240, 332..466, 598..819, 922..958		
GI Descrip.	(AC011623) putative ATPase (ISW2-like) [Arabidopsis thaliana]		

Seq. No.	365	Seq. ID	OJ990423_06.9819.C26
Gene No.	676	Strand	-
Start	1	End	958
Name	OJ990423_06.9819.C26.o1.ts	Method	TBLASTX:Soybean
Start	1	End	822
GI	none	Score	295
Exons	1..243, 2..241, 4..243, 11..259, 316..468, 329..472, 368..472, 568..783, 570..785, 574..822, 659..814		

Seq. No.	365	Seq. ID	OJ990423_06.9819.C26
Gene No.	676	Strand	-
Start	1	End	958
Name	OJ990423_06.9819.C26.o1.tc	Method	TBLASTX:Cress
Start	1	End	738
GI	none	Score	121
Exons	1..180, 2..124, 124..243, 128..241, 128..262, 198..242, 316..396, 329..448, 366..443, 371..448, 596..715, 604..738, 616..735		

Seq. No.	365	Seq. ID	OJ990423_06.9819.C26
Gene No.	676	Strand	-
Start	1	End	958
Name	OJ990423_06.9819.C26.o1.tm	Method	TBLASTX:Maize
Start	1	End	822
GI	none	Score	374
Exons	1..243, 2..241, 4..258, 329..472, 331..468, 573..818, 589..819, 589..822, 659..820		

Seq. No.	365	Seq. ID	OJ990423_06.9819.C26
Gene No.	676	Strand	-
Start	1	End	958
Name	OJ990423_06.9819.C26.o1.gs	Method	GENSCAN
Start	84	End	819
GI	none	Score	.52
Exons	84..267, 332..466, 598..819		

Seq. No.	366	Seq. ID	OJ990423_06.9819.C27
Gene No.	677	Strand	-
Start	831	End	997
Name	OJ990423_06.9819.C27.o1.gs	Method	GENSCAN
Start	831	End	997
GI	none	Score	.75
Exons	831..997		

Seq. No.	367	Seq. ID	OJ990423_06.9819.C28
Gene No.	678	Strand	-
Start	232	End	327
Name	OJ990423_06.9819.C28.o1.gs	Method	GENSCAN
Start	232	End	327
GI	none	Score	.89
Exons	232..327		

Seq. No.	368	Seq. ID	OJ990423_06.9819.C30
Gene No.	679	Strand	-
Start	1	End	771
Name	OJ990423_06.9819.C30.o1.gp	Method	AAT/GAP
Start	1	End	332
GI	11553_1.R1084	Score	480
Exons	1..21, 84..332		
GI Descrip.	'6041757/gb|AC011806.1|AC011806 0.0e+00 Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence, complete sequence'		

Seq. No.	368	Seq. ID	OJ990423_06.9819.C30
Gene No.	679	Strand	-
Start	1	End	771
Name	OJ990423_06.9819.C30.o1.np	Method	AAT/NAP
Start	1	End	771
GI	2281115	Score	644
Exons	1..368, 464..519, 595..771		
GI Descrip.	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]		

Seq. No.	368	Seq. ID	OJ990423_06.9819.C30
Gene No.	679	Strand	-
Start	1	End	771
Name	OJ990423_06.9819.C30.o1.tc	Method	TBLASTX:Cress

Start	83	End	662
GI	none	Score	258
Exons	83..412, 87..308, 215..343, 461..523, 463..522, 574..660, 594..662		

Seq. No.	368	Seq. ID	OJ990423_06.9819.C30
Gene No.	679	Strand	-
Start	1	End	771
Name	OJ990423_06.9819.C30.o1.tm	Method	TBLASTX:Maize
Start	83	End	753
GI	none	Score	321
Exons	83..370, 84..308, 86..391, 461..523, 463..522, 574..753, 593..742, 595..747		

Seq. No.	368	Seq. ID	OJ990423_06.9819.C30
Gene No.	679	Strand	-
Start	1	End	771
Name	OJ990423_06.9819.C30.o1.ts	Method	TBLASTX:Soybean
Start	83	End	760
GI	none	Score	229
Exons	83..370, 87..308, 199..375, 280..375, 461..523, 463..522, 574..753, 575..760, 593..739, 595..747		

Seq. No.	368	Seq. ID	OJ990423_06.9819.C30
Gene No.	679	Strand	-
Start	1	End	771
Name	OJ990423_06.9819.C30.o1.tw	Method	TBLASTX:Wheat
Start	83	End	278
GI	none	Score	224
Exons	83..277, 84..278		

Seq. No.	368	Seq. ID	OJ990423_06.9819.C30
Gene No.	679	Strand	-
Start	1	End	771
Name	OJ990423_06.9819.C30.o1.gs	Method	GENSCAN
Start	86	End	768
GI	none	Score	.97
Exons	86..368, 464..519, 595..768		

Seq. No.	369	Seq. ID	OJ990423_06.9819.C32
Gene No.	680	Strand	-
Start	1	End	599
Name	OJ990423_06.9819.C32.o1.np	Method	AAT/NAP
Start	1	End	587
GI	2281115	Score	173
Exons	1..328, 457..587		
GI Descrip.	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]		

Seq. No.	369	Seq. ID	OJ990423_06.9819.C32
Gene No.	680	Strand	-
Start	1	End	599
Name	OJ990423_06.9819.C32.o1.gs	Method	GENSCAN
Start	229	End	599
GI	none	Score	.88
Exons	229..328, 457..599		

Seq. No.	370	Seq. ID	OJ990423_06.9819.C33

Gene No.	681	Strand	+
Start	1	End	1155
Name	OJ990423_06.9819.C33.o1.np	Method	AAT/NAP
Start	1	End	552
GI	5852084	Score	88
Exons	1..98, 469..552		
GI Descrip.	(AL117264) zwh0007.1 [Oryza sativa]		

Seq. No.	370	Seq. ID	OJ990423_06.9819.C33
Gene No.	681	Strand	+
Start	1	End	1155
Name	OJ990423_06.9819.C33.o1.gs	Method	GENSCAN
Start	214	End	1136
GI	none	Score	.71
Exons	214..276, 883..1136		

Seq. No.	370	Seq. ID	OJ990423_06.9819.C33
Gene No.	681	Strand	+
Start	1	End	1155
Name	OJ990423_06.9819.C33.o2.np	Method	AAT/NAP
Start	853	End	1155
GI	2654088	Score	230
Exons	853..1155		
GI Descrip.	(AF033118) potassium transporter [Arabidopsis thaliana] gi|2688979 (AF029876) high-affinity potassium transporter; AtKUP1p [Arabidopsis thaliana] gi|3150413|gb|AAC16965.1| (AC004165) high affinity K+ transporter (AtKUP1/AtKT1p) [Arabidopsis thaliana]		

Seq. No.	370	Seq. ID	OJ990423_06.9819.C33
Gene No.	681	Strand	+
Start	1	End	1155
Name	OJ990423_06.9819.C33.o1.tm	Method	TBLASTX:Maize
Start	892	End	1140
GI	none	Score	131
Exons	892..993, 912..992, 1063..1095, 1075..1140, 1089..1139		

Seq. No.	370	Seq. ID	OJ990423_06.9819.C33
Gene No.	681	Strand	+
Start	1	End	1155
Name	OJ990423_06.9819.C33.o1.tc	Method	TBLASTX:Cress
Start	901	End	1155
GI	none	Score	130
Exons	901..993, 903..992, 1072..1101, 1075..1155, 1089..1142		

Seq. No.	370	Seq. ID	OJ990423_06.9819.C33
Gene No.	681	Strand	+
Start	1	End	1155
Name	OJ990423_06.9819.C33.o1.ts	Method	TBLASTX:Soybean
Start	901	End	1155
GI	none	Score	123
Exons	901..993, 915..989, 1075..1155, 1089..1142		

Seq. No.	371	Seq. ID	OJ990423_06.9819.C34
Gene No.	682	Strand	-
Start	1	End	1959
Name	OJ990423_06.9819.C34.o1.np	Method	AAT/NAP

Start	1	End	1959
GI	4680203	Score	1081
Exons	1..1051, 1804..1959		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	371	Seq. ID	OJ990423_06.9819.C34
Gene No.	682	Strand	-
Start	1	End	1959
Name	OJ990423_06.9819.C34.o1.tw	Method	TBLASTX:Wheat
Start	99	End	649
GI	none	Score	45
Exons	99..143, 141..260, 202..264, 285..356, 286..333, 342..542, 346..477, 530..649		

Seq. No.	371	Seq. ID	OJ990423_06.9819.C34
Gene No.	682	Strand	-
Start	1	End	1959
Name	OJ990423_06.9819.C34.o1.ts	Method	TBLASTX:Soybean
Start	288	End	558
GI	none	Score	105
Exons	288..353, 360..554, 364..558		

Seq. No.	371	Seq. ID	OJ990423_06.9819.C34
Gene No.	682	Strand	-
Start	1	End	1959
Name	OJ990423_06.9819.C34.o1.gp	Method	AAT/GAP
Start	913	End	1501
GI	2310235	Score	292
Exons	913..1051, 1464..1501		
GI Descrip.	5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]		

Seq. No.	372	Seq. ID	OJ990423_06.9819.C35
Gene No.	683	Strand	+
Start	94	End	446
Name	OJ990423_06.9819.C35.o1.gs	Method	GENSCAN
Start	94	End	446
GI	none	Score	.81
Exons	94..252, 419..446		

Seq. No.	372	Seq. ID	OJ990423_06.9819.C35
Gene No.	684	Strand	+
Start	880	End	1169
Name	OJ990423_06.9819.C35.o2.gs	Method	GENSCAN
Start	880	End	1169
GI	none	Score	.86
Exons	880..1032, 1041..1169		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36
Gene No.	685	Strand	+
Start	4439	End	5705
Name	OJ990423_06.9819.C36.o2.gs	Method	GENSCAN
Start	4439	End	5705
GI	none	Score	.65
Exons	4439..5048, 5542..5705		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36

Gene No.	686	Strand	+
Start	10473	End	10781
Name	OJ990423_06.9819.C36.o2.np	Method	AAT/NAP
Start	10473	End	10781
GI	2244926	Score	315
Exons	10473..10781		
GI Descrip.	(Z97339) glutaredoxin homolog [Arabidopsis thaliana]		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36
Gene No.	687	Strand	-
Start	6726	End	12604
Name	OJ990423_06.9819.C36.o2.tm	Method	TBLASTX:Maize
Start	4469	End	5008
GI	none	Score	84
Exons	4469..4582, 4574..4678, 4697..4741, 4784..5008		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36
Gene No.	687	Strand	-
Start	6726	End	12604
Name	OJ990423_06.9819.C36.o3.gs	Method	GENSCAN
Start	6726	End	12604
GI	none	Score	.59
Exons	6726..6873, 6935..6995, 7227..7317, 7346..7405, 8502..8644, 8691..8882, 10098..10259, 10550..10897, 11993..12144, 12600..12604		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36
Gene No.	687	Strand	-
Start	6726	End	12604
Name	OJ990423_06.9819.C36.o1.gp	Method	AAT/GAP
Start	10310	End	10943
GI	1631_1.R1084	Score	1229
Exons	10310..10943		
GI Descrip.	'2244926/emb|CAB10348.1| 5.0e-29 (Z97339) glutaredoxin homolog [Arabidopsis thaliana]'		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36
Gene No.	687	Strand	-
Start	6726	End	12604
Name	OJ990423_06.9819.C36.o1.tc	Method	TBLASTX:Cress
Start	10464	End	10784
GI	none	Score	179
Exons	10464..10649, 10650..10784, 10652..10780		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36
Gene No.	687	Strand	-
Start	6726	End	12604
Name	OJ990423_06.9819.C36.o1.tm	Method	TBLASTX:Maize
Start	10472	End	10790
GI	none	Score	225
Exons	10472..10555, 10473..10655, 10638..10790, 10643..10783		

Seq. No.	373	Seq. ID	OJ990423_06.9819.C36
Gene No.	687	Strand	-
Start	6726	End	12604
Name	OJ990423_06.9819.C36.o1.ts	Method	TBLASTX:Soybean
Start	10473	End	10784

GI	none	Score	187
Exons	10473..10619, 10487..10567, 10620..10784, 10646..10780		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	688	Strand	+
Start	1	End	2895
Name	OJ990423_06.9819.C37.o1.np	Method	AAT/NAP
Start	1	End	2895
GI	133435	Score	205
Exons	1..198, 2872..2895		
GI Descrip.	DNA-DIRECTED RNA POLYMERASE BETA' CHAIN gi|66983|pir||RNRZC1 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-1 chain - rice chloroplast gi|11972|emb|CAA33987| (X15901) RNA polymerase beta' subunit-1 [Oryza sativa] gi|226690|prf||1603356Q RNA polymerase beta'-1 [Oryza sativa]		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	689	Strand	+
Start	13433	End	24494
Name	OJ990423_06.9819.C37.o3.gs	Method	GENSCAN
Start	13433	End	24494
GI	none	Score	.7
Exons	13433..13715, 14569..14740, 17089..17289, 18656..18841, 18970..19069, 20098..20283, 20402..20449, 20531..20734, 21001..21090, 21192..21272, 21352..21414, 22628..22777, 22856..22911, 23018..23300, 23514..23657, 23758..23976, 24053..24220, 24393..24494		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	689	Strand	+
Start	13433	End	24494
Name	OJ990423_06.9819.C37.o4.np	Method	AAT/NAP
Start	18711	End	24491
GI	2281115	Score	1871
Exons	18711..18841, 18970..19069, 20098..20283, 20531..20596, 20809..20886, 21001..21090, 21192..21272, 21352..21414, 22413..22525, 22628..22777, 22856..22911, 23018..23300, 23514..23657, 23758..23976, 24053..24220, 24393..24491		
GI Descrip.	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	690	Strand	-
Start	465	End	2385
Name	OJ990423_06.9819.C37.o1.gs	Method	GENSCAN
Start	465	End	2385
GI	none	Score	.76
Exons	465..793, 1587..1642, 1663..1757, 1918..2121, 2200..2385		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	691	Strand	-
Start	4004	End	11771
Name	OJ990423_06.9819.C37.o1.gp	Method	AAT/GAP
Start	3832	End	6329
GI	11553_1.R1084	Score	1989
Exons	3832..4105, 4475..4642, 5536..5754, 5828..5971, 6083..6329		
GI Descrip.	'6041757/gb|AC011806.1|AC011806 0.0e+00 Genomic Sequence For Oryza sativa Clone 10P20, Lemont Strain, Complete Sequence,		

complete sequence'

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	691	Strand	-
Start	4004	End	11771
Name	OJ990423_06.9819.C37.o2.gs	Method	GENSCAN
Start	4004	End	11771
GI	none	Score	.97
Exons	4004..4105, 4475..4642, 5536..5754, 5828..5971, 6083..6365, 6461..6516, 6592..6741, 6824..6910, 7271..7333, 7412..7492, 7874..7951, 8035..8238, 8313..8360, 8473..8658, 11435..11534, 11632..11771		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	691	Strand	-
Start	4004	End	11771
Name	OJ990423_06.9819.C37.o2.np	Method	AAT/NAP
Start	4007	End	11762
GI	2281115	Score	2491
Exons	4007..4105, 4475..4642, 5536..5754, 5828..5971, 6083..6365, 6461..6516, 6592..6741, 6824..6930, 7264..7333, 7412..7492, 7578..7667, 7874..7951, 8173..8238, 8473..8658, 11435..11534, 11632..11762		
GI Descrip.	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	692	Strand	-
Start	15879	End	18025
Name	OJ990423_06.9819.C37.o3.np	Method	AAT/NAP
Start	15879	End	18025
GI	2586082	Score	686
Exons	15879..16626, 17804..18025		
GI Descrip.	(U72725) retrofit [Oryza longistaminata]		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o1.tm	Method	TBLASTX:Maize
Start	3994	End	24501
GI	none	Score	103
Exons	3994..4107, 3995..4111, 3998..4108, 3999..4112, 4000..4113, 4475..4579, 4475..4585, 4479..4604, 4527..4640, 5533..5754, 5534..5704, 5534..5755, 5614..5757, 5828..5971, 5828..5971, 5844..5972, 6063..6305, 6078..6365, 6080..6388, 6080..6367, 6458..6520, 6460..6519, 6571..6753, 6590..6742, 6592..6753, 6824..6910, 6825..6911, 6983..7024, 6985..7026, 7271..7333, 7272..7334, 7415..7495, 7416..7514, 7427..7534, 7575..7670, 7575..7670, 7576..7677, 7577..7675, 7874..7927, 7875..7922, 7922..7951, 7923..7952, 8035..8058, 20711..20734, 20809..20838, 20855..20911, 21120..21149, 21173..21268, 21195..21269, 21351..21413, 22436..22510, 22438..22503, 22442..22525, 22611..22694, 22625..22780, 22627..22707, 22847..22912, 23010..23306, 23090..23302, 23218..23421, 23502..23657, 23513..23659, 23513..23650, 23514..23660, 23518..23676, 23753..23977, 23755..23982, 23755..23997, 24047..24220, 24051..24233, 24051..24218, 24384..24485, 24412..24501		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o1.ts	Method	TBLASTX:Soybean
Start	4003	End	24485
GI	none	Score	92

Exons 4003..4107, 4004..4111, 4004..4108, 4433..4585, 4475..4585, 4476..4598, 4530..4643, 5533..5754, 5552..5704, 5607..5756, 5608..5757, 5826..5966, 5827..5964, 5828..5971, 5844..5966, 6063..6305, 6080..6367, 6083..6388, 6196..6372, 6458..6520, 6460..6519, 6571..6753, 6572..6757, 6590..6742, 6592..6744, 6819..6911, 6820..6930, 6824..6910, 6983..7021, 6985..7020, 7271..7333, 7272..7334, 7412..7495, 7413..7514, 7414..7497, 7556..7672, 7575..7673, 7575..7670, 7576..7677, 7576..7677, 7874..7951, 7875..7952, 7883..7954, 8030..8107, 8035..8238, 8041..8235, 8310..8360, 8314..8352, 8471..8659, 8476..8658, 8480..8659, 11432..11533, 11433..11537, 11625..11759, 11625..11759, 11638..11760, 18726..18890, 18971..19096, 20097..20285, 20098..20286, 20531..20734, 20546..20734, 20548..20736, 20575..20742, 20808..20885, 20809..20880, 20983..21093, 21173..21268, 21195..21272, 21327..21413, 21349..21414, 22325..22369, 22438..22503, 22442..22525, 22625..22780, 22626..22715, 22847..22912, 22847..22912, 23009..23269, 23010..23306, 23017..23229, 23090..23299, 23502..23678, 23516..23653, 23755..23982, 23755..23997, 24047..24220, 24060..24218, 24118..24246, 24384..24485,

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o3.tw	Method	TBLASTX:Wheat
Start	4003	End	24502
GI	none	Score	105

Exons 4003..4107, 4004..4111, 4004..4108, 4005..4112, 4475..4639, 4475..4585, 4479..4604, 5533..5580, 23923..23982, 24047..24220, 24063..24239, 24063..24218, 24118..24246, 24384..24485, 24401..24502, 24409..24501

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o2.tc	Method	TBLASTX:Cress
Start	4004	End	24485
GI	none	Score	71

Exons 4004..4108, 4008..4112, 4433..4585, 4452..4643, 4475..4660, 4500..4604, 5533..5643, 5671..5754, 5828..5971, 5844..5966, 6063..6305, 6080..6409, 6212..6340, 6458..6520, 6460..6519, 6571..6657, 6591..6659, 22712..22780, 22847..22912, 23010..23033, 23016..23306, 23059..23286, 23090..23299, 23502..23657, 23516..23638, 23755..23841, 23869..23982, 23932..24000, 24047..24220, 24118..24246, 24384..24485

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o1.tw	Method	TBLASTX:Wheat
Start	5632	End	23880

GI	none	Score	93
Exons	5632..5754, 5633..5704, 5634..5756, 5828..5971, 5828..5971, 6080..6274, 6081..6275, 23104..23301, 23105..23302, 23108..23302, 23109..23306, 23501..23626, 23502..23657, 23514..23657, 23753..23854, 23755..23880, 23755..23868, 23802..23879		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o4.tc	Method	TBLASTX:Cress
Start	6706	End	22663
GI	none	Score	67
Exons	6706..6753, 6819..6911, 6821..6913, 6824..6910, 7274..7333, 7278..7334, 7412..7495, 7413..7514, 7571..7669, 7575..7670, 7576..7668, 20857..20880, 20983..21093, 21195..21272, 21327..21407, 21349..21411, 22438..22503, 22445..22525, 22625..22663		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o3.tc	Method	TBLASTX:Cress
Start	7902	End	20856
GI	none	Score	51
Exons	7902..7955, 7904..7951, 8035..8238, 8041..8235, 8310..8360, 8471..8671, 8472..8651, 8476..8658, 11432..11533, 18967..19029, 18971..19096, 20088..20285, 20098..20286, 20531..20734, 20543..20734, 20809..20856		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o3.tm	Method	TBLASTX:Maize
Start	8058	End	20710
GI	none	Score	192
Exons	8058..8231, 8059..8238, 8059..8238, 8310..8360, 8318..8392, 8476..8658, 8477..8671, 11432..11533, 11433..11537, 11625..11747, 11625..11759, 11632..11760, 11823..11885, 18726..18890, 18729..18842, 18971..19096, 18979..19029, 20091..20279, 20098..20286, 20116..20286, 20531..20710, 20562..20705, 20570..20710		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o6.tm	Method	TBLASTX:Maize
Start	17462	End	17747
GI	none	Score	73
Exons	17462..17563, 17576..17746, 17577..17747		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o2.tm	Method	TBLASTX:Maize
Start	25007	End	26608
GI	none	Score	109

Exons	25007..25243, 25028..25234, 25517..26005, 25602..26279, 26126..26383, 26159..26311, 26304..26375, 26537..26608		
Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o1.tc	Method	TBLASTX:Cress
Start	25011	End	27772
GI	none	Score	110
Exons	25011..25181, 25019..25243, 25511..26005, 25515..26378, 26063..26428, 26537..26611, 26733..26804, 26810..27220, 26871..27143, 27288..27437, 27299..27439, 27455..27691, 27489..27695, 27648..27770, 27686..27772		
Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o2.ts	Method	TBLASTX:Soybean
Start	25019	End	26929
GI	none	Score	310
Exons	25019..25234, 25523..26005, 25605..26018, 26036..26215, 26112..26378, 26126..26383, 26543..26611, 26861..26929		
Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o4.tw	Method	TBLASTX:Wheat
Start	25019	End	25249
GI	none	Score	206
Exons	25019..25249		
Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o4.gs	Method	GENSCAN
Start	25019	End	27796
GI	none	Score	.66
Exons	25019..26388, 26491..26608, 26751..26951, 27002..27796		
Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o5.np	Method	AAT/NAP
Start	25022	End	28266
GI	6513926	Score	2286
Exons	25022..26388, 26491..26608, 26751..26803, 26887..27198, 27298..27775, 28201..28266		
GI Descrip.	(AC011664) putative potassium transporter [Arabidopsis thaliana]		
Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o5.tm	Method	TBLASTX:Maize
Start	26748	End	27022
GI	none	Score	125
Exons	26748..26804, 26810..27022, 26871..27020		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o4.ts	Method	TBLASTX:Soybean
Start	26930	End	27202
GI	none	Score	118
Exons	26930..27202, 26934..27200		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o4.tm	Method	TBLASTX:Maize
Start	27026	End	27757
GI	none	Score	84
Exons	27026..27220, 27027..27296, 27299..27430, 27440..27631, 27489..27665, 27686..27757, 27687..27752		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o2.tw	Method	TBLASTX:Wheat
Start	27288	End	27557
GI	none	Score	93
Exons	27288..27401, 27299..27427, 27443..27556, 27486..27557		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o3.ts	Method	TBLASTX:Soybean
Start	27299	End	27766
GI	none	Score	94
Exons	27299..27409, 27300..27401, 27455..27556, 27492..27560, 27552..27662, 27554..27679, 27684..27764, 27686..27766		

Seq. No.	374	Seq. ID	OJ990423_06.9819.C37
Gene No.	693	Strand	-
Start	25019	End	28296
Name	OJ990423_06.9819.C37.o6.np	Method	AAT/NAP
Start	28127	End	28296
GI	5852084	Score	112
Exons	28127..28296		
GI Descrip.	(AL117264) zwh0007.1 [Oryza sativa]		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	694	Strand	+
Start	1018	End	6083
Name	OJ990423_06.9819.C38.o2.np	Method	AAT/NAP
Start	1018	End	4446
GI	4063770	Score	112
Exons	1018..1039, 2538..2610, 4122..4446		
GI Descrip.	(AB004906) transposase [Ipomoea purpurea]		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	694	Strand	+
Start	1018	End	6083
Name	OJ990423_06.9819.C38.o2.gs	Method	GENSCAN
Start	4289	End	6055

GI	none	Score	.66
Exons	4289..4351, 4865..5677, 5700..6055		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	694	Strand	+
Start	1018	End	6083
Name	OJ990423_06.9819.C38.o1.gp	Method	AAT/GAP
Start	5072	End	6075
GI	29585_1.R1084	Score	1898
Exons	5072..6075		
GI Descrip.	'2055230/dbj|BAA19769| 2.0e-17 (AB000130) SRC2 [Glycine max]'		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	694	Strand	+
Start	1018	End	6083
Name	OJ990423_06.9819.C38.o3.np	Method	AAT/NAP
Start	5180	End	6083
GI	2055230	Score	331
Exons	5180..5667, 5712..6083		
GI Descrip.	(AB000130) SRC2 [Glycine max]		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	695	Strand	-
Start	261	End	1686
Name	OJ990423_06.9819.C38.o1.np	Method	AAT/NAP
Start	261	End	1686
GI	5852084	Score	91
Exons	261..344, 1619..1686		
GI Descrip.	(AL117264) zwh0007.1 [Oryza sativa]		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	696	Strand	
Start	4182	End	4370
Name	OJ990423_06.9819.C38.o2.tm	Method	TBLASTX:Maize
Start	4182	End	4370
GI	none	Score	146
Exons	4182..4361, 4182..4250, 4183..4362, 4189..4365, 4190..4366, 4314..4370		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	697	Strand	
Start	5182	End	6075
Name	OJ990423_06.9819.C38.o1.tm	Method	TBLASTX:Maize
Start	5182	End	6075
GI	none	Score	534
Exons	5182..5604, 5183..5605, 5836..5913, 5858..5947, 5938..6075, 5988..6071		

Seq. No.	375	Seq. ID	OJ990423_06.9819.C38
Gene No.	697	Strand	
Start	5182	End	6075
Name	OJ990423_06.9819.C38.o1.ts	Method	TBLASTX:Soybean
Start	5183	End	5551
GI	none	Score	103
Exons	5183..5290, 5318..5374, 5405..5551		

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39

Gene No.	698	Strand	+
Start	253	End	8421
Name	OJ990423_06.9819.C39.o1.gs	Method	GENSCAN
Start	253	End	8421
GI	none	Score	.48
Exons	253..396, 2629..2698, 3304..3342, 5436..5457, 7176..7551, 7714..7950, 8034..8301, 8306..8421		

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39
Gene No.	699	Strand	-
Start	8394	End	9270
Name	OJ990423_06.9819.C39.o1.gp	Method	AAT/GAP
Start	8394	End	9002
GI	16273_1.R1084	Score	1011
Exons	8394..9002		
GI Descrip.	'121695/sp|P12653|GTH1_MAIZE 3.0e-26 GLUTATHIONE S-TRANSFERASE I (GST-I) (GST-29) (GST CLASS-PHI) >gi_22315_emb_CAA29928_ (X06754) GST I (AA 1-214) [Zea mays]'		

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39
Gene No.	699	Strand	-
Start	8394	End	9270
Name	OJ990423_06.9819.C39.o1.tm	Method	TBLASTX:Maize
Start	8553	End	9082
GI	none	Score	153
Exons	8553..8597, 8615..8830, 8629..8988, 8815..8853, 8906..9001, 9005..9082, 9028..9075		

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39
Gene No.	699	Strand	-
Start	8394	End	9270
Name	OJ990423_06.9819.C39.o2.gs	Method	GENSCAN
Start	8596	End	8985
GI	none	Score	.99
Exons	8596..8985		

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39
Gene No.	699	Strand	-
Start	8394	End	9270
Name	OJ990423_06.9819.C39.o1.np	Method	AAT/NAP
Start	8623	End	9270
GI	3891705	Score	396
Exons	8623..9270		
GI Descrip.	Chain A, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate gi|3891706|pdb|1BYE|B Chain B, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate gi|3891707|pdb|1BYE|C Chain C, Glutathione S-Transferase I From Mais In Complex With Atrazine Glutathione Conjugate gi|3891708|pdb|1BYE|D Chain D, Glutathione S-Transf		

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39
Gene No.	699	Strand	-
Start	8394	End	9270
Name	OJ990423_06.9819.C39.o1.tw	Method	TBLASTX:Wheat
Start	8629	End	9115
GI	none	Score	154
Exons	8629..8895, 8630..8827, 8905..9075, 8916..8960, 8926..9069,		

8963..9115

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39
Gene No.	699	Strand	-
Start	8394	End	9270
Name	OJ990423_06.9819.C39.o1.tc	Method	TBLASTX:Cress
Start	8642	End	9075
GI	none	Score	93
Exons	8642..8827, 8644..9075		

Seq. No.	376	Seq. ID	OJ990423_06.9819.C39
Gene No.	699	Strand	-
Start	8394	End	9270
Name	OJ990423_06.9819.C39.o1.ts	Method	TBLASTX:Soybean
Start	8759	End	9075
GI	none	Score	80
Exons	8759..8827, 8761..8985, 9028..9075		

Seq. No.	377	Seq. ID	OJ990423_06.9819.C40
Gene No.	700	Strand	+
Start	1	End	707
Name	OJ990423_06.9819.C40.o1.np	Method	AAT/NAP
Start	1	End	707
GI	2119980	Score	839
Exons	1..707		
GI Descrip.	transposase (transposons) - Escherichia coli gi|43089|emb|CAA42760| (X60200) transposase [Escherichia coli] gi|303566|dbj|BAA03914| (D16449) transposase [Escherichia coli]		

Seq. No.	377	Seq. ID	OJ990423_06.9819.C40
Gene No.	700	Strand	+
Start	1	End	707
Name	OJ990423_06.9819.C40.o1.gs	Method	GENSCAN
Start	141	End	647
GI	none	Score	.85
Exons	141..647		

Seq. No.	378	Seq. ID	OJ990423_06.9819.C41
Gene No.	701	Strand	+
Start	246	End	724
Name	OJ990423_06.9819.C41.o1.np	Method	AAT/NAP
Start	246	End	724
GI	1170092	Score	152
Exons	246..724		
GI Descrip.	GLUTATHIONE S-TRANSFERASE IV (GST-IV) (GST-27) (GST CLASS PHI) gi|1076807|pir||S52037 glutathione transferase (EC 2.5.1.18) 27K chain - maize gi|529015 (U12679) glutathione S-transferase IV [Zea mays] gi|695789|emb|CAA56047| (X79515) glutathione transferase [Zea mays] gi|1094866|prf||2106424A glutathione S-transferase:ISOTYPE=IV [Zea mays]		

Seq. No.	378	Seq. ID	OJ990423_06.9819.C41
Gene No.	701	Strand	+
Start	246	End	724
Name	OJ990423_06.9819.C41.o1.tm	Method	TBLASTX:Maize
Start	246	End	602
GI	none	Score	79

Exons	246..314, 251..295, 321..602, 327..401		
Seq. No.	378	Seq. ID	OJ990423_06.9819.C41
Gene No.	701	Strand	+
Start	246	End	724
Name	OJ990423_06.9819.C41.o1.gs	Method	GENSCAN
Start	253	End	524
GI	none	Score	.78
Exons	253..389, 414..524		
Seq. No.	379	Seq. ID	OJ990423_01.9819.C1
Gene No.	702	Strand	+
Start	1	End	736
Name	OJ990423_01.9819.C1.o1.np	Method	AAT/NAP
Start	1	End	736
GI	6523035	Score	159
Exons	1..337, 678..736		
GI Descrip.	(AL132976) kinesin-like protein [Arabidopsis thaliana]		
Seq. No.	379	Seq. ID	OJ990423_01.9819.C1
Gene No.	702	Strand	+
Start	1	End	736
Name	OJ990423_01.9819.C1.o1.ts	Method	TBLASTX:Soybean
Start	107	End	314
GI	none	Score	274
Exons	107..304, 108..314, 108..314		
Seq. No.	379	Seq. ID	OJ990423_01.9819.C1
Gene No.	702	Strand	+
Start	1	End	736
Name	OJ990423_01.9819.C1.o1.tm	Method	TBLASTX:Maize
Start	114	End	340
GI	none	Score	344
Exons	114..338, 114..332, 118..333, 119..340		
Seq. No.	379	Seq. ID	OJ990423_01.9819.C1
Gene No.	702	Strand	+
Start	1	End	736
Name	OJ990423_01.9819.C1.o1.gs	Method	GENSCAN
Start	171	End	337
GI	none	Score	.72
Exons	171..337		
Seq. No.	380	Seq. ID	OJ990423_01.9819.C2
Gene No.	703	Strand	+
Start	149	End	408
Name	OJ990423_01.9819.C2.o1.gs	Method	GENSCAN
Start	149	End	408
GI	none	Score	.46
Exons	149..408		
Seq. No.	380	Seq. ID	OJ990423_01.9819.C2
Gene No.	704	Strand	-
Start	113	End	334
Name	OJ990423_01.9819.C2.o1.gp	Method	AAT/GAP
Start	113	End	334
GI	uC-osflm202111h06b1	Score	388

Exons	113..334		
GI Descrip.	'287938/emb|X54204|CVPRSET5C 6.0e-47 Cloning vector pRSET5c (pBluescript KS plus derivative)'		
Seq. No.	381	Seq. ID	OJ990423_01.9819.C3
Gene No.	705	Strand	-
Start	195	End	577
Name	OJ990423_01.9819.C3.o1.gs	Method	GENSCAN
Start	195	End	577
GI	none	Score	.58
Exons	195..259, 372..456, 575..577		
Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	706	Strand	+
Start	12973	End	13221
Name	OJ990423_01.9819.C6.o3.gs	Method	GENSCAN
Start	12973	End	13221
GI	none	Score	.95
Exons	12973..13083, 13090..13221		
Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	707	Strand	+
Start	18233	End	19900
Name	OJ990423_01.9819.C6.o5.gs	Method	GENSCAN
Start	18233	End	19900
GI	none	Score	.6
Exons	18233..18516, 18845..19060, 19145..19315, 19496..19541, 19712..19900		
Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o6.gs	Method	GENSCAN
Start	20203	End	22758
GI	none	Score	.89
Exons	20203..22758		
Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o1.np	Method	AAT/NAP
Start	20206	End	23133
GI	6539553	Score	4727
Exons	20206..23133		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		
Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o2.tw	Method	TBLASTX:Wheat
Start	20342	End	20818
GI	none	Score	353
Exons	20342..20728, 20380..20727, 20743..20817, 20747..20818		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o4.ts	Method	TBLASTX:Soybean
Start	20470	End	20811
GI	none	Score	83
Exons	20470..20679, 20549..20674, 20698..20811, 20705..20785		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o2.tm	Method	TBLASTX:Maize
Start	20674	End	21013
GI	none	Score	206
Exons	20674..21012, 20675..21013		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o2.ts	Method	TBLASTX:Soybean
Start	20824	End	21169
GI	none	Score	124
Exons	20824..21168, 20969..21169		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o3.tw	Method	TBLASTX:Wheat
Start	21022	End	21567
GI	none	Score	48
Exons	21022..21228, 21032..21154, 21223..21567, 21247..21420		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o1.tm	Method	TBLASTX:Maize
Start	21103	End	21568
GI	none	Score	55
Exons	21103..21567, 21206..21316, 21250..21432, 21386..21568		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o1.ts	Method	TBLASTX:Soybean
Start	21238	End	21702
GI	5509260	Score	58
Exons	21238..21702, 21257..21316, 21389..21484, 21533..21601		
GI Descrip.	-		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o1.tc	Method	TBLASTX:Cress
Start	21349	End	21609
GI	none	Score	286
Exons	21349..21609		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o1.tw	Method	TBLASTX:Wheat
Start	21622	End	22369
GI	none	Score	442
Exons	21622..22359, 21622..21861, 21639..21950, 21890..22369, 21913..22362		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o2.tc	Method	TBLASTX:Cress
Start	22003	End	22392
GI	none	Score	115
Exons	22003..22197, 22210..22392		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o3.ts	Method	TBLASTX:Soybean
Start	22027	End	22425
GI	none	Score	38
Exons	22027..22200, 22154..22192, 22201..22425, 22247..22417		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o3.tm	Method	TBLASTX:Maize
Start	22213	End	22647
GI	none	Score	84
Exons	22213..22647, 22238..22438		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o4.tw	Method	TBLASTX:Wheat
Start	22371	End	22569
GI	none	Score	82
Exons	22371..22442, 22372..22569, 22372..22566		

Seq. No.	382	Seq. ID	OJ990423_01.9819.C6
Gene No.	708	Strand	-
Start	20203	End	23133
Name	OJ990423_01.9819.C6.o5.ts	Method	TBLASTX:Soybean
Start	22435	End	22821
GI	none	Score	88
Exons	22435..22683, 22666..22821		

Seq. No.	383	Seq. ID	OJ990423_01.9819.C7
Gene No.	709	Strand	+
Start	55	End	774
Name	OJ990423_01.9819.C7.o1.gp	Method	AAT/GAP
Start	55	End	774
GI	1523_1.R1084	Score	948
Exons	55..164, 249..306, 384..774		
GI Descrip.	'4006881/emb|CAB16799.1| 4.0e-61 (Z99707) putative protein		

[Arabidopsis thaliana]'

Seq. No.	383	Seq. ID	OJ990423_01.9819.C7
Gene No.	709	Strand	+
Start	55	End	774
Name	OJ990423_01.9819.C7.o1.np	Method	AAT/NAP
Start	78	End	455
GI	4006881	Score	96
Exons	78..164, 249..306, 384..455		
GI Descrip.	(Z99707) putative protein [Arabidopsis thaliana]		

Seq. No.	383	Seq. ID	OJ990423_01.9819.C7
Gene No.	709	Strand	+
Start	55	End	774
Name	OJ990423_01.9819.C7.o1.gs	Method	GENSCAN
Start	249	End	306
GI	none	Score	.73
Exons	249..306		

Seq. No.	384	Seq. ID	OJ990423_01.9819.C9
Gene No.	710	Strand	-
Start	415	End	472
Name	OJ990423_01.9819.C9.o1.gs	Method	GENSCAN
Start	415	End	472
GI	none	Score	.93
Exons	415..472		

Seq. No.	385	Seq. ID	OJ990423_01.9819.C10
Gene No.	711	Strand	+
Start	1	End	286
Name	OJ990423_01.9819.C10.o1.np	Method	AAT/NAP
Start	1	End	286
GI	5295971	Score	338
Exons	1..286		
GI Descrip.	(AB026295) EST D24315(R1718) corresponds to a region of the predicted gene.; Similar to Tobacco DNA for retroviral-like transposon Tnt 1-94.(X13777) [Oryza sativa]		

Seq. No.	385	Seq. ID	OJ990423_01.9819.C10
Gene No.	712	Strand	-
Start	1	End	1189
Name	OJ990423_01.9819.C10.o2.np	Method	AAT/NAP
Start	1	End	1189
GI	6907106	Score	212
Exons	1..116, 674..854, 950..1054, 1124..1189		
GI Descrip.	(AP001129) EST AU068291(C12960) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	385	Seq. ID	OJ990423_01.9819.C10
Gene No.	712	Strand	-
Start	1	End	1189
Name	OJ990423_01.9819.C10.o1.gp	Method	AAT/GAP
Start	299	End	581
GI	86158_1.R1084	Score	399
Exons	299..581		
GI Descrip.	'5295936/dbj|AB026295.2|AB026295 5.0e-42 Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence'		

Seq. No.	386	Seq. ID	OJ990423_01.9819.C14
Gene No.	713	Strand	-
Start	365	End	684
Name	OJ990423_01.9819.C14.o1.gs	Method	GENSCAN
Start	365	End	684
GI	none	Score	.66
Exons	365..453, 545..684		

Seq. No.	387	Seq. ID	OJ990423_01.9819.C15
Gene No.	714	Strand	-
Start	1	End	784
Name	OJ990423_01.9819.C15.o1.np	Method	AAT/NAP
Start	1	End	784
GI	6523035	Score	65
Exons	1..74, 171..274, 668..784		
GI Descrip.	(AL132976) kinesin-like protein [Arabidopsis thaliana]		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o1.gs	Method	GENSCAN
Start	553	End	5378
GI	none	Score	.46
Exons	553..5378		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o1.np	Method	AAT/NAP
Start	573	End	5375
GI	5295971	Score	8110
Exons	573..5375		
GI Descrip.	(AB026295) EST D24315(R1718) corresponds to a region of the predicted gene.; Similar to Tobacco DNA for retroviral-like transposon Tnt 1-94.(X13777) [Oryza sativa]		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o6.tm	Method	TBLASTX:Maize
Start	965	End	1256
GI	none	Score	360
Exons	965..1180, 966..1256, 1035..1256		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o1.tm	Method	TBLASTX:Maize
Start	1491	End	2210
GI	none	Score	399
Exons	1491..1766, 1508..1765, 1683..1778, 1748..1780, 1785..2210, 1786..2109, 1845..2210		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378

Name	OJ990423_01.9819.C17.o2.tw	Method	TBLASTX:Wheat
Start	2135	End	2588
GI	none	Score	331
Exons	2135..2374, 2136..2501, 2139..2516, 2496..2588, 2508..2588		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o7.tm	Method	TBLASTX:Maize
Start	2225	End	2465
GI	none	Score	290
Exons	2225..2374, 2226..2465, 2232..2456, 2432..2464		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o4.ts	Method	TBLASTX:Soybean
Start	2526	End	2801
GI	none	Score	194
Exons	2526..2801, 2622..2702		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o3.tw	Method	TBLASTX:Wheat
Start	2661	End	3212
GI	none	Score	105
Exons	2661..2801, 2859..3125, 2876..3025, 3128..3199, 3132..3212		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o2.tm	Method	TBLASTX:Maize
Start	2864	End	3290
GI	none	Score	697
Exons	2864..3289, 2868..3290		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o1.ts	Method	TBLASTX:Soybean
Start	2895	End	3374
GI	none	Score	355
Exons	2895..3203, 2900..3190, 3228..3374		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o2.tc	Method	TBLASTX:Cress
Start	2910	End	3350
GI	none	Score	203
Exons	2910..3206, 2960..2992, 3050..3196, 3228..3350		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o2.ts	Method	TBLASTX:Soybean

Start	3825	End	4322
GI	5509260	Score	419
Exons	3825..4322, 3905..4081, 4145..4303		
GI Descrip.	-		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o5.tm	Method	TBLASTX:Maize
Start	3876	End	4172
GI	none	Score	387
Exons	3876..4172, 3902..4171		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o3.tc	Method	TBLASTX:Cress
Start	3947	End	4211
GI	none	Score	244
Exons	3947..4078, 3948..4211, 4041..4211		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o1.tw	Method	TBLASTX:Wheat
Start	3992	End	4547
GI	none	Score	317
Exons	3992..4081, 3993..4337, 4146..4313, 4148..4333, 4323..4547		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o3.tm	Method	TBLASTX:Maize
Start	4374	End	4765
GI	none	Score	603
Exons	4374..4763, 4374..4763, 4376..4765		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o5.tw	Method	TBLASTX:Wheat
Start	4548	End	4859
GI	none	Score	64
Exons	4548..4655, 4680..4859		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o1.tc	Method	TBLASTX:Cress
Start	4680	End	5342
GI	none	Score	255
Exons	4680..4967, 4742..4852, 4874..4966, 4976..5053, 4977..5057, 5124..5342, 5132..5203		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378

Name	OJ990423_01.9819.C17.o3.ts	Method	TBLASTX:Soybean
Start	4701	End	5351
GI	none	Score	147
Exons	4701..4862, 4874..5035, 4875..5063, 5070..5228, 5118..5351		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o8.tm	Method	TBLASTX:Maize
Start	4767	End	4946
GI	none	Score	195
Exons	4767..4946, 4769..4945		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o4.tw	Method	TBLASTX:Wheat
Start	4893	End	5312
GI	none	Score	124
Exons	4893..5063, 4976..5053, 5109..5312, 5118..5300		

Seq. No.	388	Seq. ID	OJ990423_01.9819.C17
Gene No.	715	Strand	+
Start	553	End	5378
Name	OJ990423_01.9819.C17.o4.tm	Method	TBLASTX:Maize
Start	4952	End	5341
GI	none	Score	512
Exons	4952..5059, 4953..5339, 4955..5341, 4984..5214, 5034..5339, 5263..5340		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	716	Strand	+
Start	6267	End	15427
Name	OJ990423_01.9819.C18.o2.gs	Method	GENSCAN
Start	6267	End	15218
GI	none	Score	.6
Exons	6267..6652, 7117..7221, 12862..13013, 13206..13305, 13394..13441, 13619..15218		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	716	Strand	+
Start	6267	End	15427
Name	OJ990423_01.9819.C18.o4.np	Method	AAT/NAP
Start	13635	End	15427
GI	6539553	Score	2764
Exons	13635..15281, 15403..15427		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o1.gs	Method	GENSCAN
Start	1249	End	3385
GI	none	Score	.67

Exons	1249..1292, 1399..1542, 2179..2293, 2614..2712, 2813..2950, 3317..3385		
Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o1.tw	Method	TBLASTX:Wheat
Start	1374	End	1663
GI	none	Score	386
Exons	1374..1661, 1376..1663		
Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o1.tc	Method	TBLASTX:Cress
Start	1400	End	2682
GI	none	Score	213
Exons	1400..1702, 1401..1700, 1421..1702, 2599..2682		
Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o5.tm	Method	TBLASTX:Maize
Start	1400	End	2718
GI	none	Score	144
Exons	1400..1597, 1404..1592, 1616..1702, 1617..1700, 2599..2718, 2614..2718		
Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o1.ts	Method	TBLASTX:Soybean
Start	1400	End	1667
GI	none	Score	198
Exons	1400..1666, 1401..1667		
Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o1.np	Method	AAT/NAP
Start	1401	End	7224
GI	4006878	Score	574
Exons	1401..1702, 2614..2712, 2813..2950, 3053..3189, 7184..7224		
GI Descrip.	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]		
Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o2.ts	Method	TBLASTX:Soybean
Start	2599	End	3178
GI	none	Score	109
Exons	2599..2718, 2614..2718, 2813..2950, 2829..2951, 3050..3178		
Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o2.tc	Method	TBLASTX:Cress

Start	2684	End	3295
GI	none	Score	41
Exons	2684..2713, 2686..2718, 2813..2950, 2814..2951, 3050..3181, 3254..3295		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o7.tm	Method	TBLASTX:Maize
Start	2835	End	3178
GI	none	Score	99
Exons	2835..2948, 2837..2947, 3060..3107, 3062..3178		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	717	Strand	-
Start	1249	End	7224
Name	OJ990423_01.9819.C18.o1.gp	Method	AAT/GAP
Start	2858	End	3567
GI	5056120	Score	829
Exons	2858..2950, 3053..3175, 3317..3567		
GI Descrip.	4006878/emb|CAB16796.1| 7.0e-11 (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	718	Strand	
Start	7669	End	7959
Name	OJ990423_01.9819.C18.o6.tm	Method	TBLASTX:Maize
Start	7669	End	7959
GI	none	Score	42
Exons	7669..7767, 7688..7780, 7762..7959, 7763..7915, 7765..7959		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	719	Strand	
Start	8038	End	9201
Name	OJ990423_01.9819.C18.o3.tw	Method	TBLASTX:Wheat
Start	8038	End	8406
GI	none	Score	330
Exons	8038..8406		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	719	Strand	
Start	8038	End	9201
Name	OJ990423_01.9819.C18.o1.tm	Method	TBLASTX:Maize
Start	8131	End	8602
GI	none	Score	79
Exons	8131..8217, 8132..8212, 8227..8601, 8414..8602		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	719	Strand	
Start	8038	End	9201
Name	OJ990423_01.9819.C18.o4.tw	Method	TBLASTX:Wheat
Start	8500	End	9052
GI	none	Score	127
Exons	8500..8616, 8644..8682, 8689..9051, 8702..9052		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	719	Strand	

Start	8038	End	9201
Name	OJ990423_01.9819.C18.o3.ts	Method	TBLASTX:Soybean
Start	8674	End	9201
GI	none	Score	115
Exons	8674..8859, 8848..9075, 8849..9085, 9145..9201		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	719	Strand	
Start	8038	End	9201
Name	OJ990423_01.9819.C18.o4.tm	Method	TBLASTX:Maize
Start	8789	End	9127
GI	none	Score	179
Exons	8789..9127, 8803..9114		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	720	Strand	
Start	13629	End	14077
Name	OJ990423_01.9819.C18.o2.tw	Method	TBLASTX:Wheat
Start	13629	End	14016
GI	none	Score	355
Exons	13629..14015, 13640..14014, 13753..14016		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	720	Strand	
Start	13629	End	14077
Name	OJ990423_01.9819.C18.o3.tm	Method	TBLASTX:Maize
Start	13764	End	14077
GI	none	Score	363
Exons	13764..14075, 13772..14077		

Seq. No.	389	Seq. ID	OJ990423_01.9819.C18
Gene No.	721	Strand	
Start	14583	End	14898
Name	OJ990423_01.9819.C18.o2.tm	Method	TBLASTX:Maize
Start	14583	End	14898
GI	none	Score	394
Exons	14583..14897, 14603..14896, 14731..14898		

Seq. No.	390	Seq. ID	OJ990423_01.9819.C20
Gene No.	722	Strand	-
Start	775	End	838
Name	OJ990423_01.9819.C20.o1.gs	Method	GENSCAN
Start	775	End	838
GI	none	Score	.66
Exons	775..838		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21
Gene No.	723	Strand	+
Start	1	End	3487
Name	OJ990423_01.9819.C21.o1.gs	Method	GENSCAN
Start	1	End	2658
GI	none	Score	.86
Exons	1..9, 281..374, 487..515, 598..695, 793..888, 1127..1348, 1730..1886, 2200..2355, 2431..2658		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21
Gene No.	723	Strand	+

Start	1	End	3487
Name	OJ990423_01.9819.C21.o1.np	Method	AAT/NAP
Start	281	End	3487
GI	6523035	Score	564
Exons	281..382, 492..695, 793..891, 1136..1348, 1730..1886, 2186..2355, 2458..2619, 3428..3487		
GI Descrip.	(AL132976) kinesin-like protein [Arabidopsis thaliana]		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21
Gene No.	724	Strand	+
Start	5482	End	5704
Name	OJ990423_01.9819.C21.o2.gp	Method	AAT/GAP
Start	5482	End	5704
GI	uC-osflm202111h06b1	Score	417
Exons	5482..5704		
GI Descrip.	'287938/emb|X54204|CVPRSET5C 6.0e-47 Cloning vector pRSET5c (pBluescript KS plus derivative)'		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21
Gene No.	725	Strand	-
Start	2965	End	6723
Name	OJ990423_01.9819.C21.o1.tm	Method	TBLASTX:Maize
Start	608	End	3059
GI	none	Score	137
Exons	608..700, 610..696, 614..700, 793..888, 794..889, 1125..1349, 1125..1343, 1129..1344, 1130..1351, 1727..1885, 1728..1886, 1801..1887, 2175..2333, 2201..2332, 2203..2358, 2205..2354, 2425..2601, 2428..2520, 2430..2609, 2430..2600, 2674..2721, 2710..2736, 2711..2737, 2755..2778, 2756..2785, 2783..2803, 2800..2835, 2928..3035, 2928..3008, 3021..3059		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21
Gene No.	725	Strand	-
Start	2965	End	6723
Name	OJ990423_01.9819.C21.o2.ts	Method	TBLASTX:Soybean
Start	1118	End	1325
GI	none	Score	274
Exons	1118..1315, 1119..1325, 1126..1323		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21
Gene No.	725	Strand	-
Start	2965	End	6723
Name	OJ990423_01.9819.C21.o1.ts	Method	TBLASTX:Soybean
Start	2196	End	2601
GI	none	Score	116
Exons	2196..2339, 2197..2346, 2419..2601, 2421..2600		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21
Gene No.	725	Strand	-
Start	2965	End	6723
Name	OJ990423_01.9819.C21.o2.gs	Method	GENSCAN
Start	2965	End	6723
GI	none	Score	.45
Exons	2965..3176, 3755..3883, 4542..4585, 5271..5298, 5454..5719, 6481..6723		

Seq. No.	391	Seq. ID	OJ990423_01.9819.C21

Gene No.	725	Strand	-
Start	2965	End	6723
Name	OJ990423_01.9819.C21.o1.gp	Method	AAT/GAP
Start	3715	End	3799
GI	5771201	Score	103
Exons	3715..3799		
GI Descrip.	287938/emb|X54204|CVPRSET5C 6.0e-47 Cloning vector pRSET5c (pBluescript KS plus derivative)		

Seq. No.	392	Seq. ID	OJ990423_01.9819.C22
Gene No.	726	Strand	+
Start	367	End	9126
Name	OJ990423_01.9819.C22.o1.np	Method	AAT/NAP
Start	367	End	9126
GI	5852180	Score	431
Exons	367..401, 3976..4029, 5013..5131, 5183..5630, 9100..9126		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	392	Seq. ID	OJ990423_01.9819.C22
Gene No.	727	Strand	-
Start	902	End	8907
Name	OJ990423_01.9819.C22.o1.gp	Method	AAT/GAP
Start	902	End	1452
GI	uC-osflm202111h06b1	Score	505
Exons	902..1024, 1293..1452		
GI Descrip.	'287938/emb|X54204|CVPRSET5C 6.0e-47 Cloning vector pRSET5c (pBluescript KS plus derivative)'		

Seq. No.	392	Seq. ID	OJ990423_01.9819.C22
Gene No.	727	Strand	-
Start	902	End	8907
Name	OJ990423_01.9819.C22.o1.gs	Method	GENSCAN
Start	902	End	8907
GI	none	Score	.54
Exons	902..1096, 1293..1434, 4210..4314, 5142..5246, 5339..5577, 7069..7154, 8833..8907		

Seq. No.	392	Seq. ID	OJ990423_01.9819.C22
Gene No.	727	Strand	-
Start	902	End	8907
Name	OJ990423_01.9819.C22.o2.gp	Method	AAT/GAP
Start	3878	End	4259
GI	uC-osflcyp033a04b1	Score	655
Exons	3878..4259		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	728	Strand	+
Start	6480	End	17353
Name	OJ990423_01.9819.C23.o1.np	Method	AAT/NAP
Start	6480	End	17353
GI	6815052	Score	805
Exons	6480..6633, 6715..6789, 7867..7990, 12172..12300, 12373..12433, 13449..13589, 13664..14175, 14272..14421, 17287..17353		
GI Descrip.	(AP001080) hypothetical protein [Oryza sativa]		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	729	Strand	-
Start	18981	End	19394
Name	OJ990423_01.9819.C23.o3.gs	Method	GENSCAN
Start	18981	End	19394
GI	none	Score	.86
Exons	18981..19394		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	730	Strand	-
Start	24028	End	29304
Name	OJ990423_01.9819.C23.o2.np	Method	AAT/NAP
Start	24028	End	29304
GI	6721516	Score	566
Exons	24028..24197, 28326..28656, 29067..29304		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	731	Strand	-
Start	32982	End	39689
Name	OJ990423_01.9819.C23.o2.gp	Method	AAT/GAP
Start	32695	End	37512
GI	14411_1.R1084	Score	4167
Exons	32695..33230, 33322..33528, 33650..33820, 34751..34888, 35203..35292, 35373..35450, 35529..36185, 36264..36382, 37324..37512		
GI Descrip.	'1737492 0.0e+00 (U81318) poly(A)-binding protein [Triticum aestivum]'		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	731	Strand	-
Start	32982	End	39689
Name	OJ990423_01.9819.C23.o5.gs	Method	GENSCAN
Start	32982	End	39689
GI	none	Score	.81
Exons	32982..33230, 33322..33528, 33650..33820, 34751..34888, 35203..35292, 35373..35450, 35529..36185, 36264..36382, 37324..37519, 37806..37969, 39620..39689		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	731	Strand	-
Start	32982	End	39689
Name	OJ990423_01.9819.C23.o3.np	Method	AAT/NAP
Start	32985	End	37579
GI	1737492	Score	2703
Exons	32985..33230, 33322..33528, 33650..33820, 34751..34888, 35203..35292, 35373..35450, 35529..36185, 36264..36382, 37324..37579		
GI Descrip.	(U81318) poly(A)-binding protein [Triticum aestivum]		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o3.tw	Method	TBLASTX:Wheat
Start	12639	End	13124
GI	none	Score	89
Exons	12639..12782, 12639..12764, 12665..13111, 12804..13112,		

12816..13124

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o3.ts	Method	TBLASTX:Soybean
Start	12645	End	13034
GI	none	Score	88
Exons	12645..12785, 12813..13034		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o4.tm	Method	TBLASTX:Maize
Start	30563	End	30843
GI	none	Score	59
Exons	30563..30646, 30582..30644, 30656..30823, 30724..30825, 30724..30843		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o1.tm	Method	TBLASTX:Maize
Start	32886	End	36203
GI	none	Score	37
Exons	32886..32909, 32889..32927, 32982..33050, 32989..33033, 33024..33230, 33025..33231, 33319..33396, 33326..33400, 33374..33445, 33394..33450, 33397..33450, 33433..33480, 33442..33531, 33452..33508, 33658..33684, 33661..33693, 33696..33758, 33729..33767, 33752..33769, 33773..33823, 34739..34798, 34749..34889, 34751..34891, 34847..34894, 35188..35286, 35197..35292, 35201..35305, 35204..35320, 35361..35450, 35362..35451, 35370..35450, 35370..35450, 35374..35451, 35518..35625, 35527..35625, 35528..35821, 35529..36179, 35529..35615, 35655..35927, 35673..36203, 35674..36186, 35682..35966, 35682..35924, 35702..36187, 35955..36188, 35958..36188		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o2.tw	Method	TBLASTX:Wheat
Start	32950	End	33430
GI	none	Score	41
Exons	32950..32976, 32967..33056, 32968..33036, 33027..33230, 33028..33231, 33289..33429, 33319..33429, 33323..33430		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o1.ts	Method	TBLASTX:Soybean
Start	33003	End	37495
GI	none	Score	168
Exons	33003..33230, 33073..33231, 33323..33406, 33325..33396, 33397..33570, 33397..33480, 34751..34798, 34767..34889, 34769..34891, 34847..34894, 35197..35301, 35209..35283, 35325..35453, 35361..35450, 35370..35450, 35374..35484,		

35528..35617, 35529..36188, 35529..35633, 35655..35927,
35667..35975, 35670..36194, 35701..35859, 35745..35816,
35958..36188, 36264..36371, 36264..36368, 36265..36372,
37325..37495, 37332..37487

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o1.tc	Method	TBLASTX:Cress
Start	33063	End	37495
GI	none	Score	170

Exons 33063..33230, 33070..33231, 33732..33821, 34751..34798,
34770..34889, 34772..34891, 34847..34894, 35197..35292,
35204..35275, 35352..35450, 35367..35450, 35374..35469,
35529..36188, 35529..35618, 35655..35969, 35682..35960,
35701..35859, 35704..36186, 35745..35816, 35826..35927,
35958..36188, 36264..36383, 36264..36362, 36268..36381,
37307..37495, 37326..37487

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o4.tw	Method	TBLASTX:Wheat
Start	33649	End	35320
GI	none	Score	75

Exons 33649..33759, 33655..33708, 33696..33758, 33729..33821,
33752..33823, 34751..34774, 34772..34798, 34809..34892,
34811..34894, 34847..34894, 35197..35316, 35204..35320

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o1.tw	Method	TBLASTX:Wheat
Start	35370	End	36189
GI	none	Score	61

Exons 35370..35450, 35535..35618, 35541..35936, 35542..35631,
35552..35935, 35953..36189, 35955..36185

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o3.tm	Method	TBLASTX:Maize
Start	36240	End	37496
GI	none	Score	81

Exons 36240..36368, 36268..36372, 36270..36383, 37304..37492,
37326..37496

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o5.tw	Method	TBLASTX:Wheat
Start	36264	End	37463
GI	none	Score	146

Exons 36264..36368, 36265..36372, 37304..37462, 37326..37463

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-

Start	40452	End	49263
Name	OJ990423_01.9819.C23.o6.gs	Method	GENSCAN
Start	40452	End	48812
GI	none	Score	.81
Exons	40452..40556, 41393..41450, 41535..41650, 42329..42387, 42851..42899, 43333..43397, 43496..43583, 45027..45125, 46738..46809, 46968..47054, 48308..48379, 48615..48812		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o3.gp	Method	AAT/GAP
Start	40828	End	44499
GI	1523_1.R1084	Score	2163
Exons	40828..41315, 41393..41450, 41535..41650, 42329..42387, 42851..42899, 43333..43397, 43496..43583, 44151..44499		
GI Descrip.	'4006881/emb|CAB16799.1| 4.0e-61 (Z99707) putative protein [Arabidopsis thaliana]'		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o2.ts	Method	TBLASTX:Soybean
Start	41241	End	43581
GI	none	Score	60
Exons	41241..41315, 41266..41316, 41390..41452, 41391..41453, 41528..41653, 41535..41651, 42302..42373, 42849..42899, 42850..42900, 43330..43398, 43497..43577, 43498..43581		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o4.np	Method	AAT/NAP
Start	41244	End	44494
GI	4006881	Score	395
Exons	41244..41315, 41393..41450, 41535..41650, 42329..42387, 42851..42899, 43333..43397, 43496..43580, 44289..44494		
GI Descrip.	(Z99707) putative protein [Arabidopsis thaliana]		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o2.tm	Method	TBLASTX:Maize
Start	41245	End	43584
GI	none	Score	67
Exons	41245..41316, 41247..41315, 41390..41452, 41391..41453, 41528..41653, 41535..41651, 42849..42899, 42850..42900, 43330..43407, 43330..43398, 43331..43408, 43497..43580, 43498..43584		

Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o5.np	Method	AAT/NAP
Start	45439	End	49263
GI	4006878	Score	179
Exons	45439..45532, 46738..46809, 46968..47054, 47141..47424,		

	49195..49263		
GI Descrip.	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]		
Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o4.gp	Method	AAT/GAP
Start	46270	End	46586
GI	5056119	Score	601
Exons	46270..46586		
Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o2.tc	Method	TBLASTX:Cress
Start	46968	End	47335
GI	none	Score	52
Exons	46968..47060, 46975..47052, 47144..47335, 47154..47333		
Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o4.ts	Method	TBLASTX:Soybean
Start	47144	End	47342
GI	none	Score	85
Exons	47144..47341, 47154..47342		
Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o5.gp	Method	AAT/GAP
Start	48180	End	48561
GI	91923_1.R1084	Score	509
Exons	48180..48346, 48367..48561		
GI Descrip.	'4006878/emb|CAB16796.1| 7.0e-11 (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]'		
Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o6.np	Method	AAT/NAP
Start	48614	End	49263
GI	6907106	Score	218
Exons	48614..48877, 49148..49263		
GI Descrip.	(AP001129) EST AU068291(C12960) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		
Seq. No.	393	Seq. ID	OJ990423_01.9819.C23
Gene No.	732	Strand	-
Start	40452	End	49263
Name	OJ990423_01.9819.C23.o6.gp	Method	AAT/GAP
Start	48879	End	49162
GI	86158_1.R1084	Score	396
Exons	48879..49162		
GI Descrip.	'5295936/dbj|AB026295.2|AB026295 5.0e-42 Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence'		

Seq. No.	394	Seq. ID	OJ990423_01.9819.C25
Gene No.	733	Strand	+
Start	756	End	899
Name	OJ990423_01.9819.C25.o1.gs	Method	GENSCAN
Start	756	End	899
GI	none	Score	.77
Exons	756..899		

Seq. No.	395	Seq. ID	OJ990423_01.9819.C27
Gene No.	734	Strand	+
Start	13	End	53
Name	OJ990423_01.9819.C27.o1.gs	Method	GENSCAN
Start	13	End	53
GI	none	Score	.42
Exons	13..53		

Seq. No.	395	Seq. ID	OJ990423_01.9819.C27
Gene No.	735	Strand	-
Start	1	End	580
Name	OJ990423_01.9819.C27.o1.np	Method	AAT/NAP
Start	1	End	580
GI	6705984	Score	305
Exons	1..580		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	395	Seq. ID	OJ990423_01.9819.C27
Gene No.	735	Strand	-
Start	1	End	580
Name	OJ990423_01.9819.C27.o1.tw	Method	TBLASTX:Wheat
Start	69	End	542
GI	none	Score	158
Exons	69..377, 70..516, 399..542, 417..542		

Seq. No.	395	Seq. ID	OJ990423_01.9819.C27
Gene No.	735	Strand	-
Start	1	End	580
Name	OJ990423_01.9819.C27.o1.ts	Method	TBLASTX:Soybean
Start	147	End	536
GI	none	Score	88
Exons	147..368, 396..536		

Seq. No.	396	Seq. ID	OJ990423_01.9819.C29
Gene No.	736	Strand	-
Start	67	End	776
Name	OJ990423_01.9819.C29.o1.gp	Method	AAT/GAP
Start	67	End	776
GI	1523_1.R1084	Score	96
Exons	67..140, 747..776		
GI Descrip.	'4006881/emb|CAB16799.1| 4.0e-61 (Z99707) putative protein [Arabidopsis thaliana]'		

Seq. No.	397	Seq. ID	OJ990423_01.9819.C30
Gene No.	737	Strand	-
Start	169	End	476
Name	OJ990423_01.9819.C30.o1.tw	Method	TBLASTX:Wheat
Start	144	End	433
GI	none	Score	386

Exons	144..431, 146..433		
Seq. No.	397	Seq. ID	OJ990423_01.9819.C30
Gene No.	737	Strand	-
Start	169	End	476
Name	OJ990423_01.9819.C30.o1.gs	Method	GENSCAN
Start	169	End	373
GI	none	Score	.76
Exons	169..373		
Seq. No.	397	Seq. ID	OJ990423_01.9819.C30
Gene No.	737	Strand	-
Start	169	End	476
Name	OJ990423_01.9819.C30.o1.np	Method	AAT/NAP
Start	169	End	476
GI	4006878	Score	248
Exons	169..476		
GI Descrip.	(Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]		
Seq. No.	397	Seq. ID	OJ990423_01.9819.C30
Gene No.	737	Strand	-
Start	169	End	476
Name	OJ990423_01.9819.C30.o1.tc	Method	TBLASTX:Cress
Start	170	End	460
GI	none	Score	201
Exons	170..454, 171..458, 191..460		
Seq. No.	397	Seq. ID	OJ990423_01.9819.C30
Gene No.	737	Strand	-
Start	169	End	476
Name	OJ990423_01.9819.C30.o1.tm	Method	TBLASTX:Maize
Start	170	End	460
GI	none	Score	144
Exons	170..367, 174..362, 386..460, 387..455		
Seq. No.	397	Seq. ID	OJ990423_01.9819.C30
Gene No.	737	Strand	-
Start	169	End	476
Name	OJ990423_01.9819.C30.o1.ts	Method	TBLASTX:Soybean
Start	170	End	437
GI	none	Score	198
Exons	170..436, 171..437		
Seq. No.	398	Seq. ID	OJ990423_02.9819.C4
Gene No.	738	Strand	-
Start	1	End	455
Name	OJ990423_02.9819.C4.o1.np	Method	AAT/NAP
Start	1	End	455
GI	6539588	Score	250
Exons	1..44, 124..455		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		
Seq. No.	398	Seq. ID	OJ990423_02.9819.C4
Gene No.	738	Strand	-
Start	1	End	455
Name	OJ990423_02.9819.C4.o1.gs	Method	GENSCAN
Start	153	End	334

GI	none	Score	.64
Exons	153..334		

Seq. No.	399	Seq. ID	OJ990423_02.9819.C5
Gene No.	739	Strand	+
Start	697	End	1988
Name	OJ990423_02.9819.C5.o1.gs	Method	GENSCAN
Start	697	End	1988
GI	none	Score	.52
Exons	697..948, 1824..1988		

Seq. No.	399	Seq. ID	OJ990423_02.9819.C5
Gene No.	740	Strand	-
Start	1858	End	3303
Name	OJ990423_02.9819.C5.o1.np	Method	AAT/NAP
Start	1858	End	3303
GI	2119353	Score	69
Exons	1858..1884, 2732..2896, 3144..3303		
GI Descrip.	calmodulin - moss (Physcomitrella patens)		

Seq. No.	399	Seq. ID	OJ990423_02.9819.C5
Gene No.	741	Strand	-
Start	5809	End	7158
Name	OJ990423_02.9819.C5.o1.gp	Method	AAT/GAP
Start	4405	End	4496
GI	5867_1.R1084	Score	135
Exons	4405..4496		
GI Descrip.	'464986/sp|P35132|UBC9_ARATH 5.0e-58 UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis'		

Seq. No.	399	Seq. ID	OJ990423_02.9819.C5
Gene No.	741	Strand	-
Start	5809	End	7158
Name	OJ990423_02.9819.C5.o2.gs	Method	GENSCAN
Start	5809	End	6099
GI	none	Score	.49
Exons	5809..6099		

Seq. No.	399	Seq. ID	OJ990423_02.9819.C5
Gene No.	741	Strand	-
Start	5809	End	7158
Name	OJ990423_02.9819.C5.o2.np	Method	AAT/NAP
Start	5831	End	7158
GI	6705984	Score	388
Exons	5831..6616, 6876..7158		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	400	Seq. ID	OJ990423_02.9819.C6
Gene No.	742	Strand	-
Start	1669	End	1950
Name	OJ990423_02.9819.C6.o1.np	Method	AAT/NAP
Start	1669	End	1950

GI	6539588	Score	155
Exons	1669..1950		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	400	Seq. ID	OJ990423_02.9819.C6
Gene No.	743	Strand	-
Start	3842	End	3954
Name	OJ990423_02.9819.C6.o1.gp	Method	AAT/GAP
Start	3842	End	3954
GI	69953_1.R1084	Score	111
Exons	3842..3954		
GI Descrip.	'5295936/dbj|AB026295.2|AB026295 7.0e-34 Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence'		

Seq. No.	401	Seq. ID	OJ990423_02.9819.C7
Gene No.	744	Strand	-
Start	884	End	12157
Name	OJ990423_02.9819.C7.o1.gs	Method	GENSCAN
Start	884	End	11179
GI	none	Score	.45
Exons	884..999, 2513..5689, 9353..9403, 9862..9978, 10558..11179		

Seq. No.	401	Seq. ID	OJ990423_02.9819.C7
Gene No.	744	Strand	-
Start	884	End	12157
Name	OJ990423_02.9819.C7.o2.np	Method	AAT/NAP
Start	2670	End	5153
GI	2792220	Score	652
Exons	2670..2811, 3514..4969, 5009..5153		
GI Descrip.	(AF032688) NBS-LRR type resistance protein [Oryza sativa]		

Seq. No.	401	Seq. ID	OJ990423_02.9819.C7
Gene No.	744	Strand	-
Start	884	End	12157
Name	OJ990423_02.9819.C7.o1.ts	Method	TBLASTX:Soybean
Start	3975	End	4412
GI	none	Score	67
Exons	3975..4136, 4143..4412, 4149..4337		

Seq. No.	401	Seq. ID	OJ990423_02.9819.C7
Gene No.	744	Strand	-
Start	884	End	12157
Name	OJ990423_02.9819.C7.o1.tm	Method	TBLASTX:Maize
Start	4127	End	4610
GI	none	Score	116
Exons	4127..4384, 4128..4448, 4129..4437, 4557..4610		

Seq. No.	401	Seq. ID	OJ990423_02.9819.C7
Gene No.	744	Strand	-
Start	884	End	12157
Name	OJ990423_02.9819.C7.o3.np	Method	AAT/NAP
Start	9523	End	12157
GI	5091601	Score	81
Exons	9523..9562, 10821..11034, 12131..12157		
GI Descrip.	(AC007858) This gene is a member of PF|00501 AMP-binding enzymes. [Oryza sativa]		

Seq. No.	402	Seq. ID	OJ990423_02.9819.C9
Gene No.	745	Strand	+
Start	51	End	453
Name	OJ990423_02.9819.C9.o1.gs	Method	GENSCAN
Start	51	End	453
GI	none	Score	.8
Exons	51..165, 386..453		

Seq. No.	403	Seq. ID	OJ990423_02.9819.C10
Gene No.	746	Strand	-
Start	1	End	1262
Name	OJ990423_02.9819.C10.o1.np	Method	AAT/NAP
Start	1	End	1262
GI	6705984	Score	157
Exons	1..125, 385..607, 1207..1262		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	403	Seq. ID	OJ990423_02.9819.C10
Gene No.	746	Strand	-
Start	1	End	1262
Name	OJ990423_02.9819.C10.o1.gs	Method	GENSCAN
Start	543	End	905
GI	none	Score	.84
Exons	543..681, 715..905		

Seq. No.	404	Seq. ID	OJ990423_02.9819.C11
Gene No.	747	Strand	+
Start	454	End	1240
Name	OJ990423_02.9819.C11.o1.np	Method	AAT/NAP
Start	454	End	1240
GI	6539588	Score	248
Exons	454..759, 1145..1240		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	404	Seq. ID	OJ990423_02.9819.C11
Gene No.	747	Strand	+
Start	454	End	1240
Name	OJ990423_02.9819.C11.o1.gs	Method	GENSCAN
Start	570	End	1119
GI	none	Score	.72
Exons	570..751, 893..1119		

Seq. No.	405	Seq. ID	OJ990423_02.9819.C14
Gene No.	748	Strand	-
Start	547	End	690
Name	OJ990423_02.9819.C14.o1.gs	Method	GENSCAN
Start	547	End	690
GI	none	Score	.41
Exons	547..690		

Seq. No.	406	Seq. ID	OJ990423_02.9819.C15
Gene No.	749	Strand	-
Start	26	End	80
Name	OJ990423_02.9819.C15.o1.gs	Method	GENSCAN
Start	26	End	80
GI	none	Score	.55
Exons	26..80		

Seq. No.	407	Seq. ID	OJ990423_02.9819.C16
Gene No.	750	Strand	-
Start	54	End	208
Name	OJ990423_02.9819.C16.o1.gs	Method	GENSCAN
Start	54	End	208
GI	none	Score	.61
Exons	54..208		

Seq. No.	408	Seq. ID	OJ990423_02.9819.C17
Gene No.	751	Strand	+
Start	152	End	342
Name	OJ990423_02.9819.C17.o1.gs	Method	GENSCAN
Start	152	End	342
GI	none	Score	.97
Exons	152..342		

Seq. No.	408	Seq. ID	OJ990423_02.9819.C17
Gene No.	752	Strand	+
Start	456	End	628
Name	OJ990423_02.9819.C17.o1.np	Method	AAT/NAP
Start	456	End	628
GI	6705984	Score	82
Exons	456..628		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	409	Seq. ID	OJ990423_02.9819.C18
Gene No.	753	Strand	+
Start	57	End	833
Name	OJ990423_02.9819.C18.o1.np	Method	AAT/NAP
Start	57	End	833
GI	4379369	Score	70
Exons	57..132, 325..409, 657..833		
GI Descrip.	(X90560) Calmodulin [Cloning vector pBluescript]		

Seq. No.	410	Seq. ID	OJ990423_02.9819.C19
Gene No.	754	Strand	+
Start	17	End	822
Name	OJ990423_02.9819.C19.o1.np	Method	AAT/NAP
Start	17	End	822
GI	6539588	Score	164
Exons	17..321, 760..822		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	410	Seq. ID	OJ990423_02.9819.C19
Gene No.	754	Strand	+
Start	17	End	822
Name	OJ990423_02.9819.C19.o1.gs	Method	GENSCAN
Start	137	End	689
GI	none	Score	.79
Exons	137..321, 463..689		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o1.gp	Method	AAT/GAP
Start	1	End	2685

GI	342_1.R1084	Score	4353
Exons	1..2685		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o1.np	Method	AAT/NAP
Start	1	End	1876
GI	6742729	Score	2630
Exons	1..1876		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o1.gs	Method	GENSCAN
Start	180	End	2689
GI	none	Score	.64
Exons	180..1540, 1675..2689		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o1.tw	Method	TBLASTX:Wheat
Start	199	End	750
GI	none	Score	398
Exons	199..249, 249..311, 333..749, 334..750		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o2.tm	Method	TBLASTX:Maize
Start	393	End	707
GI	none	Score	68
Exons	393..623, 393..707, 421..696		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o3.tw	Method	TBLASTX:Wheat
Start	751	End	1161
GI	none	Score	81
Exons	751..837, 753..842, 753..836, 870..1088, 910..1092, 1098..1160, 1111..1161		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o2.ts	Method	TBLASTX:Soybean
Start	1194	End	1436
GI	none	Score	216
Exons	1194..1436		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-

Start	1	End	3830
Name	OJ990423_02.9819.C21.o1.tm	Method	TBLASTX:Maize
Start	1266	End	1723
GI	none	Score	52
Exons	1266..1460, 1470..1589, 1470..1595, 1589..1711, 1595..1723		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o2.tw	Method	TBLASTX:Wheat
Start	1300	End	1768
GI	none	Score	173
Exons	1300..1506, 1300..1509, 1305..1529, 1509..1595, 1510..1596, 1610..1714, 1614..1703, 1715..1768, 1716..1760		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o1.tc	Method	TBLASTX:Cress
Start	1589	End	1904
GI	none	Score	74
Exons	1589..1897, 1617..1712, 1752..1904		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o3.gp	Method	AAT/GAP
Start	1616	End	3137
GI	2310235	Score	304
Exons	1616..1673, 2550..2689, 3100..3137		
GI Descrip.	5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o1.ts	Method	TBLASTX:Soybean
Start	1637	End	2066
GI	none	Score	121
Exons	1637..1933, 1655..1879, 1928..1990, 1983..2066, 1991..2065		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o4.tw	Method	TBLASTX:Wheat
Start	1987	End	2338
GI	none	Score	187
Exons	1987..2238, 1997..2248, 1998..2240, 2231..2338		

Seq. No.	411	Seq. ID	OJ990423_02.9819.C21
Gene No.	755	Strand	-
Start	1	End	3830
Name	OJ990423_02.9819.C21.o2.np	Method	AAT/NAP
Start	2360	End	3830
GI	5852182	Score	432
Exons	2360..2689, 3759..3830		
GI Descrip.	(AL117265) zhb0012.1 [Oryza sativa]		

Seq. No.	412	Seq. ID	OJ990423_02.9819.C22
Gene No.	756	Strand	-
Start	257	End	718
Name	OJ990423_02.9819.C22.o1.gs	Method	GENSCAN
Start	257	End	718
GI	none	Score	.9
Exons	257..329, 414..524, 621..718		

Seq. No.	413	Seq. ID	OJ990423_02.9819.C24
Gene No.	757	Strand	+
Start	544	End	5724
Name	OJ990423_02.9819.C24.o1.gs	Method	GENSCAN
Start	544	End	5411
GI	none	Score	.43
Exons	544..735, 821..1004, 1432..1544, 1968..2149, 2291..2701, 2939..3247, 3332..3484, 3672..4740, 4749..5411		

Seq. No.	413	Seq. ID	OJ990423_02.9819.C24
Gene No.	757	Strand	+
Start	544	End	5724
Name	OJ990423_02.9819.C24.o2.np	Method	AAT/NAP
Start	1852	End	3528
GI	6539588	Score	258
Exons	1852..2171, 3503..3528		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	413	Seq. ID	OJ990423_02.9819.C24
Gene No.	757	Strand	+
Start	544	End	5724
Name	OJ990423_02.9819.C24.o1.tw	Method	TBLASTX:Wheat
Start	5172	End	5724
GI	none	Score	101
Exons	5172..5384, 5440..5724, 5548..5718, 5556..5723		

Seq. No.	413	Seq. ID	OJ990423_02.9819.C24
Gene No.	757	Strand	+
Start	544	End	5724
Name	OJ990423_02.9819.C24.o1.tm	Method	TBLASTX:Maize
Start	5298	End	5724
GI	none	Score	46
Exons	5298..5384, 5395..5724, 5400..5480, 5523..5723		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	758	Strand	+
Start	1	End	1714
Name	OJ990423_02.9819.C25.o1.np	Method	AAT/NAP
Start	1	End	1711
GI	6630685	Score	1682
Exons	1..1711		
GI Descrip.	(AP000969) Similar to copia-type pol polyprotein. (AF105716) [Oryza sativa]		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	758	Strand	+
Start	1	End	1714
Name	OJ990423_02.9819.C25.o1.gs	Method	GENSCAN

Start	231	End	1714
GI	none	Score	.73
Exons	231..1053, 1134..1714		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	759	Strand	+
Start	3322	End	5547
Name	OJ990423_02.9819.C25.o2.gs	Method	GENSCAN
Start	3322	End	5547
GI	none	Score	.57
Exons	3322..3402, 3734..3915, 3987..4133, 4565..4790, 4827..5061, 5441..5547		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	759	Strand	+
Start	3322	End	5547
Name	OJ990423_02.9819.C25.o2.np	Method	AAT/NAP
Start	3613	End	5294
GI	6539588	Score	248
Exons	3613..3946, 5268..5294		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	760	Strand	+
Start	6350	End	18824
Name	OJ990423_02.9819.C25.o3.gs	Method	GENSCAN
Start	6350	End	8136
GI	none	Score	.53
Exons	6350..6391, 6881..7082, 7135..7221, 7752..7809, 7842..8136		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	760	Strand	+
Start	6350	End	18824
Name	OJ990423_02.9819.C25.o4.np	Method	AAT/NAP
Start	7852	End	18824
GI	5922631	Score	3082
Exons	7852..7976, 11609..11868, 12130..12322, 12350..12922, 12965..13124, 13251..14178, 16263..17126, 18762..18824		
GI Descrip.	(AP000492) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] gi|6016864|dbj|BAA85207.1| (AP000570) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativ		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	760	Strand	+
Start	6350	End	18824
Name	OJ990423_02.9819.C25.o4.gs	Method	GENSCAN
Start	10323	End	14186
GI	none	Score	.85
Exons	10323..10366, 10741..10758, 11645..11893, 11955..12054, 12099..12229, 12305..12623, 12683..13124, 13166..13281, 13337..13562, 13573..14186		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25

Gene No.	760	Strand	+
Start	6350	End	18824
Name	OJ990423_02.9819.C25.o5.gs	Method	GENSCAN
Start	16202	End	17121
GI	none	Score	.45
Exons	16202..16480, 16673..16762, 16864..17121		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	761	Strand	-
Start	1	End	4638
Name	OJ990423_02.9819.C25.o3.np	Method	AAT/NAP
Start	1	End	4638
GI	6705984	Score	233
Exons	1..27, 4143..4638		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o1.ts	Method	TBLASTX:Soybean
Start	72	End	685
GI	5509260	Score	659
Exons	72..122, 135..371, 144..680, 161..382, 428..685		
GI Descrip.	-		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o1.tw	Method	TBLASTX:Wheat
Start	200	End	677
GI	none	Score	83
Exons	200..289, 201..290, 324..671, 332..382, 418..450, 469..672, 491..661, 498..677		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o1.tc	Method	TBLASTX:Cress
Start	306	End	566
GI	none	Score	235
Exons	306..566		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o2.tm	Method	TBLASTX:Maize
Start	347	End	785
GI	none	Score	508
Exons	347..721, 348..785, 501..785		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o4.ts	Method	TBLASTX:Soybean
Start	822	End	1055
GI	none	Score	185
Exons	822..1055		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o5.tm	Method	TBLASTX:Maize
Start	854	End	1055
GI	none	Score	213
Exons	854..991, 855..1055, 867..1049		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o1.tm	Method	TBLASTX:Maize
Start	1057	End	1693
GI	none	Score	695
Exons	1057..1542, 1058..1693, 1346..1678, 1624..1683		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o2.ts	Method	TBLASTX:Soybean
Start	1058	End	1723
GI	none	Score	280
Exons	1058..1444, 1246..1401, 1463..1723		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o5.tw	Method	TBLASTX:Wheat
Start	1193	End	1648
GI	none	Score	119
Exons	1193..1453, 1472..1648, 1472..1648		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o2.tc	Method	TBLASTX:Cress
Start	1328	End	1693
GI	none	Score	88
Exons	1328..1459, 1448..1693		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o6.tw	Method	TBLASTX:Wheat
Start	12533	End	12934
GI	none	Score	87
Exons	12533..12637, 12534..12641, 12656..12934		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o3.tw	Method	TBLASTX:Wheat
Start	13519	End	14379
GI	none	Score	41
Exons	13519..13569, 13572..13691, 13581..13679, 13737..13973, 13739..13975, 14109..14270, 14111..14275, 14314..14379		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o4.tw	Method	TBLASTX:Wheat
Start	15842	End	16073
GI	none	Score	270
Exons	15842..16051, 15873..16070, 15876..16073		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o4.tm	Method	TBLASTX:Maize
Start	15875	End	16159
GI	none	Score	239
Exons	15875..16072, 15876..16073, 16076..16159		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o3.tm	Method	TBLASTX:Maize
Start	16187	End	16570
GI	none	Score	317
Exons	16187..16570, 16195..16551		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o2.tw	Method	TBLASTX:Wheat
Start	16244	End	16668
GI	none	Score	431
Exons	16244..16663, 16249..16668		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o3.ts	Method	TBLASTX:Soybean
Start	16292	End	16690
GI	none	Score	265
Exons	16292..16690, 16339..16482		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o7.tw	Method	TBLASTX:Wheat
Start	16835	End	17106
GI	none	Score	79
Exons	16835..16915, 16906..17025, 17056..17106		

Seq. No.	414	Seq. ID	OJ990423_02.9819.C25
Gene No.	762	Strand	-
Start	17905	End	18538
Name	OJ990423_02.9819.C25.o6.gs	Method	GENSCAN
Start	17905	End	18538
GI	none	Score	.77
Exons	17905..18012, 18339..18538		

Seq. No.	415	Seq. ID	OJ990423_02.9819.C26
Gene No.	763	Strand	+
Start	156	End	836
Name	OJ990423_02.9819.C26.o1.gs	Method	GENSCAN
Start	156	End	836
GI	none	Score	.65
Exons	156..202, 284..305, 555..596, 801..836		

Seq. No.	415	Seq. ID	OJ990423_02.9819.C26
Gene No.	764	Strand	+
Start	6229	End	6287
Name	OJ990423_02.9819.C26.o1.gp	Method	AAT/GAP
Start	6229	End	6287
GI	2312838	Score	66
Exons	6229..6287		
GI Descrip.	1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence		

Seq. No.	415	Seq. ID	OJ990423_02.9819.C26
Gene No.	765	Strand	-
Start	3587	End	3821
Name	OJ990423_02.9819.C26.o1.np	Method	AAT/NAP
Start	3587	End	3821
GI	6016874	Score	230
Exons	3587..3821		
GI Descrip.	(AP000570) ESTs C19143(E10020),D25076(R3116) correspond to a region of the predicted gene.; Similar to putative AC9 transposase. (P03010) [Oryza sativa]		

Seq. No.	415	Seq. ID	OJ990423_02.9819.C26
Gene No.	766	Strand	-
Start	5796	End	8855
Name	OJ990423_02.9819.C26.o2.np	Method	AAT/NAP
Start	5796	End	8855
GI	2258319	Score	69
Exons	5796..5946, 6032..6148, 6466..6573, 8825..8855		
GI Descrip.	(AF004880) resistance complex protein I2C-3 [Lycopersicon esculentum]		

Seq. No.	415	Seq. ID	OJ990423_02.9819.C26
Gene No.	766	Strand	-
Start	5796	End	8855
Name	OJ990423_02.9819.C26.o3.np	Method	AAT/NAP
Start	5821	End	8476
GI	2792220	Score	604
Exons	5821..6012, 6862..7065, 7094..8292, 8332..8476		
GI Descrip.	(AF032688) NBS-LRR type resistance protein [Oryza sativa]		

Seq. No.	415	Seq. ID	OJ990423_02.9819.C26
Gene No.	766	Strand	-
Start	5796	End	8855
Name	OJ990423_02.9819.C26.o1.ts	Method	TBLASTX:Soybean
Start	7301	End	7738
GI	none	Score	213
Exons	7301..7462, 7469..7738		

Seq. No.	415	Seq. ID	OJ990423_02.9819.C26

Gene No.	766	Strand	-
Start	5796	End	8855
Name	OJ990423_02.9819.C26.o1.tm	Method	TBLASTX:Maize
Start	7454	End	7930
GI	none	Score	123
Exons	7454..7762, 7455..7751, 7862..7930		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	767	Strand	+
Start	1395	End	4824
Name	OJ990423_02.9819.C27.o1.gs	Method	GENSCAN
Start	1395	End	2676
GI	none	Score	.89
Exons	1395..1458, 1603..1804, 2004..2084, 2403..2676		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	767	Strand	+
Start	1395	End	4824
Name	OJ990423_02.9819.C27.o1.np	Method	AAT/NAP
Start	1424	End	2680
GI	6721505	Score	78
Exons	1424..1482, 2557..2680		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	767	Strand	+
Start	1395	End	4824
Name	OJ990423_02.9819.C27.o2.np	Method	AAT/NAP
Start	2373	End	4821
GI	2088651	Score	175
Exons	2373..2477, 4535..4821		
GI Descrip.	(AF002109) putative anthocyanin 5-aromatic acyltransferase [Arabidopsis thaliana]		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	767	Strand	+
Start	1395	End	4824
Name	OJ990423_02.9819.C27.o2.gs	Method	GENSCAN
Start	4342	End	4824
GI	none	Score	.6
Exons	4342..4824		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	768	Strand	+
Start	7475	End	7619
Name	OJ990423_02.9819.C27.o1.gp	Method	AAT/GAP
Start	7475	End	7619
GI	21474_1.R1084	Score	247
Exons	7475..7619		
GI Descrip.	'3894159 2.0e-10 (AC005312) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	769	Strand	-
Start	7949	End	11661
Name	OJ990423_02.9819.C27.o1.ts	Method	TBLASTX:Soybean
Start	4587	End	4815

GI	none	Score	211
Exons	4587..4763, 4588..4815		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	769	Strand	-
Start	7949	End	11661
Name	OJ990423_02.9819.C27.o1.tm	Method	TBLASTX:Maize
Start	4632	End	4821
GI	none	Score	187
Exons	4632..4763, 4633..4821, 4684..4821		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	769	Strand	-
Start	7949	End	11661
Name	OJ990423_02.9819.C27.o3.np	Method	AAT/NAP
Start	5103	End	11661
GI	4680204	Score	1056
Exons	5103..5143, 8008..8104, 8455..8674, 8771..8944, 9054..10150, 10225..11661		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	769	Strand	-
Start	7949	End	11661
Name	OJ990423_02.9819.C27.o3.gs	Method	GENSCAN
Start	7949	End	11646
GI	none	Score	.69
Exons	7949..8134, 8214..8312, 8407..8479, 8564..8674, 8771..8944, 9054..10150, 10225..11646		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	769	Strand	-
Start	7949	End	11661
Name	OJ990423_02.9819.C27.o2.tw	Method	TBLASTX:Wheat
Start	8605	End	9127
GI	none	Score	68
Exons	8605..8676, 8776..8958, 8783..8908, 9047..9127		

Seq. No.	416	Seq. ID	OJ990423_02.9819.C27
Gene No.	769	Strand	-
Start	7949	End	11661
Name	OJ990423_02.9819.C27.o1.tw	Method	TBLASTX:Wheat
Start	10615	End	11016
GI	none	Score	84
Exons	10615..10785, 10748..10915, 10780..11016, 10867..11016		

Seq. No.	417	Seq. ID	OJ990423_02.9819.C28
Gene No.	770	Strand	-
Start	39	End	1304
Name	OJ990423_02.9819.C28.o1.gp	Method	AAT/GAP
Start	39	End	1304
GI	342_1.R1084	Score	1716
Exons	39..564, 674..778, 897..1304		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	417	Seq. ID	OJ990423_02.9819.C28

Gene No.	770	Strand	-
Start	39	End	1304
Name	OJ990423_02.9819.C28.o3.gp	Method	AAT/GAP
Start	227	End	1304
GI	342_1.R1084	Score	1447
Exons	227..564, 674..778, 897..1304		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	417	Seq. ID	OJ990423_02.9819.C28
Gene No.	770	Strand	-
Start	39	End	1304
Name	OJ990423_02.9819.C28.o1.gs	Method	GENSCAN
Start	981	End	1250
GI	none	Score	.93
Exons	981..1250		

Seq. No.	417	Seq. ID	OJ990423_02.9819.C28
Gene No.	770	Strand	-
Start	39	End	1304
Name	OJ990423_02.9819.C28.o1.np	Method	AAT/NAP
Start	1002	End	1304
GI	4680203	Score	216
Exons	1002..1304		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	418	Seq. ID	OJ990423_02.9819.C29
Gene No.	771	Strand	-
Start	1	End	905
Name	OJ990423_02.9819.C29.o1.gp	Method	AAT/GAP
Start	1	End	822
GI	342_1.R1084	Score	1422
Exons	1..822		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	418	Seq. ID	OJ990423_02.9819.C29
Gene No.	771	Strand	-
Start	1	End	905
Name	OJ990423_02.9819.C29.o1.tw	Method	TBLASTX:Wheat
Start	27	End	822
GI	none	Score	43
Exons	27..71, 32..67, 66..818, 81..398, 82..813, 259..822		

Seq. No.	418	Seq. ID	OJ990423_02.9819.C29
Gene No.	771	Strand	-
Start	1	End	905
Name	OJ990423_02.9819.C29.o1.np	Method	AAT/NAP
Start	151	End	905
GI	6742729	Score	1040
Exons	151..905		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	418	Seq. ID	OJ990423_02.9819.C29
Gene No.	771	Strand	-
Start	1	End	905
Name	OJ990423_02.9819.C29.o1.tc	Method	TBLASTX:Cress

Start	249	End	700
GI	none	Score	188
Exons	249..686, 249..692, 253..696, 259..696, 518..700		

Seq. No.	418	Seq. ID	OJ990423_02.9819.C29
Gene No.	771	Strand	-
Start	1	End	905
Name	OJ990423_02.9819.C29.o1.tm	Method	TBLASTX:Maize
Start	627	End	818
GI	none	Score	91
Exons	627..818, 655..813		

Seq. No.	419	Seq. ID	OJ990423_02.9819.C30
Gene No.	772	Strand	+
Start	180	End	822
Name	OJ990423_02.9819.C30.o1.gs	Method	GENSCAN
Start	180	End	822
GI	none	Score	.87
Exons	180..290, 375..447, 542..640, 720..822		

Seq. No.	420	Seq. ID	OJ990323_32.9917.C1
Gene No.	773	Strand	-
Start	1	End	505
Name	OJ990323_32.9917.C1.o1.np	Method	AAT/NAP
Start	1	End	505
GI	5902445	Score	461
Exons	1..505		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	420	Seq. ID	OJ990323_32.9917.C1
Gene No.	773	Strand	-
Start	1	End	505
Name	OJ990323_32.9917.C1.o1.gs	Method	GENSCAN
Start	9	End	435
GI	none	Score	.63
Exons	9..435		

Seq. No.	420	Seq. ID	OJ990323_32.9917.C1
Gene No.	773	Strand	-
Start	1	End	505
Name	OJ990323_32.9917.C1.o1.tw	Method	TBLASTX:Wheat
Start	107	End	419
GI	none	Score	67
Exons	107..319, 114..311, 197..316, 323..418, 324..419		

Seq. No.	421	Seq. ID	OJ990323_32.9917.C2
Gene No.	774	Strand	-
Start	199	End	291
Name	OJ990323_32.9917.C2.o1.gs	Method	GENSCAN
Start	199	End	291
GI	none	Score	.42
Exons	199..291		

Seq. No.	422	Seq. ID	OJ990323_32.9917.C3
Gene No.	775	Strand	+
Start	110	End	209
Name	OJ990323_32.9917.C3.o1.gs	Method	GENSCAN

Start	110	End	209
GI	none	Score	.78
Exons	110..209		

Seq. No.	423	Seq. ID	OJ990323_32.9917.C5
Gene No.	776	Strand	+
Start	266	End	347
Name	OJ990323_32.9917.C5.o1.gs	Method	GENSCAN
Start	266	End	347
GI	none	Score	.66
Exons	266..347		

Seq. No.	424	Seq. ID	OJ990323_32.9917.C7
Gene No.	777	Strand	-
Start	645	End	1033
Name	OJ990323_32.9917.C7.o1.gs	Method	GENSCAN
Start	645	End	1033
GI	none	Score	.9
Exons	645..749, 911..1033		

Seq. No.	425	Seq. ID	OJ990323_32.9917.C8
Gene No.	778	Strand	-
Start	484	End	1797
Name	OJ990323_32.9917.C8.o1.gs	Method	GENSCAN
Start	484	End	1797
GI	none	Score	.58
Exons	484..552, 1227..1417, 1572..1797		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	779	Strand	+
Start	698	End	4886
Name	OJ990323_32.9917.C9.o1.gs	Method	GENSCAN
Start	698	End	4886
GI	none	Score	.73
Exons	698..890, 985..1226, 1238..1780, 2208..2312, 2405..2587, 2625..2750, 2975..3077, 3153..3233, 3742..3895, 4252..4396, 4510..4615, 4738..4886		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	779	Strand	+
Start	698	End	4886
Name	OJ990323_32.9917.C9.o1.np	Method	AAT/NAP
Start	1417	End	2880
GI	2642433	Score	100
Exons	1417..1692, 2859..2880		
GI Descrip.	(AC002391) putative receptor-like protein kinase [Arabidopsis thaliana]		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	780	Strand	+
Start	5528	End	6418
Name	OJ990323_32.9917.C9.o2.gs	Method	GENSCAN
Start	5528	End	6418
GI	none	Score	.84
Exons	5528..5548, 5912..6017, 6037..6183, 6288..6418		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9

Gene No.	781	Strand	+
Start	14999	End	18511
Name	OJ990323_32.9917.C9.o1.gp	Method	AAT/GAP
Start	14999	End	16085
GI	2311182	Score	627
Exons	14999..15247, 15955..16085		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	781	Strand	+
Start	14999	End	18511
Name	OJ990323_32.9917.C9.o4.gs	Method	GENSCAN
Start	15958	End	18511
GI	none	Score	.79
Exons	15958..16323, 16681..17261, 17551..18511		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	781	Strand	+
Start	14999	End	18511
Name	OJ990323_32.9917.C9.o4.np	Method	AAT/NAP
Start	15958	End	18466
GI	2864618	Score	1515
Exons	15958..16225, 16280..16323, 16421..16513, 16788..17247, 17537..18466		
GI Descrip.	(AL021811) putative protein [Arabidopsis thaliana]		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	781	Strand	+
Start	14999	End	18511
Name	OJ990323_32.9917.C9.o2.gp	Method	AAT/GAP
Start	16847	End	17752
GI	LIB3434-047-P1-K1-E9	Score	1038
Exons	16847..17261, 17605..17752		
GI Descrip.	'2864618/emb|CAA16965| 2.0e-55 (AL021811) putative protein [Arabidopsis thaliana]'		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	782	Strand	+
Start	19346	End	20843
Name	OJ990323_32.9917.C9.o5.np	Method	AAT/NAP
Start	19346	End	20843
GI	128855	Score	168
Exons	19346..19367, 20606..20843		
GI Descrip.	NADH-PLASTOQUINONE OXIDOREDUCTASE SUBUNIT J (ORF 159) gi|1363530|pir||S58555 ndhJ protein - maize chloroplast gi|12428|emb|CAA35483| (X17438) ORF 159 (AA 1 - 159) [Zea mays] gi|902225|emb|CAA60289| (X86563) ndhJ [Zea mays]		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	783	Strand	-
Start	7525	End	15614
Name	OJ990323_32.9917.C9.o3.gs	Method	GENSCAN
Start	7525	End	15614
GI	none	Score	.57
Exons	7525..7666, 8195..8363, 8380..8480, 9058..9331, 9700..9798, 11613..11647, 11848..11945, 11988..12275, 13524..13647, 15145..15270, 15520..15614		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o6.ts	Method	TBLASTX:Soybean
Start	2310	End	3863
GI	none	Score	91
Exons	2310..2387, 2702..2737, 2853..2900, 2946..3071, 2953..3078, 2963..3079, 3181..3213, 3182..3259, 3738..3809, 3813..3863		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o4.tm	Method	TBLASTX:Maize
Start	2529	End	4611
GI	none	Score	73
Exons	2529..2591, 2669..2737, 2670..2738, 2675..2740, 2832..2897, 2841..2897, 2849..2905, 2971..3078, 2972..3079, 2972..3079, 2973..3080, 3181..3237, 3182..3280, 3738..3893, 3739..3894, 3740..3928, 4253..4399, 4258..4398, 4259..4399, 4506..4604, 4509..4604, 4510..4611		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o3.tm	Method	TBLASTX:Maize
Start	15952	End	16278
GI	none	Score	464
Exons	15952..16278, 15954..16277		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o3.ts	Method	TBLASTX:Soybean
Start	15979	End	16260
GI	none	Score	299
Exons	15979..16260, 16038..16253		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o2.tm	Method	TBLASTX:Maize
Start	16795	End	17124
GI	none	Score	533
Exons	16795..17124, 16796..16987, 16797..17105, 16837..17124		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o2.ts	Method	TBLASTX:Soybean
Start	16819	End	17293
GI	none	Score	44
Exons	16819..16851, 16858..16956, 16957..17262, 16963..17262, 16968..17264, 17240..17293		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009

Name	OJ990323_32.9917.C9.o1.ts	Method	TBLASTX:Soybean
Start	17633	End	18165
GI	none	Score	141
Exons	17633..17767, 17665..17766, 17773..18165, 17774..18160		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o1.tm	Method	TBLASTX:Maize
Start	17663	End	18511
GI	none	Score	1109
Exons	17663..18400, 17663..18391, 17665..18399, 18375..18437, 18436..18510, 18452..18511, 18452..18511		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o1.tc	Method	TBLASTX:Cress
Start	18175	End	18376
GI	none	Score	220
Exons	18175..18348, 18185..18376		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o5.ts	Method	TBLASTX:Soybean
Start	18190	End	18361
GI	none	Score	196
Exons	18190..18348, 18191..18361		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o5.gs	Method	GENSCAN
Start	18641	End	22009
GI	none	Score	.64
Exons	18641..18858, 18921..18980, 19168..19335, 19364..19520, 19576..19667, 19759..19892, 20317..20500, 20952..21027, 21117..21266, 21480..21550, 21859..22009		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o4.ts	Method	TBLASTX:Soybean
Start	19606	End	19921
GI	none	Score	78
Exons	19606..19671, 19606..19671, 19760..19921, 19761..19919		

Seq. No.	426	Seq. ID	OJ990323_32.9917.C9
Gene No.	784	Strand	-
Start	18641	End	22009
Name	OJ990323_32.9917.C9.o5.tm	Method	TBLASTX:Maize
Start	20602	End	20775
GI	none	Score	99
Exons	20602..20688, 20608..20688, 20610..20693, 20610..20693, 20689..20775, 20692..20760		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o1.np	Method	AAT/NAP
Start	338	End	4913
GI	4388818	Score	2658
Exons	338..463, 1068..4913		
GI Descrip.	(AC006528) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o4.tw	Method	TBLASTX:Wheat
Start	1260	End	1682
GI	none	Score	176
Exons	1260..1409, 1277..1402, 1389..1499, 1406..1498, 1491..1553, 1502..1543, 1620..1682, 1637..1672		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o1.gp	Method	AAT/GAP
Start	2224	End	2660
GI	2428449	Score	818
Exons	2224..2660		
GI Descrip.	4388818/gb|AAD19773| 3.0e-40 (AC006528) putative pol polyprotein with a Zn-finger CCHC type domain (prosite:QDOC50158) and a DDE integrase signature motif [Arabidopsis thaliana]		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o4.tm	Method	TBLASTX:Maize
Start	2373	End	2858
GI	none	Score	337
Exons	2373..2858, 2562..2726, 2567..2857		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o3.tw	Method	TBLASTX:Wheat
Start	2387	End	3041
GI	none	Score	332
Exons	2387..2797, 2388..2837, 2934..3041		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o2.ts	Method	TBLASTX:Soybean
Start	2607	End	3059
GI	none	Score	287
Exons	2607..2936, 2636..2854, 2922..3059		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913

Name	OJ990323_32.9917.C10.o1.tc	Method	TBLASTX:Cress
Start	2625	End	3056
GI	none	Score	187
Exons	2625..2918, 2933..3049, 2934..3056		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o1.tw	Method	TBLASTX:Wheat
Start	3271	End	3707
GI	none	Score	633
Exons	3271..3459, 3273..3707, 3273..3707		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o3.tm	Method	TBLASTX:Maize
Start	3546	End	3977
GI	none	Score	349
Exons	3546..3647, 3549..3977, 3584..3844		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o2.tc	Method	TBLASTX:Cress
Start	3549	End	3755
GI	none	Score	204
Exons	3549..3755, 3549..3755		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o1.ts	Method	TBLASTX:Soybean
Start	3573	End	3962
GI	none	Score	387
Exons	3573..3962, 3593..3868, 3594..3917, 3667..3924		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o2.gp	Method	AAT/GAP
Start	3708	End	3950
GI	1621494	Score	446
Exons	3708..3950		
GI Descrip.	1621495/dbj|BAA12903| 4.0e-35 (D85877) reverse transcriptase [Oryza sativa]		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o2.tw	Method	TBLASTX:Wheat
Start	3708	End	4331
GI	none	Score	169
Exons	3708..3860, 3897..4331, 3953..4087, 4026..4181, 4148..4312		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+

Start	338	End	4913
Name	OJ990323_32.9917.C10.o2.tm	Method	TBLASTX:Maize
Start	3980	End	4426
GI	none	Score	125
Exons	3980..4072, 3981..4139, 4115..4426, 4116..4421, 4175..4423		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o3.tc	Method	TBLASTX:Cress
Start	4428	End	4907
GI	none	Score	78
Exons	4428..4532, 4533..4679, 4695..4907		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o5.tw	Method	TBLASTX:Wheat
Start	4445	End	4880
GI	none	Score	168
Exons	4445..4636, 4458..4661, 4679..4756, 4680..4880, 4689..4820		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o1.tm	Method	TBLASTX:Maize
Start	4482	End	4907
GI	none	Score	556
Exons	4482..4907, 4484..4906, 4503..4907		

Seq. No.	427	Seq. ID	OJ990323_32.9917.C10
Gene No.	785	Strand	+
Start	338	End	4913
Name	OJ990323_32.9917.C10.o3.ts	Method	TBLASTX:Soybean
Start	4506	End	4904
GI	none	Score	300
Exons	4506..4778, 4508..4789, 4791..4904, 4805..4903		

Seq. No.	428	Seq. ID	OJ990323_32.9917.C11
Gene No.	786	Strand	+
Start	4716	End	6200
Name	OJ990323_32.9917.C11.o2.gs	Method	GENSCAN
Start	4716	End	5720
GI	none	Score	.78
Exons	4716..5720		

Seq. No.	428	Seq. ID	OJ990323_32.9917.C11
Gene No.	786	Strand	+
Start	4716	End	6200
Name	OJ990323_32.9917.C11.o1.np	Method	AAT/NAP
Start	4752	End	6200
GI	5915836	Score	440
Exons	4752..5643, 6142..6200		
GI Descrip.	CYTOCHROME P450 71D7 gi|1762144 (U48435) putative cytochrome P450 [Solanum chacoense]		

Seq. No.	428	Seq. ID	OJ990323_32.9917.C11

Gene No.	786	Strand	+
Start	4716	End	6200
Name	OJ990323_32.9917.C11.o1.ts	Method	TBLASTX:Soybean
Start	4809	End	5387
GI	none	Score	320
Exons	4809..5195, 4922..5044, 5301..5387		

Seq. No.	428	Seq. ID	OJ990323_32.9917.C11
Gene No.	786	Strand	+
Start	4716	End	6200
Name	OJ990323_32.9917.C11.o1.tc	Method	TBLASTX:Cress
Start	4830	End	5195
GI	none	Score	78
Exons	4830..4904, 4844..4903, 4887..5195, 4940..5038		

Seq. No.	428	Seq. ID	OJ990323_32.9917.C11
Gene No.	786	Strand	+
Start	4716	End	6200
Name	OJ990323_32.9917.C11.o1.tm	Method	TBLASTX:Maize
Start	4839	End	5195
GI	none	Score	414
Exons	4839..5195, 4841..5182		

Seq. No.	428	Seq. ID	OJ990323_32.9917.C11
Gene No.	786	Strand	+
Start	4716	End	6200
Name	OJ990323_32.9917.C11.o1.tw	Method	TBLASTX:Wheat
Start	4887	End	5174
GI	none	Score	61
Exons	4887..4940, 4947..5048, 5091..5174		

Seq. No.	429	Seq. ID	OJ990323_32.9917.C12
Gene No.	787	Strand	+
Start	905	End	1019
Name	OJ990323_32.9917.C12.o1.gs	Method	GENSCAN
Start	905	End	1019
GI	none	Score	.66
Exons	905..1019		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	788	Strand	+
Start	322	End	985
Name	OJ990323_32.9917.C14.o1.np	Method	AAT/NAP
Start	322	End	967
GI	5915839	Score	509
Exons	322..967		
GI Descrip.	CYTOCHROME P450 71D10 gi|2739000|gb|AAB94588| (AF022459) CYP71D10p [Glycine max]		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	788	Strand	+
Start	322	End	985
Name	OJ990323_32.9917.C14.o1.gs	Method	GENSCAN
Start	326	End	985
GI	none	Score	.9
Exons	326..985		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	789	Strand	+
Start	1663	End	2631
Name	OJ990323_32.9917.C14.o2.gs	Method	GENSCAN
Start	1663	End	2631
GI	none	Score	.58
Exons	1663..1695, 1886..1914, 2372..2393, 2458..2631		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o2.tw	Method	TBLASTX:Wheat
Start	319	End	9404
GI	none	Score	104
Exons	319..432, 326..433, 446..640, 9083..9196, 9090..9197, 9210..9404, 9234..9404		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o1.tc	Method	TBLASTX:Cress
Start	320	End	9692
GI	none	Score	100
Exons	320..448, 479..658, 586..657, 680..724, 728..931, 730..870, 6570..6653, 6642..7088, 6695..6994, 9048..9212, 9243..9422, 9350..9421, 9447..9485, 9489..9692, 9491..9667		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o2.tm	Method	TBLASTX:Maize
Start	320	End	9820
GI	none	Score	82
Exons	320..436, 488..658, 577..657, 680..718, 730..915, 731..937, 1026..1058, 9084..9200, 9131..9199, 9252..9422, 9269..9421, 9444..9479, 9491..9676, 9492..9698, 9788..9820		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o1.ts	Method	TBLASTX:Soybean
Start	320	End	9698
GI	none	Score	134
Exons	320..466, 325..465, 479..658, 577..657, 689..712, 728..937, 733..918, 6663..7001, 7056..7175, 7299..7343, 9051..9236, 9089..9193, 9234..9422, 9257..9421, 9489..9698, 9494..9679		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o1.tw	Method	TBLASTX:Wheat
Start	686	End	9701
GI	none	Score	54
Exons	686..718, 730..918, 731..937, 731..940, 7639..7716, 9446..9475, 9447..9479, 9450..9479, 9491..9679, 9492..9698, 9492..9701		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14

Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o1.tm	Method	TBLASTX:Maize
Start	6028	End	7235
GI	none	Score	100
Exons	6028..6084, 6581..6646, 6582..6647, 6582..6689, 6589..6648, 6652..6741, 6657..7004, 6695..6964, 7011..7235, 7022..7162, 7032..7235		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o3.gs	Method	GENSCAN
Start	6477	End	9743
GI	none	Score	.94
Exons	6477..7403, 9090..9743		

Seq. No.	430	Seq. ID	OJ990323_32.9917.C14
Gene No.	790	Strand	+
Start	6477	End	9820
Name	OJ990323_32.9917.C14.o2.np	Method	AAT/NAP
Start	6508	End	9728
GI	5915836	Score	937
Exons	6508..7403, 9090..9728		
GI Descrip.	CYTOCHROME P450 71D7 gi|1762144 (U48435) putative cytochrome P450 [Solanum chacoense]		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	791	Strand	+
Start	56	End	7105
Name	OJ990323_32.9917.C15.o1.gs	Method	GENSCAN
Start	56	End	7105
GI	none	Score	.82
Exons	56..159, 1866..1978, 2017..2113, 2475..2744, 3172..3269, 4055..4804, 4884..5012, 5071..5225, 5332..5390, 5460..5599, 5668..6088, 6344..6489, 6594..7105		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	791	Strand	+
Start	56	End	7105
Name	OJ990323_32.9917.C15.o1.np	Method	AAT/NAP
Start	4042	End	6221
GI	6721561	Score	1025
Exons	4042..4111, 5077..5261, 5332..5390, 5460..6221		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	792	Strand	+
Start	16975	End	21082
Name	OJ990323_32.9917.C15.o4.np	Method	AAT/NAP
Start	16975	End	21082
GI	5915836	Score	813
Exons	16975..17865, 20772..21082		

GI Descrip.	CYTOCHROME P450 71D7 gi|1762144 (U48435) putative cytochrome P450 [Solanum chacoense]		
Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	792	Strand	+
Start	16975	End	21082
Name	OJ990323_32.9917.C15.o4.gs	Method	GENSCAN
Start	20766	End	21053
GI	none	Score	.87
Exons	20766..21053		
Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o1.tm	Method	TBLASTX:Maize
Start	5776	End	17685
GI	none	Score	65
Exons	5776..5895, 17055..17114, 17068..17118, 17125..17445, 17136..17402, 17497..17685, 17508..17657		
Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o9.tw	Method	TBLASTX:Wheat
Start	5857	End	17397
GI	none	Score	57
Exons	5857..5910, 17110..17163, 17170..17280, 17314..17397		
Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o2.gs	Method	GENSCAN
Start	7299	End	14062
GI	none	Score	.67
Exons	7299..7606, 7739..7969, 8072..9813, 10053..10810, 10979..11220, 11255..11366, 11420..11545, 11569..13176, 13250..14062		
Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o2.np	Method	AAT/NAP
Start	7725	End	10801
GI	5902445	Score	3077
Exons	7725..10801		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		
Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o3.tw	Method	TBLASTX:Wheat
Start	7734	End	8342
GI	none	Score	61
Exons	7734..7865, 7735..7860, 7854..8342, 8086..8193, 8242..8328		
Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080

Name	OJ990323_32.9917.C15.o4.tw	Method	TBLASTX:Wheat
Start	8466	End	8849
GI	none	Score	207
Exons	8466..8849, 8467..8841		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o3.tm	Method	TBLASTX:Maize
Start	8544	End	8849
GI	none	Score	174
Exons	8544..8849, 8545..8832		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o6.tw	Method	TBLASTX:Wheat
Start	9309	End	9716
GI	none	Score	48
Exons	9309..9371, 9309..9482, 9490..9663, 9492..9716		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o2.ts	Method	TBLASTX:Soybean
Start	9807	End	10237
GI	none	Score	96
Exons	9807..9887, 9899..10237, 10047..10232		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o2.tw	Method	TBLASTX:Wheat
Start	9867	End	10285
GI	none	Score	267
Exons	9867..10280, 9885..10241, 9899..10285		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o4.tm	Method	TBLASTX:Maize
Start	9959	End	10342
GI	none	Score	185
Exons	9959..10342, 9960..10307, 10070..10315		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o2.tm	Method	TBLASTX:Maize
Start	10370	End	10726
GI	none	Score	235
Exons	10370..10726, 10371..10691		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o1.tw	Method	TBLASTX:Wheat

Start	10401	End	10855
GI	none	Score	347
Exons	10401..10847, 10412..10855, 10415..10855		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o3.ts	Method	TBLASTX:Soybean
Start	10451	End	10816
GI	none	Score	107
Exons	10451..10585, 10592..10816		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o3.np	Method	AAT/NAP
Start	10868	End	15355
GI	5902444	Score	1018
Exons	10868..12517, 12704..12923, 15305..15355		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o5.tw	Method	TBLASTX:Wheat
Start	11005	End	11503
GI	none	Score	89
Exons	11005..11058, 11048..11284, 11166..11282, 11321..11503, 11322..11495		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o7.tw	Method	TBLASTX:Wheat
Start	12085	End	12483
GI	none	Score	260
Exons	12085..12483		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o6.tm	Method	TBLASTX:Maize
Start	12247	End	12486
GI	none	Score	186
Exons	12247..12486		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o1.tc	Method	TBLASTX:Cress
Start	17067	End	21080
GI	none	Score	72
Exons	17067..17126, 17068..17127, 17110..17550, 17145..17405, 20766..20879, 20783..20872, 20928..21080		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-

Start	7299	End	21080
Name	OJ990323_32.9917.C15.o1.ts	Method	TBLASTX:Soybean
Start	17067	End	21080
GI	none	Score	354
Exons	17067..17273, 17068..17445, 17527..17862, 20772..20882, 20777..20878, 21000..21080		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o5.tm	Method	TBLASTX:Maize
Start	17731	End	21080
GI	none	Score	85
Exons	17731..17862, 17772..17894, 20772..20960, 20780..20950, 20904..21071, 21000..21080, 21014..21079		

Seq. No.	431	Seq. ID	OJ990323_32.9917.C15
Gene No.	793	Strand	-
Start	7299	End	21080
Name	OJ990323_32.9917.C15.o8.tw	Method	TBLASTX:Wheat
Start	17775	End	21080
GI	none	Score	235
Exons	17775..17861, 20772..21080, 20777..20875, 20904..21080		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	794	Strand	+
Start	136	End	823
Name	OJ990323_32.9917.C18.o1.gs	Method	GENSCAN
Start	136	End	823
GI	none	Score	.56
Exons	136..170, 457..823		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	795	Strand	+
Start	5944	End	10483
Name	OJ990323_32.9917.C18.o3.gs	Method	GENSCAN
Start	5944	End	7624
GI	none	Score	.73
Exons	5944..6834, 6977..7624		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	795	Strand	+
Start	5944	End	10483
Name	OJ990323_32.9917.C18.o1.np	Method	AAT/NAP
Start	5965	End	7609
GI	5915835	Score	937
Exons	5965..6834, 6977..7609		
GI Descrip.	CYTOCHROME P450 71D6 gi|1762142 (U48434) putative cytochrome P450 [Solanum chacoense]		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	795	Strand	+
Start	5944	End	10483
Name	OJ990323_32.9917.C18.o2.np	Method	AAT/NAP
Start	5997	End	10458
GI	5852181	Score	112
Exons	5997..6035, 9099..9407, 10200..10458		

GI Descrip. (AL117265) zhb0011.1 [Oryza sativa]

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	795	Strand	+
Start	5944	End	10483
Name	OJ990323_32.9917.C18.o4.gs	Method	GENSCAN
Start	9561	End	10483
GI	none	Score	.68
Exons	9561..9565, 10303..10483		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233
Name	OJ990323_32.9917.C18.o3.tm	Method	TBLASTX:Maize
Start	1874	End	2117
GI	none	Score	70
Exons	1874..2116, 1875..2117		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233
Name	OJ990323_32.9917.C18.o1.tm	Method	TBLASTX:Maize
Start	5977	End	6693
GI	none	Score	93
Exons	5977..6012, 6018..6104, 6058..6105, 6115..6405, 6117..6398, 6475..6693, 6513..6674, 6550..6693		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233
Name	OJ990323_32.9917.C18.o1.ts	Method	TBLASTX:Soybean
Start	6054	End	7573
GI	none	Score	240
Exons	6054..6119, 6121..6405, 6153..6263, 6297..6404, 6475..6633, 6739..6783, 6974..7126, 6976..7125, 7238..7309, 7316..7348, 7367..7573, 7375..7560		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233
Name	OJ990323_32.9917.C18.o1.tc	Method	TBLASTX:Cress
Start	6058	End	6405
GI	none	Score	54
Exons	6058..6105, 6100..6405		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233
Name	OJ990323_32.9917.C18.o2.tc	Method	TBLASTX:Cress
Start	6977	End	7570
GI	none	Score	100
Exons	6977..7162, 6991..7164, 7232..7309, 7313..7360, 7369..7488, 7373..7570		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233

Name	OJ990323_32.9917.C18.o2.tm	Method	TBLASTX:Maize
Start	6977	End	7573
GI	none	Score	75
Exons	6977..7141, 7238..7309, 7322..7573, 7322..7504, 7363..7521		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233
Name	OJ990323_32.9917.C18.o1.tw	Method	TBLASTX:Wheat
Start	7247	End	7573
GI	none	Score	78
Exons	7247..7309, 7322..7504, 7360..7506, 7511..7573		

Seq. No.	432	Seq. ID	OJ990323_32.9917.C18
Gene No.	796	Strand	+
Start	11258	End	14233
Name	OJ990323_32.9917.C18.o5.gs	Method	GENSCAN
Start	11258	End	14233
GI	none	Score	.5
Exons	11258..11278, 11499..11630, 12651..12736, 13953..14233		

Seq. No.	433	Seq. ID	OJ990323_32.9917.C19
Gene No.	797	Strand	+
Start	1108	End	1713
Name	OJ990323_32.9917.C19.o1.np	Method	AAT/NAP
Start	1108	End	1713
GI	5915835	Score	407
Exons	1108..1713		
GI Descrip.	CYTOCHROME P450 71D6 gi|1762142 (U48434) putative cytochrome P450 [Solanum chacoense]		

Seq. No.	433	Seq. ID	OJ990323_32.9917.C19
Gene No.	797	Strand	+
Start	1108	End	1713
Name	OJ990323_32.9917.C19.o1.ts	Method	TBLASTX:Soybean
Start	1183	End	1548
GI	none	Score	308
Exons	1183..1548, 1278..1406		

Seq. No.	433	Seq. ID	OJ990323_32.9917.C19
Gene No.	797	Strand	+
Start	1108	End	1713
Name	OJ990323_32.9917.C19.o1.tm	Method	TBLASTX:Maize
Start	1189	End	1542
GI	none	Score	406
Exons	1189..1542, 1224..1538		

Seq. No.	433	Seq. ID	OJ990323_32.9917.C19
Gene No.	797	Strand	+
Start	1108	End	1713
Name	OJ990323_32.9917.C19.o1.tc	Method	TBLASTX:Cress
Start	1198	End	1548
GI	none	Score	77
Exons	1198..1260, 1243..1548, 1278..1538		

Seq. No.	434	Seq. ID	OJ990323_32.9917.C20
Gene No.	798	Strand	+

Start	17	End	845
Name	OJ990323_32.9917.C20.o1.gs	Method	GENSCAN
Start	17	End	845
GI	none	Score	.44
Exons	17..43, 705..845		

Seq. No.	435	Seq. ID	OJ990613_37.9922.C1
Gene No.	799	Strand	-
Start	58	End	175
Name	OJ990613_37.9922.C1.o1.gs	Method	GENSCAN
Start	58	End	175
GI	none	Score	.45
Exons	58..175		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	800	Strand	+
Start	1992	End	8869
Name	OJ990613_37.9922.C3.o2.gs	Method	GENSCAN
Start	1992	End	6582
GI	none	Score	.49
Exons	1992..2055, 2193..2252, 2844..2981, 3537..3757, 4126..4248, 5610..5714, 6538..6582		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	800	Strand	+
Start	1992	End	8869
Name	OJ990613_37.9922.C3.o1.gp	Method	AAT/GAP
Start	2561	End	8869
GI	967_1.R1084	Score	2622
Exons	2561..2690, 2844..2981, 3961..4037, 4126..4248, 5610..5714, 7680..7752, 7868..7939, 8020..8215, 8292..8421, 8503..8869		
GI Descrip.	'6094330/sp|O48659|SPE2_HYONI 1.0e-150 SPERMIDINE SYNTHASE 2 (PUTRESCINE AMINOPROPYLTRANSFERASE 2) (SPDSY 2) >gi_2821957_dbj_BAA24534_ (AB006691) spermidine synthase 2 [Hyoscyamus niger]'		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	800	Strand	+
Start	1992	End	8869
Name	OJ990613_37.9922.C3.o2.np	Method	AAT/NAP
Start	2852	End	8565
GI	6468656	Score	1448
Exons	2852..2981, 3961..4037, 4126..4248, 5610..5714, 7680..7752, 7868..7939, 8020..8215, 8292..8421, 8503..8565		
GI Descrip.	(AJ251298) spermidine synthase 1 [Oryza sativa]		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	801	Strand	-
Start	1	End	1497
Name	OJ990613_37.9922.C3.o1.np	Method	AAT/NAP
Start	1	End	976
GI	5441880	Score	669
Exons	1..976		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	801	Strand	-
Start	1	End	1497
Name	OJ990613_37.9922.C3.o1.gs	Method	GENSCAN
Start	21	End	1497
GI	none	Score	.83
Exons	21..1186, 1300..1497		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	802	Strand	-
Start	8515	End	8838
Name	OJ990613_37.9922.C3.o2.tm	Method	TBLASTX:Maize
Start	11	End	407
GI	none	Score	169
Exons	11..253, 12..254, 254..406, 285..407		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	802	Strand	-
Start	8515	End	8838
Name	OJ990613_37.9922.C3.o1.tm	Method	TBLASTX:Maize
Start	2924	End	8582
GI	none	Score	97
Exons	2924..2998, 2929..3009, 2939..2998, 3959..4036, 3960..4037, 4119..4250, 4120..4254, 4120..4251, 5604..5717, 5609..5740, 5609..5716, 5653..5745, 7665..7763, 7677..7751, 7679..7762, 7863..7940, 7867..7941, 8016..8213, 8018..8230, 8019..8213, 8074..8223, 8289..8420, 8290..8424, 8293..8430, 8500..8568, 8502..8582, 8502..8570		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	802	Strand	-
Start	8515	End	8838
Name	OJ990613_37.9922.C3.o2.tc	Method	TBLASTX:Cress
Start	2929	End	4254
GI	none	Score	96
Exons	2929..3000, 2939..2998, 3959..4030, 3960..4037, 3960..4037, 4109..4249, 4115..4192, 4117..4251, 4120..4254		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	802	Strand	-
Start	8515	End	8838
Name	OJ990613_37.9922.C3.o1.ts	Method	TBLASTX:Soybean
Start	2938	End	8568
GI	none	Score	89
Exons	2938..2997, 2939..2998, 3925..3966, 3959..4030, 3960..4037, 4119..4250, 4120..4254, 5604..5717, 5609..5716, 7665..7763, 7679..7753, 7857..7940, 7867..7941, 8018..8215, 8019..8213, 8289..8351, 8289..8351, 8290..8376, 8380..8424, 8500..8568		

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	802	Strand	-
Start	8515	End	8838
Name	OJ990613_37.9922.C3.o1.tc	Method	TBLASTX:Cress
Start	5627	End	8568
GI	none	Score	65
Exons	5627..5716, 5629..5709, 5640..5717, 7665..7763, 7679..7762, 7863..7940, 7867..7941, 8018..8230, 8019..8213, 8289..8372,		

8290..8373, 8371..8430, 8373..8420, 8500..8568, 8508..8564

Seq. No.	436	Seq. ID	OJ990613_37.9922.C3
Gene No.	802	Strand	-
Start	8515	End	8838
Name	OJ990613_37.9922.C3.o3.gs	Method	GENSCAN
Start	8515	End	8838
GI	none	Score	.85
Exons	8515..8838		

Seq. No.	437	Seq. ID	OJ990613_37.9922.C4
Gene No.	803	Strand	-
Start	1	End	4340
Name	OJ990613_37.9922.C4.o1.np	Method	AAT/NAP
Start	1	End	4340
GI	6573747	Score	170
Exons	1..40, 1172..1530, 2222..2359, 2589..2641, 4303..4340		
GI Descrip.	(AC009398) F20B24.17 [Arabidopsis thaliana]		

Seq. No.	437	Seq. ID	OJ990613_37.9922.C4
Gene No.	803	Strand	-
Start	1	End	4340
Name	OJ990613_37.9922.C4.o1.gs	Method	GENSCAN
Start	213	End	4038
GI	none	Score	.73
Exons	213..309, 564..690, 1172..1440, 2060..2202, 2598..2694, 2728..2854, 2899..3193, 3298..3416, 3506..4038		

Seq. No.	437	Seq. ID	OJ990613_37.9922.C4
Gene No.	803	Strand	-
Start	1	End	4340
Name	OJ990613_37.9922.C4.o1.tm	Method	TBLASTX:Maize
Start	1171	End	2634
GI	none	Score	62
Exons	1171..1188, 1189..1323, 1204..1323, 1313..1369, 1320..1367, 1411..1530, 2589..2633, 2590..2634		

Seq. No.	437	Seq. ID	OJ990613_37.9922.C4
Gene No.	803	Strand	-
Start	1	End	4340
Name	OJ990613_37.9922.C4.o1.tw	Method	TBLASTX:Wheat
Start	1171	End	1515
GI	none	Score	119
Exons	1171..1188, 1189..1323, 1313..1369, 1411..1515		

Seq. No.	437	Seq. ID	OJ990613_37.9922.C4
Gene No.	803	Strand	-
Start	1	End	4340
Name	OJ990613_37.9922.C4.o2.np	Method	AAT/NAP
Start	2808	End	4340
GI	3283026	Score	373
Exons	2808..3012, 3076..3193, 3298..3416, 3518..4045, 4121..4340		
GI Descrip.	(AF051562) putative transposase [Arabidopsis thaliana]		

Seq. No.	437	Seq. ID	OJ990613_37.9922.C4
Gene No.	803	Strand	-
Start	1	End	4340

Name	OJ990613_37.9922.C4.o1.ts	Method	TBLASTX:Soybean
Start	3080	End	3438
GI	none	Score	111
Exons	3080..3205, 3293..3412, 3300..3410, 3301..3438, 3304..3438		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	804	Strand	+
Start	1	End	114
Name	OJ990613_37.9922.C5.o1.np	Method	AAT/NAP
Start	1	End	114
GI	6069646	Score	144
Exons	1..114		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	805	Strand	+
Start	2399	End	12155
Name	OJ990613_37.9922.C5.o2.np	Method	AAT/NAP
Start	2399	End	6283
GI	3695059	Score	775
Exons	2399..2815, 2947..3067, 3204..3323, 3882..4112, 4202..4344, 6225..6283		
GI Descrip.	(AF064787) rac GTPase activating protein 1 [Lotus japonicus]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	805	Strand	+
Start	2399	End	12155
Name	OJ990613_37.9922.C5.o1.gs	Method	GENSCAN
Start	2472	End	7517
GI	none	Score	.4
Exons	2472..2815, 2947..3067, 3204..3323, 3999..4112, 4202..4831, 6063..6171, 6176..6383, 7409..7517		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	805	Strand	+
Start	2399	End	12155
Name	OJ990613_37.9922.C5.o3.np	Method	AAT/NAP
Start	7091	End	12155
GI	6063554	Score	360
Exons	7091..7198, 8251..8374, 9592..9872, 9952..10168, 11933..12155		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	805	Strand	+
Start	2399	End	12155
Name	OJ990613_37.9922.C5.o3.gs	Method	GENSCAN
Start	10959	End	11342
GI	none	Score	.81
Exons	10959..11342		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5

Gene No.	806	Strand	+
Start	26167	End	42442
Name	OJ990613_37.9922.C5.o7.gs	Method	GENSCAN
Start	26167	End	27914
GI	none	Score	.74
Exons	26167..26376, 26468..26692, 27556..27691, 27748..27914		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	806	Strand	+
Start	26167	End	42442
Name	OJ990613_37.9922.C5.o5.np	Method	AAT/NAP
Start	26176	End	31584
GI	6723388	Score	564
Exons	26176..26376, 26468..26581, 30033..30160, 30233..30371, 30487..30686, 31445..31584		
GI Descrip.	(AL132956) putative protein [Arabidopsis thaliana]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	806	Strand	+
Start	26167	End	42442
Name	OJ990613_37.9922.C5.o8.gs	Method	GENSCAN
Start	28483	End	42442
GI	none	Score	.68
Exons	28483..28580, 29077..29161, 30033..30160, 30233..30371, 30487..30686, 31445..31572, 33150..33343, 33441..33558, 34471..34561, 34773..34941, 35257..35336, 36616..36820, 38831..38863, 39043..39183, 39320..39464, 39773..39814, 40167..40550, 41275..41348, 41852..42442		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	806	Strand	+
Start	26167	End	42442
Name	OJ990613_37.9922.C5.o1.gp	Method	AAT/GAP
Start	31077	End	31435
GI	LIB3477-008-P1-K1-A9	Score	242
Exons	31077..31193, 31338..31435		
GI Descrip.	'1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence'		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	806	Strand	+
Start	26167	End	42442
Name	OJ990613_37.9922.C5.o3.gp	Method	AAT/GAP
Start	33138	End	34224
GI	none	Score	1311
Exons	33138..33343, 33441..33636, 33901..34224		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	807	Strand	+
Start	45757	End	47722
Name	OJ990613_37.9922.C5.o6.np	Method	AAT/NAP
Start	45757	End	47722
GI	140298	Score	663
Exons	45757..45802, 47280..47722		
GI Descrip.	CYTOCHROME C BIOGENESIS PROTEIN CCSA gi|82524|pir||JQ0288 hypothetical 36.7K protein (trnL-trnN intergenic region) - rice chloroplast gi|12049|emb|CAA33952| (X15901) ORF321 [Oryza		

sativa] gi|226669|prf||1603356CW ORF 321 [Oryza sativa]

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	808	Strand	+
Start	53939	End	54681
Name	OJ990613_37.9922.C5.o4.gp	Method	AAT/GAP
Start	53939	End	54681
GI	none	Score	725
Exons	53939..54258, 54367..54430, 54620..54681		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	809	Strand	+
Start	54858	End	55266
Name	OJ990613_37.9922.C5.o5.gp	Method	AAT/GAP
Start	54858	End	55266
GI	3761538	Score	518
Exons	54858..55266		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	810	Strand	+
Start	55517	End	57442
Name	OJ990613_37.9922.C5.o6.gp	Method	AAT/GAP
Start	55517	End	57442
GI	none	Score	680
Exons	55517..55643, 57198..57442		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	811	Strand	+
Start	59373	End	60472
Name	OJ990613_37.9922.C5.o12.np	Method	AAT/NAP
Start	59373	End	60472
GI	6815053	Score	745
Exons	59373..59517, 60008..60185, 60235..60472		
GI Descrip.	(AP001080) hypothetical protein [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	812	Strand	-
Start	11696	End	12085
Name	OJ990613_37.9922.C5.o4.gs	Method	GENSCAN
Start	11696	End	12085
GI	none	Score	.77
Exons	11696..12085		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	813	Strand	-
Start	14582	End	23260
Name	OJ990613_37.9922.C5.o4.np	Method	AAT/NAP
Start	14582	End	22023
GI	4263831	Score	925
Exons	14582..14615, 16349..16961, 17087..17461, 17502..17674, 17828..18050, 18193..19268, 19960..20115, 22000..22023		
GI Descrip.	(AC006067) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	813	Strand	-
Start	14582	End	23260

Name	OJ990613_37.9922.C5.o6.gs	Method	GENSCAN
Start	16306	End	23260
GI	none	Score	.57
Exons	16306..16799, 17395..17674, 17705..19090, 19133..19419, 19937..20162, 20174..20424, 20456..20879, 21135..21907, 22113..22208, 22259..22389, 22545..22975, 23135..23260		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	814	Strand	-
Start	31277	End	31336
Name	OJ990613_37.9922.C5.o2.gp	Method	AAT/GAP
Start	31277	End	31336
GI	2312838	Score	80
Exons	31277..31336		
GI Descrip.	1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	815	Strand	-
Start	44314	End	45102
Name	OJ990613_37.9922.C5.o9.gs	Method	GENSCAN
Start	44314	End	45102
GI	none	Score	1
Exons	44314..45102		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	816	Strand	-
Start	47926	End	49428
Name	OJ990613_37.9922.C5.o7.np	Method	AAT/NAP
Start	47926	End	49428
GI	128732	Score	2555
Exons	47926..49428		
GI Descrip.	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST gi|66181|pir||DERZN4 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - rice chloroplast gi|12050|emb|CAA33953| (X15901) NADH dehydrogenase ND4 [Oryza sativa] gi|226670|prf||1603356CX NADH dehydrogenase ND4 [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	817	Strand	-
Start	49551	End	49793
Name	OJ990613_37.9922.C5.o8.np	Method	AAT/NAP
Start	49551	End	49793
GI	131164	Score	449
Exons	49551..49793		
GI Descrip.	PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C) gi|65727|pir||FERZA photosystem I iron-sulfur protein psaC - rice chloroplast gi|65728|pir||FEWT1 photosystem I iron-sulfur protein psaC - wheat chloroplast gi|12051|emb|CAA33954| (X15901) PSI 9kDa protein [Oryza sativa] gi|12350|emb|CAA31555| (X13158) photosystem I 8 kDa subunit		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	818	Strand	-
Start	50243	End	50545
Name	OJ990613_37.9922.C5.o9.np	Method	AAT/NAP
Start	50243	End	50545

GI	128874	Score	490
Exons	50243..50545		
GI Descrip.	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4L, CHLOROPLAST gi|66168|pir||DERZNL NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4L - rice chloroplast gi|12052|emb|CAA33955| (X15901) NADH dehydrogenase ND4L [Oryza sativa] gi|226673|prf||1603356DA NADH dehydrogenase ND4L [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	819	Strand	-
Start	50758	End	51273
Name	OJ990613_37.9922.C5.o10.np	Method	AAT/NAP
Start	50758	End	51273
GI	128803	Score	849
Exons	50758..51273		
GI Descrip.	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 6, CHLOROPLAST gi|66198|pir||DERZN6 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 6 - rice chloroplast gi|12053|emb|CAA33908| (X15901) NADH dehydrogenase ND6 [Oryza sativa] gi|226674|prf||1603356DB NADH dehydrogenase ND6 [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	820	Strand	-
Start	54552	End	58947
Name	OJ990613_37.9922.C5.o11.np	Method	AAT/NAP
Start	54552	End	58947
GI	5922636	Score	342
Exons	54552..54570, 58221..58354, 58633..58947		
GI Descrip.	(AP000492) ESTs C99517(E20319),AU078130(E20319) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6016869|dbj|BAA85212.1| (AP000570) ESTs C99517(E20319),AU078130(E20319) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	821	Strand	-
Start	59869	End	73456
Name	OJ990613_37.9922.C5.o13.np	Method	AAT/NAP
Start	59869	End	64535
GI	5852181	Score	124
Exons	59869..59927, 61136..61352, 64513..64535		
GI Descrip.	(AL117265) zhb0011.1 [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	821	Strand	-
Start	59869	End	73456
Name	OJ990613_37.9922.C5.o12.gs	Method	GENSCAN
Start	62790	End	68968
GI	none	Score	.54
Exons	62790..62951, 63540..63642, 63935..64228, 64233..64614, 64646..64789, 64813..65063, 65643..65818, 66830..66940, 67007..67123, 67166..67257, 67350..67463, 68407..68968		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	821	Strand	-
Start	59869	End	73456
Name	OJ990613_37.9922.C5.o14.np	Method	AAT/NAP

Start	64808	End	68380
GI	4567294	Score	218
Exons	64808..65075, 68295..68380		
GI Descrip.	(AC006918) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	821	Strand	-
Start	59869	End	73456
Name	OJ990613_37.9922.C5.o16.np	Method	AAT/NAP
Start	68790	End	73456
GI	5852181	Score	146
Exons	68790..68898, 70062..70309, 73405..73456		
GI Descrip.	(AL117265) zhb0011.1 [Oryza sativa]		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	821	Strand	-
Start	59869	End	73456
Name	OJ990613_37.9922.C5.o13.gs	Method	GENSCAN
Start	69156	End	72128
GI	none	Score	.75
Exons	69156..69553, 69797..69938, 70117..70222, 71125..71335, 71849..72128		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o13.ts	Method	TBLASTX:Soybean
Start	2637	End	3238
GI	none	Score	192
Exons	2637..2807, 2646..2813, 2944..3078, 2945..3067, 3203..3238		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o5.tc	Method	TBLASTX:Cress
Start	2954	End	4115
GI	none	Score	140
Exons	2954..3067, 2959..3078, 3203..3319, 3204..3323, 3855..4115, 3881..4108		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o4.ts	Method	TBLASTX:Soybean
Start	3258	End	4291
GI	none	Score	105
Exons	3258..3323, 3855..4115, 3873..3977, 3881..4108, 4008..4115, 4195..4266, 4199..4291, 4202..4285		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o4.tm	Method	TBLASTX:Maize
Start	3270	End	4415
GI	none	Score	83
Exons	3270..3323, 3278..3322, 3855..4115, 3869..4111, 3873..4115,		

4027..4122, 4199..4291, 4201..4266, 4202..4297, 4293..4415

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o2.tw	Method	TBLASTX:Wheat
Start	3897	End	4352
GI	none	Score	320
Exons	3897..4115, 3899..4111, 3900..4115, 4199..4291, 4200..4235, 4202..4303, 4278..4352		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o8.ts	Method	TBLASTX:Soybean
Start	16321	End	42991
GI	none	Score	41
Exons	16321..16566, 16325..16354, 16394..16564, 42790..42963, 42796..42825, 42896..42991		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o5.tw	Method	TBLASTX:Wheat
Start	16342	End	42930
GI	none	Score	77
Exons	16342..16758, 16376..16549, 42811..42930		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o10.ts	Method	TBLASTX:Soybean
Start	17126	End	17407
GI	none	Score	210
Exons	17126..17407		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o9.ts	Method	TBLASTX:Soybean
Start	17775	End	18174
GI	none	Score	56
Exons	17775..17882, 17777..18028, 17876..18016, 18050..18127, 18054..18125, 18127..18174		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o12.ts	Method	TBLASTX:Soybean
Start	18321	End	18784
GI	none	Score	74
Exons	18321..18458, 18506..18784, 18546..18746		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o6.tw	Method	TBLASTX:Wheat

Start	18464	End	18812
GI	none	Score	93
Exons	18464..18811, 18468..18812		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o3.tm	Method	TBLASTX:Maize
Start	18470	End	18931
GI	none	Score	209
Exons	18470..18931, 18471..18776, 18650..18931		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o1.tw	Method	TBLASTX:Wheat
Start	18814	End	19205
GI	none	Score	211
Exons	18814..19143, 18815..19144, 18821..19153, 19005..19145, 19148..19204, 19158..19205		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o7.tm	Method	TBLASTX:Maize
Start	18932	End	19150
GI	none	Score	117
Exons	18932..19150, 18950..19141, 19005..19145		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o11.ts	Method	TBLASTX:Soybean
Start	19001	End	64999
GI	none	Score	138
Exons	19001..19135, 19142..19366, 64775..64999, 64776..64973		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o7.tw	Method	TBLASTX:Wheat
Start	21468	End	69743
GI	none	Score	196
Exons	21468..21599, 69390..69743		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o8.tc	Method	TBLASTX:Cress
Start	26188	End	30092
GI	none	Score	136
Exons	26188..26364, 26465..26584, 26467..26583, 30033..30092		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o9.tm	Method	TBLASTX:Maize

Start	26338	End	30107
GI	none	Score	61
Exons	26338..26376, 26351..26374, 26465..26584, 26465..26581, 26467..26583, 30032..30097, 30033..30107		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o5.tm	Method	TBLASTX:Maize
Start	30108	End	33612
GI	none	Score	69
Exons	30108..30152, 31442..31573, 31443..31574, 31444..31575, 31444..31578, 33148..33342, 33149..33343, 33149..33343, 33438..33578, 33446..33601, 33447..33593, 33451..33612		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o6.tm	Method	TBLASTX:Maize
Start	44335	End	44878
GI	none	Score	120
Exons	44335..44577, 44629..44877, 44636..44878		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o9.tc	Method	TBLASTX:Cress
Start	44641	End	44881
GI	none	Score	116
Exons	44641..44877, 44693..44881		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o3.ts	Method	TBLASTX:Soybean
Start	47321	End	47713
GI	none	Score	481
Exons	47321..47596, 47323..47712, 47324..47713, 47630..47713		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o4.tc	Method	TBLASTX:Cress
Start	47324	End	47715
GI	none	Score	89
Exons	47324..47446, 47325..47444, 47359..47469, 47485..47715, 47486..47713, 47533..47715		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o2.tm	Method	TBLASTX:Maize
Start	47859	End	48310
GI	none	Score	54
Exons	47859..47918, 47884..47919, 47909..47980, 47911..48309, 47913..48110, 47920..48309, 47939..48310		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o2.tc	Method	TBLASTX:Cress
Start	47925	End	48390
GI	none	Score	350
Exons	47925..48110, 47932..48390, 48035..48388		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o5.ts	Method	TBLASTX:Soybean
Start	47977	End	48231
GI	none	Score	219
Exons	47977..48213, 47980..48231, 47985..48215, 48041..48229		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o1.tc	Method	TBLASTX:Cress
Start	48442	End	48984
GI	none	Score	340
Exons	48442..48885, 48443..48892, 48487..48900, 48509..48889, 48606..48896, 48895..48984, 48905..48967		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o1.ts	Method	TBLASTX:Soybean
Start	48511	End	49015
GI	none	Score	376
Exons	48511..48948, 48511..48978, 48587..48961, 48949..49014, 48953..49015, 48962..49015		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o8.tm	Method	TBLASTX:Maize
Start	48616	End	49062
GI	none	Score	65
Exons	48616..48774, 48617..48757, 48865..49026, 48866..48961, 48949..49062, 48953..49006		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o7.tc	Method	TBLASTX:Cress
Start	48985	End	49266
GI	none	Score	206
Exons	48985..49146, 48986..49144, 49145..49258, 49146..49259, 49146..49259, 49192..49266		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o6.ts	Method	TBLASTX:Soybean
Start	49016	End	49291

GI	none	Score	291
Exons	49016..49291, 49017..49103, 49048..49284		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o2.ts	Method	TBLASTX:Soybean
Start	49292	End	50592
GI	none	Score	96
Exons	49292..49435, 49309..49434, 49434..49475, 49435..49479, 49517..49798, 49527..49808, 49528..49830, 49868..49921, 49871..49915, 49948..49983, 50240..50581, 50241..50582, 50359..50592		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o3.tc	Method	TBLASTX:Cress
Start	49292	End	49810
GI	none	Score	148
Exons	49292..49435, 49294..49434, 49435..49452, 49522..49611, 49533..49610, 49605..49808, 49606..49809, 49606..49809, 49607..49810		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o1.tm	Method	TBLASTX:Maize
Start	49599	End	50046
GI	none	Score	610
Exons	49599..49658, 49628..50044, 49629..50045, 49630..50046		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o4.tw	Method	TBLASTX:Wheat
Start	49816	End	50052
GI	none	Score	65
Exons	49816..49860, 49816..49860, 49817..49861, 49859..49912, 49860..49913, 49864..49914, 49870..49917, 49915..49989, 49916..50005, 49926..49997, 50001..50051, 50001..50051, 50005..50052		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o6.tc	Method	TBLASTX:Cress
Start	50258	End	50583
GI	none	Score	309
Exons	50258..50581, 50259..50582, 50353..50583, 50359..50583		

Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o10.tc	Method	TBLASTX:Cress
Start	50728	End	50953
GI	none	Score	187

Exons	50728..50952, 50749..50952, 50756..50953		
Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o7.ts	Method	TBLASTX:Soybean
Start	50901	End	51150
GI	none	Score	81
Exons	50901..51062, 50902..51084, 50903..51070, 51067..51132, 51068..51133, 51127..51150, 51128..51148		
Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o3.tw	Method	TBLASTX:Wheat
Start	64823	End	65074
GI	none	Score	114
Exons	64823..65074, 64824..65015		
Seq. No.	438	Seq. ID	OJ990613_37.9922.C5
Gene No.	822	Strand	-
Start	73440	End	73612
Name	OJ990613_37.9922.C5.o14.gs	Method	GENSCAN
Start	73440	End	73612
GI	none	Score	.86
Exons	73440..73548, 73572..73612		
Seq. No.	439	Seq. ID	OJ990503_25.9922.C3
Gene No.	823	Strand	-
Start	1	End	656
Name	OJ990503_25.9922.C3.o1.np	Method	AAT/NAP
Start	1	End	656
GI	6069646	Score	308
Exons	1..656		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		
Seq. No.	440	Seq. ID	OJ990503_25.9922.C4
Gene No.	824	Strand	
Start	2	End	652
Name	OJ990503_25.9922.C4.o1.tm	Method	TBLASTX:Maize
Start	2	End	652
GI	none	Score	60
Exons	2..109, 5..103, 5..106, 6..101, 120..158, 169..324, 170..319, 214..345, 214..327, 215..352, 220..297, 223..333, 227..328, 341..466, 341..478, 344..484, 353..454, 360..482, 361..477, 361..483, 369..512, 375..485, 375..488, 378..500, 493..612, 522..608, 522..623, 523..615, 523..630, 531..629, 532..630, 533..652, 533..634, 534..623		
Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	825	Strand	+
Start	376	End	1028
Name	OJ990503_25.9922.C5.o1.gs	Method	GENSCAN

Start	376	End	1028
GI	none	Score	.91
Exons	376..510, 606..1028		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	826	Strand	+
Start	6111	End	6472
Name	OJ990503_25.9922.C5.o1.gp	Method	AAT/GAP
Start	6111	End	6472
GI	426662	Score	656
Exons	6111..6472		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	827	Strand	+
Start	8127	End	11948
Name	OJ990503_25.9922.C5.o3.gs	Method	GENSCAN
Start	8127	End	11948
GI	none	Score	.51
Exons	8127..8210, 9194..9218, 10371..10556, 10574..10862, 10927..11090, 11092..11279, 11850..11948		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	827	Strand	+
Start	8127	End	11948
Name	OJ990503_25.9922.C5.o1.np	Method	AAT/NAP
Start	10152	End	11920
GI	6907087	Score	909
Exons	10152..10528, 10574..11279, 11819..11920		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	828	Strand	+
Start	14105	End	18438
Name	OJ990503_25.9922.C5.o3.np	Method	AAT/NAP
Start	14105	End	18438
GI	4539660	Score	379
Exons	14105..14932, 15071..15412, 18410..18438		
GI Descrip.	(AF061282) polyprotein [Sorghum bicolor]		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	828	Strand	+
Start	14105	End	18438
Name	OJ990503_25.9922.C5.o4.np	Method	AAT/NAP
Start	17551	End	18438
GI	6907087	Score	632
Exons	17551..17927, 17973..18438		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	829	Strand	-
Start	2621	End	6675
Name	OJ990503_25.9922.C5.o2.gs	Method	GENSCAN
Start	2621	End	6520

GI	none	Score	.55
Exons	2621..2665, 3318..3531, 3624..3904, 6308..6520		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	829	Strand	-
Start	2621	End	6675
Name	OJ990503_25.9922.C5.o2.gp	Method	AAT/GAP
Start	6363	End	6675
GI	14719_1.R1084	Score	450
Exons	6363..6675		
GI Descrip.	'5091617/gb|AAD39605.1|AC007454_4 1.0e-23 (AC007454) Contains similarity to gi_479356 protein kinase PK1 from Zea mays, is a member of the PF_00954 S-locus glycoprotein family and contains a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]'		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	830	Strand	-
Start	12314	End	14268
Name	OJ990503_25.9922.C5.o1.tm	Method	TBLASTX:Maize
Start	8531	End	9238
GI	none	Score	70
Exons	8531..8593, 8551..8601, 8894..8977, 8895..8969, 8896..8970, 8953..9102, 8958..9104, 8978..9103, 9190..9234, 9191..9238, 9194..9238		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	830	Strand	-
Start	12314	End	14268
Name	OJ990503_25.9922.C5.o1.tc	Method	TBLASTX:Cress
Start	8886	End	9238
GI	none	Score	61
Exons	8886..8954, 8908..8970, 8979..9104, 8981..9103, 9194..9238, 9205..9237		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	830	Strand	-
Start	12314	End	14268
Name	OJ990503_25.9922.C5.o2.tw	Method	TBLASTX:Wheat
Start	8895	End	9238
GI	none	Score	84
Exons	8895..8954, 8896..8970, 8958..9104, 8978..9103, 9182..9229, 9194..9238		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	830	Strand	-
Start	12314	End	14268
Name	OJ990503_25.9922.C5.o2.np	Method	AAT/NAP
Start	12314	End	14268
GI	4680186	Score	112
Exons	12314..12551, 14237..14268		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	831	Strand	
Start	14327	End	14866
Name	OJ990503_25.9922.C5.o1.tw	Method	TBLASTX:Wheat

Start	14327	End	14683
GI	none	Score	272
Exons	14327..14683, 14329..14622		

Seq. No.	441	Seq. ID	OJ990503_25.9922.C5
Gene No.	831	Strand	
Start	14327	End	14866
Name	OJ990503_25.9922.C5.o2.tm	Method	TBLASTX:Maize
Start	14567	End	14866
GI	none	Score	215
Exons	14567..14866, 14581..14670		

Seq. No.	442	Seq. ID	OJ990503_25.9922.C6
Gene No.	832	Strand	+
Start	1588	End	2704
Name	OJ990503_25.9922.C6.o1.np	Method	AAT/NAP
Start	1588	End	2704
GI	4680186	Score	271
Exons	1588..1641, 2478..2704		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	442	Seq. ID	OJ990503_25.9922.C6
Gene No.	833	Strand	+
Start	3599	End	3889
Name	OJ990503_25.9922.C6.o1.gs	Method	GENSCAN
Start	3599	End	3889
GI	none	Score	.77
Exons	3599..3889		

Seq. No.	442	Seq. ID	OJ990503_25.9922.C6
Gene No.	834	Strand	-
Start	1	End	117
Name	OJ990503_25.9922.C6.o1.gp	Method	AAT/GAP
Start	1	End	117
GI	uC-osf1M202074a03a1	Score	208
Exons	1..117		
GI Descrip.	'4521194/dbj|AB013613.1|AB013613 4.0e-38 Oryza sativa DNA, centromere sequence RCB11'		

Seq. No.	442	Seq. ID	OJ990503_25.9922.C6
Gene No.	835	Strand	-
Start	2231	End	2620
Name	OJ990503_25.9922.C6.o2.gp	Method	AAT/GAP
Start	2231	End	2620
GI	uC-osflcyp033a04b1	Score	595
Exons	2231..2620		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o1.np	Method	AAT/NAP
Start	1	End	3091
GI	5852180	Score	358
Exons	1..519, 845..889, 3065..3091		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o2.np	Method	AAT/NAP
Start	1	End	4944
GI	4680179	Score	4526
Exons	1..69, 1228..1509, 1543..4944		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o7.tw	Method	TBLASTX:Wheat
Start	1570	End	1937
GI	none	Score	127
Exons	1570..1740, 1731..1778, 1823..1936, 1824..1937		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o4.tw	Method	TBLASTX:Wheat
Start	2102	End	2589
GI	none	Score	53
Exons	2102..2338, 2103..2156, 2211..2333, 2326..2589, 2328..2546		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o5.tm	Method	TBLASTX:Maize
Start	2117	End	2406
GI	none	Score	171
Exons	2117..2329, 2118..2333, 2326..2406, 2330..2404		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o3.tm	Method	TBLASTX:Maize
Start	2476	End	2976
GI	none	Score	170
Exons	2476..2655, 2662..2976, 2802..2855, 2883..2933		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o1.ts	Method	TBLASTX:Soybean
Start	2530	End	2925
GI	none	Score	52
Exons	2530..2559, 2532..2561, 2566..2925, 2567..2599, 2568..2603, 2649..2924, 2653..2925		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o5.tw	Method	TBLASTX:Wheat
Start	2638	End	2940
GI	none	Score	374

Exons	2638..2940, 2639..2710, 2649..2924		
Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o3.tw	Method	TBLASTX:Wheat
Start	2941	End	3366
GI	none	Score	552
Exons	2941..3366, 2973..3362, 3004..3366		
Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o3.ts	Method	TBLASTX:Soybean
Start	2947	End	3192
GI	none	Score	186
Exons	2947..3192, 2964..3092		
Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o2.tm	Method	TBLASTX:Maize
Start	3012	End	3375
GI	none	Score	451
Exons	3012..3362, 3013..3366, 3013..3375		
Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o2.tw	Method	TBLASTX:Wheat
Start	3397	End	3933
GI	none	Score	620
Exons	3397..3933, 3441..3932		
Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o2.ts	Method	TBLASTX:Soybean
Start	3721	End	3981
GI	none	Score	274
Exons	3721..3981, 3726..3980, 3778..3981		
Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o4.tm	Method	TBLASTX:Maize
Start	3780	End	4071
GI	none	Score	91
Exons	3780..3983, 3780..4067, 3781..4071		
Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o2.gs	Method	GENSCAN
Start	3874	End	4809
GI	none	Score	.41
Exons	3874..4023, 4183..4809		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o1.tw	Method	TBLASTX:Wheat
Start	3940	End	4566
GI	none	Score	671
Exons	3940..4566, 3996..4454, 4312..4563		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o1.tm	Method	TBLASTX:Maize
Start	4120	End	4719
GI	none	Score	222
Exons	4120..4281, 4123..4275, 4279..4719, 4281..4454, 4435..4611, 4518..4703		

Seq. No.	443	Seq. ID	OJ990503_25.9922.C7
Gene No.	836	Strand	+
Start	1	End	4944
Name	OJ990503_25.9922.C7.o6.tw	Method	TBLASTX:Wheat
Start	4566	End	4899
GI	none	Score	309
Exons	4566..4835, 4567..4899		

Seq. No.	444	Seq. ID	OJ990503_25.9922.C10
Gene No.	837	Strand	-
Start	1	End	509
Name	OJ990503_25.9922.C10.o1.gp	Method	AAT/GAP
Start	1	End	509
GI	none	Score	989
Exons	1..509		

Seq. No.	444	Seq. ID	OJ990503_25.9922.C10
Gene No.	837	Strand	-
Start	1	End	509
Name	OJ990503_25.9922.C10.o1.gs	Method	GENSCAN
Start	401	End	509
GI	none	Score	.82
Exons	401..509		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	838	Strand	+
Start	1	End	192
Name	OJ990503_25.9922.C12.o1.np	Method	AAT/NAP
Start	1	End	192
GI	4680186	Score	293
Exons	1..192		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	839	Strand	+
Start	1899	End	2635
Name	OJ990503_25.9922.C12.o1.gp	Method	AAT/GAP
Start	1899	End	2635
GI	101153_1.R1084	Score	395

Exons	1899..1934, 2381..2635		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-115 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	840	Strand	-
Start	3612	End	3886
Name	OJ990503_25.9922.C12.o2.gp	Method	AAT/GAP
Start	3612	End	3886
GI	61605_1.R1084	Score	461
Exons	3612..3886		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	841	Strand	-
Start	4520	End	5007
Name	OJ990503_25.9922.C12.o3.gp	Method	AAT/GAP
Start	4520	End	5007
GI	uC-osflcyp162a07a1	Score	694
Exons	4520..4747, 4847..5007		
GI Descrip.	'4680179/gb|AAD27547.1|AF111709_1 2.0e-40 (AF111709) polyprotein [Oryza sativa subsp. indica]'		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o9.tw	Method	TBLASTX:Wheat
Start	4572	End	11861
GI	none	Score	179
Exons	4572..4772, 4600..4773, 4625..4774, 11662..11859, 11664..11861		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o6.tm	Method	TBLASTX:Maize
Start	4825	End	11627
GI	none	Score	215
Exons	4825..5088, 4848..5012, 11322..11627, 11449..11613		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o7.tw	Method	TBLASTX:Wheat
Start	4825	End	11628
GI	none	Score	247
Exons	4825..5088, 4917..5018, 11277..11627, 11434..11628		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o2.gs	Method	GENSCAN
Start	5831	End	11939
GI	none	Score	.5
Exons	5831..5872, 6352..6513, 6583..6822, 7069..7181, 7598..8174, 8505..11939		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o2.np	Method	AAT/NAP
Start	7584	End	11996
GI	4680179	Score	5397
Exons	7584..10985, 11019..11996		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o6.tw	Method	TBLASTX:Wheat
Start	7629	End	7962
GI	none	Score	121
Exons	7629..7961, 7650..7958, 7693..7962		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o1.tm	Method	TBLASTX:Maize
Start	7809	End	8408
GI	none	Score	113
Exons	7809..8174, 7824..8087, 7825..8178, 8164..8250, 8165..8251, 8183..8251, 8248..8319, 8255..8320, 8308..8400, 8322..8408, 8362..8400		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o2.tw	Method	TBLASTX:Wheat
Start	7962	End	8588
GI	none	Score	88
Exons	7962..8171, 8074..8172, 8164..8319, 8168..8320, 8198..8344, 8322..8588, 8328..8495		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o4.tm	Method	TBLASTX:Maize
Start	8457	End	8749
GI	none	Score	202
Exons	8457..8747, 8461..8748, 8588..8749		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o2.ts	Method	TBLASTX:Soybean
Start	8547	End	8807
GI	none	Score	148
Exons	8547..8807, 8548..8802		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o1.tc	Method	TBLASTX:Cress
Start	8571	End	8888

GI	none	Score	85
Exons	8571..8714, 8572..8712, 8715..8888		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o1.tw	Method	TBLASTX:Wheat
Start	8595	End	9173
GI	none	Score	331
Exons	8595..9173, 8596..9162		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o2.tm	Method	TBLASTX:Maize
Start	9153	End	9516
GI	none	Score	158
Exons	9153..9515, 9162..9515, 9166..9516		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o3.tw	Method	TBLASTX:Wheat
Start	9174	End	9587
GI	none	Score	338
Exons	9174..9587, 9175..9555		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o3.ts	Method	TBLASTX:Soybean
Start	9336	End	9581
GI	none	Score	66
Exons	9336..9581, 9436..9564		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o3.tm	Method	TBLASTX:Maize
Start	9552	End	10052
GI	none	Score	95
Exons	9552..9866, 9673..9801, 9873..10052, 9898..10044		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o5.tw	Method	TBLASTX:Wheat
Start	9588	End	9890
GI	none	Score	171
Exons	9588..9890, 9594..9887, 9604..9888		

Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o1.ts	Method	TBLASTX:Soybean
Start	9603	End	9998
GI	none	Score	110

Exons	9603..9875, 9603..9962, 9604..9894, 9922..9960, 9929..9961, 9966..9998, 9967..9996		
Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o4.tw	Method	TBLASTX:Wheat
Start	9939	End	10425
GI	none	Score	277
Exons	9939..10316, 9982..10425, 10371..10421		
Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o2.tc	Method	TBLASTX:Cress
Start	9975	End	10292
GI	none	Score	182
Exons	9975..10292		
Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o5.tm	Method	TBLASTX:Maize
Start	10120	End	10410
GI	none	Score	189
Exons	10120..10410, 10122..10409		
Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o8.tw	Method	TBLASTX:Wheat
Start	10536	End	10959
GI	none	Score	69
Exons	10536..10703, 10591..10704, 10749..10958, 10750..10959		
Seq. No.	445	Seq. ID	OJ990503_25.9922.C12
Gene No.	842	Strand	-
Start	5831	End	11996
Name	OJ990503_25.9922.C12.o7.tm	Method	TBLASTX:Maize
Start	10641	End	10992
GI	none	Score	68
Exons	10641..10964, 10825..10992		
Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	843	Strand	+
Start	2020	End	8080
Name	OJ990503_25.9922.C13.o2.np	Method	AAT/NAP
Start	2020	End	8080
GI	5852180	Score	610
Exons	2020..2070, 3052..3169, 3220..3645, 8020..8080		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		
Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	843	Strand	+
Start	2020	End	8080
Name	OJ990503_25.9922.C13.o2.gs	Method	GENSCAN
Start	3387	End	3917

GI	none	Score	.97
Exons	3387..3917		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	844	Strand	-
Start	220	End	1789
Name	OJ990503_25.9922.C13.o1.gs	Method	GENSCAN
Start	220	End	1789
GI	none	Score	.88
Exons	220..1029, 1736..1789		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o1.gp	Method	AAT/GAP
Start	1919	End	2302
GI	uC-osflcyp033a04b1	Score	669
Exons	1919..2302		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o3.np	Method	AAT/NAP
Start	1926	End	6551
GI	4680179	Score	937
Exons	1926..1958, 4780..4893, 4921..5885, 6435..6551		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o3.gs	Method	GENSCAN
Start	4303	End	6987
GI	none	Score	.44
Exons	4303..5831, 6246..6987		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o1.tm	Method	TBLASTX:Maize
Start	4354	End	4689
GI	none	Score	75
Exons	4354..4509, 4391..4513, 4510..4689		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o4.tw	Method	TBLASTX:Wheat
Start	4354	End	4495
GI	none	Score	121
Exons	4354..4494, 4355..4495		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987

Name	OJ990503_25.9922.C13.o1.ts	Method	TBLASTX:Soybean
Start	4360	End	4635
GI	none	Score	176
Exons	4360..4599, 4361..4597, 4362..4598, 4363..4599, 4603..4635, 4603..4635		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o1.tw	Method	TBLASTX:Wheat
Start	4496	End	4804
GI	none	Score	171
Exons	4496..4702, 4501..4698, 4702..4785, 4705..4788, 4706..4804		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o2.tw	Method	TBLASTX:Wheat
Start	5194	End	5535
GI	none	Score	34
Exons	5194..5535, 5252..5305, 5340..5423, 5405..5509		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o2.tm	Method	TBLASTX:Maize
Start	5236	End	5535
GI	none	Score	40
Exons	5236..5535, 5240..5305, 5379..5417, 5405..5509		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o3.tw	Method	TBLASTX:Wheat
Start	5587	End	5769
GI	none	Score	129
Exons	5587..5769, 5588..5767		

Seq. No.	446	Seq. ID	OJ990503_25.9922.C13
Gene No.	845	Strand	-
Start	1919	End	6987
Name	OJ990503_25.9922.C13.o4.np	Method	AAT/NAP
Start	6226	End	6987
GI	4512229	Score	1087
Exons	6226..6987		
GI Descrip.	(AB014740) ORF0 protein [Oryza sativa]		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	846	Strand	+
Start	1	End	461
Name	OJ990503_25.9922.C14.o1.np	Method	AAT/NAP
Start	1	End	461
GI	5852180	Score	158
Exons	1..461		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14

Gene No.	846	Strand	+
Start	1	End	461
Name	OJ990503_25.9922.C14.o1.gs	Method	GENSCAN
Start	122	End	451
GI	none	Score	.9
Exons	122..451		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o2.gs	Method	GENSCAN
Start	1806	End	4129
GI	none	Score	.46
Exons	1806..1873, 2103..2236, 2869..2971, 3658..4129		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o2.np	Method	AAT/NAP
Start	3489	End	6754
GI	4325357	Score	381
Exons	3489..4219, 5025..5490, 6730..6754		
GI Descrip.	(AF128395) contains similarity to Arabidopsis thaliana retrotransposon Athila hypothetical protein 1 (GB:X81801) [Arabidopsis thaliana]		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o2.tw	Method	TBLASTX:Wheat
Start	3827	End	4198
GI	none	Score	97
Exons	3827..4018, 4043..4198		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o1.ts	Method	TBLASTX:Soybean
Start	5018	End	5428
GI	none	Score	59
Exons	5018..5296, 5324..5428		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o1.tw	Method	TBLASTX:Wheat
Start	5081	End	5428
GI	none	Score	96
Exons	5081..5296, 5312..5428		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o3.gs	Method	GENSCAN
Start	5111	End	6543
GI	none	Score	.43
Exons	5111..5251, 5974..6123, 6428..6543		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o3.np	Method	AAT/NAP
Start	5834	End	6932
GI	479357	Score	697
Exons	5834..6932		
GI Descrip.	hypothetical protein 612 - maize transposon MuA2 gi|22375|emb|CAA44165| (X62251) ORF [Zea mays]		

Seq. No.	447	Seq. ID	OJ990503_25.9922.C14
Gene No.	847	Strand	-
Start	1806	End	6932
Name	OJ990503_25.9922.C14.o1.tm	Method	TBLASTX:Maize
Start	6228	End	6930
GI	none	Score	57
Exons	6228..6266, 6233..6268, 6287..6673, 6339..6386, 6456..6644, 6725..6820, 6820..6930		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	848	Strand	-
Start	1	End	1873
Name	OJ990503_25.9922.C15.o1.np	Method	AAT/NAP
Start	1	End	1873
GI	2130141	Score	401
Exons	1..415, 494..809, 849..987, 1748..1873		
GI Descrip.	mudrA protein - maize transposon MuDR gi|540581 (M76978) mudrA [Zea mays] gi|595816 (U14597) mudrA gene product [Zea mays]		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	849	Strand	-
Start	12706	End	18540
Name	OJ990503_25.9922.C15.o5.tm	Method	TBLASTX:Maize
Start	20	End	346
GI	none	Score	131
Exons	20..343, 21..236, 158..346		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	849	Strand	-
Start	12706	End	18540
Name	OJ990503_25.9922.C15.o2.np	Method	AAT/NAP
Start	12706	End	18540
GI	6016874	Score	724
Exons	12706..12764, 14790..15084, 16156..16484, 16775..16955, 17343..17502, 17890..18131, 18487..18540		
GI Descrip.	(AP000570) ESTs C19143(E10020),D25076(R3116) correspond to a region of the predicted gene.; Similar to putative AC9 transposase. (P03010) [Oryza sativa]		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	849	Strand	-
Start	12706	End	18540
Name	OJ990503_25.9922.C15.o3.tm	Method	TBLASTX:Maize
Start	16205	End	16453
GI	none	Score	206
Exons	16205..16435, 16207..16449, 16211..16453		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	849	Strand	-
Start	12706	End	18540
Name	OJ990503_25.9922.C15.o1.ts	Method	TBLASTX:Soybean
Start	16222	End	17043
GI	none	Score	90
Exons	16222..16443, 16235..16438, 16936..17043		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	849	Strand	-
Start	12706	End	18540
Name	OJ990503_25.9922.C15.o4.tm	Method	TBLASTX:Maize
Start	16764	End	17088
GI	none	Score	117
Exons	16764..16823, 16828..17088, 16829..17041, 16885..17043, 16932..17075		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	849	Strand	-
Start	12706	End	18540
Name	OJ990503_25.9922.C15.o2.tm	Method	TBLASTX:Maize
Start	17285	End	17601
GI	none	Score	151
Exons	17285..17506, 17287..17511, 17293..17532, 17521..17601		

Seq. No.	448	Seq. ID	OJ990503_25.9922.C15
Gene No.	849	Strand	-
Start	12706	End	18540
Name	OJ990503_25.9922.C15.o1.tm	Method	TBLASTX:Maize
Start	17695	End	18198
GI	none	Score	89
Exons	17695..17733, 17720..17794, 17728..17790, 17809..18066, 17810..18064, 18094..18132, 18118..18198		

Seq. No.	449	Seq. ID	OJ990503_25.9922.C16
Gene No.	850	Strand	+
Start	1838	End	5542
Name	OJ990503_25.9922.C16.o1.gs	Method	GENSCAN
Start	1838	End	5518
GI	none	Score	.75
Exons	1838..1906, 2616..2686, 2782..2878, 3816..3948, 4117..4241, 4310..4483, 4581..4612, 4693..4901, 4921..5112, 5160..5518		

Seq. No.	449	Seq. ID	OJ990503_25.9922.C16
Gene No.	850	Strand	+
Start	1838	End	5542
Name	OJ990503_25.9922.C16.o1.np	Method	AAT/NAP
Start	2348	End	4184
GI	6721512	Score	73
Exons	2348..2461, 2489..2566, 4127..4184		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	449	Seq. ID	OJ990503_25.9922.C16
Gene No.	850	Strand	+
Start	1838	End	5542
Name	OJ990503_25.9922.C16.o2.np	Method	AAT/NAP

Start	3315	End	4899
GI	6721558	Score	178
Exons	3315..3414, 4117..4342, 4793..4899		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa] gi|6815083|dbj|BAA90369.1| (AP001081) hypothetical protein [Oryza sativa]		

Seq. No.	449	Seq. ID	OJ990503_25.9922.C16
Gene No.	850	Strand	+
Start	1838	End	5542
Name	OJ990503_25.9922.C16.o3.np	Method	AAT/NAP
Start	3745	End	5542
GI	6721561	Score	574
Exons	3745..3811, 4313..4483, 4554..4612, 4693..5310, 5406..5542		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	851	Strand	+
Start	1174	End	1280
Name	OJ990503_25.9922.C17.o1.gs	Method	GENSCAN
Start	1174	End	1280
GI	none	Score	.87
Exons	1174..1280		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	852	Strand	+
Start	6614	End	9401
Name	OJ990503_25.9922.C17.o3.gp	Method	AAT/GAP
Start	6509	End	6893
GI	uC-osflcyp033a04b1	Score	678
Exons	6509..6893		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	852	Strand	+
Start	6614	End	9401
Name	OJ990503_25.9922.C17.o3.gs	Method	GENSCAN
Start	6614	End	9401
GI	none	Score	.84
Exons	6614..6679, 7753..7833, 8145..9401		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	853	Strand	+
Start	9882	End	11677
Name	OJ990503_25.9922.C17.o4.gs	Method	GENSCAN
Start	9882	End	11677
GI	none	Score	.69
Exons	9882..10182, 10585..10797, 10855..10939, 11590..11677		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	854	Strand	-
Start	1173	End	11317

Name	OJ990503_25.9922.C17.o1.np	Method	AAT/NAP
Start	1173	End	2938
GI	6907087	Score	784
Exons	1173..1274, 1815..2382, 2591..2938		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	854	Strand	-
Start	1173	End	11317
Name	OJ990503_25.9922.C17.o2.gs	Method	GENSCAN
Start	1419	End	5306
GI	none	Score	.53
Exons	1419..1472, 1815..1989, 2004..2272, 2319..2703, 3809..3831, 3954..3980, 5184..5306		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	854	Strand	-
Start	1173	End	11317
Name	OJ990503_25.9922.C17.o1.gp	Method	AAT/GAP
Start	4202	End	4451
GI	LIB3434-038-P1-K1-F1	Score	285
Exons	4202..4451		
GI Descrip.	'5257255/dbj|AP000364.1|AP000364 0.0e+00 Oryza sativa genomic DNA, chromosome 8, clone:P0026F07'		

Seq. No.	450	Seq. ID	OJ990503_25.9922.C17
Gene No.	854	Strand	-
Start	1173	End	11317
Name	OJ990503_25.9922.C17.o2.np	Method	AAT/NAP
Start	4446	End	11317
GI	5852180	Score	558
Exons	4446..4487, 5188..5602, 5653..5749, 6726..6810, 11297..11317		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	451	Seq. ID	OJ990503_25.9922.C18
Gene No.	855	Strand	-
Start	443	End	920
Name	OJ990503_25.9922.C18.o1.gs	Method	GENSCAN
Start	443	End	920
GI	none	Score	.81
Exons	443..621, 872..920		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	856	Strand	+
Start	50	End	280
Name	OJ990503_25.9922.C19.o1.gs	Method	GENSCAN
Start	50	End	280
GI	none	Score	.64
Exons	50..280		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	857	Strand	+
Start	8598	End	8979
Name	OJ990503_25.9922.C19.o2.gp	Method	AAT/GAP
Start	8598	End	8979

GI	uC-osflcyp033a04b1	Score	659
Exons	8598..8979		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	858	Strand	+
Start	10415	End	15046
Name	OJ990503_25.9922.C19.o3.np	Method	AAT/NAP
Start	10415	End	15046
GI	5091513	Score	1162
Exons	10415..10469, 11370..11857, 12698..13671, 13755..14023, 14925..15046		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	859	Strand	-
Start	1304	End	1368
Name	OJ990503_25.9922.C19.o1.gp	Method	AAT/GAP
Start	1304	End	1368
GI	uC-osflcyp158c04a1	Score	79
Exons	1304..1368		
GI Descrip.	'4581164/gb|AAD24647.1|AC006220_3 2.0e-17 (AC006220) putative polyprotein [Arabidopsis thaliana]'		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o1.np	Method	AAT/NAP
Start	1719	End	4827
GI	5902445	Score	2926
Exons	1719..2985, 3021..4827		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o3.tw	Method	TBLASTX:Wheat
Start	1746	End	2324
GI	none	Score	323
Exons	1746..1859, 1884..2324		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o2.gs	Method	GENSCAN
Start	2058	End	11066
GI	none	Score	.5
Exons	2058..2280, 2650..3194, 3280..3838, 4037..4144, 4244..4836, 5005..6523, 7285..7589, 7772..7862, 8828..8881, 10442..10570, 10942..11066		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o4.tw	Method	TBLASTX:Wheat
Start	2460	End	2843

GI	none	Score	40
Exons	2460..2843, 2461..2493, 2469..2636, 2527..2835		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o2.tm	Method	TBLASTX:Maize
Start	2496	End	2957
GI	none	Score	54
Exons	2496..2957, 2497..2613, 2638..2838		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o6.tw	Method	TBLASTX:Wheat
Start	3334	End	3741
GI	none	Score	107
Exons	3334..3492, 3515..3721, 3517..3741		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o1.ts	Method	TBLASTX:Soybean
Start	3832	End	4257
GI	none	Score	76
Exons	3832..4257, 4073..4225		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o2.tw	Method	TBLASTX:Wheat
Start	3887	End	4311
GI	none	Score	266
Exons	3887..4264, 3889..4311, 3919..4308		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o3.tm	Method	TBLASTX:Maize
Start	3985	End	4368
GI	none	Score	142
Exons	3985..4368, 3986..4264		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o1.tm	Method	TBLASTX:Maize
Start	4396	End	4752
GI	none	Score	229
Exons	4396..4752, 4397..4717		

Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o1.tw	Method	TBLASTX:Wheat
Start	4426	End	4881
GI	none	Score	369

Exons	4426..4881, 4427..4873, 4441..4881		
Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o2.np	Method	AAT/NAP
Start	4894	End	8782
GI	5902444	Score	947
Exons	4894..6523, 7504..7655, 8735..8782		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		
Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o5.tw	Method	TBLASTX:Wheat
Start	5074	End	5508
GI	none	Score	75
Exons	5074..5235, 5248..5289, 5326..5508, 5327..5500		
Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o7.tw	Method	TBLASTX:Wheat
Start	6091	End	6489
GI	none	Score	245
Exons	6091..6489		
Seq. No.	452	Seq. ID	OJ990503_25.9922.C19
Gene No.	860	Strand	-
Start	2058	End	11066
Name	OJ990503_25.9922.C19.o4.tm	Method	TBLASTX:Maize
Start	6253	End	6513
GI	none	Score	195
Exons	6253..6513		
Seq. No.	453	Seq. ID	OJ990503_25.9922.C20
Gene No.	861	Strand	+
Start	532	End	1959
Name	OJ990503_25.9922.C20.o1.tm	Method	TBLASTX:Maize
Start	488	End	889
GI	none	Score	51
Exons	488..550, 503..547, 565..618, 567..617, 620..757, 677..754, 804..887, 827..889, 827..889		
Seq. No.	453	Seq. ID	OJ990503_25.9922.C20
Gene No.	861	Strand	+
Start	532	End	1959
Name	OJ990503_25.9922.C20.o1.np	Method	AAT/NAP
Start	532	End	1959
GI	6175164	Score	225
Exons	532..756, 825..888, 1919..1959		
GI Descrip.	(AC011437) putative tryptophanyl-tRNA synthetase [Arabidopsis thaliana]		
Seq. No.	453	Seq. ID	OJ990503_25.9922.C20
Gene No.	861	Strand	+
Start	532	End	1959

Name	OJ990503_25.9922.C20.o1.ts	Method	TBLASTX:Soybean
Start	565	End	888
GI	none	Score	58
Exons	565..612, 567..611, 619..690,	620..757,	850..888

Seq. No.	453	Seq. ID	OJ990503_25.9922.C20
Gene No.	861	Strand	+
Start	532	End	1959
Name	OJ990503_25.9922.C20.o1.tc	Method	TBLASTX:Cress
Start	573	End	888
GI	none	Score	61
Exons	573..617, 574..621, 613..690, 850..888	614..757, 725..757, 825..887,	

Seq. No.	454	Seq. ID	OJ990503_25.9922.C21
Gene No.	862	Strand	+
Start	553	End	4103
Name	OJ990503_25.9922.C21.o1.np	Method	AAT/NAP
Start	553	End	3186
GI	6907087	Score	562
Exons	553..604, 1518..1831, 1876..2545, 3085..3186		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	454	Seq. ID	OJ990503_25.9922.C21
Gene No.	862	Strand	+
Start	553	End	4103
Name	OJ990503_25.9922.C21.o1.gs	Method	GENSCAN
Start	823	End	4103
GI	none	Score	.65
Exons	823..970, 1091..1315, 1644..2545, 2696..2835, 3982..4103		

Seq. No.	454	Seq. ID	OJ990503_25.9922.C21
Gene No.	863	Strand	+
Start	5505	End	9493
Name	OJ990503_25.9922.C21.o4.np	Method	AAT/NAP
Start	5505	End	9493
GI	1399945	Score	61
Exons	5505..5659, 5688..5746, 9066..9157, 9419..9493		
GI Descrip.	(U60194) RNA helicase GLH-2 [Caenorhabditis elegans] gi|1405387 (U60449) GLH-2 [Caenorhabditis elegans]		

Seq. No.	454	Seq. ID	OJ990503_25.9922.C21
Gene No.	864	Strand	-
Start	4161	End	9795
Name	OJ990503_25.9922.C21.o2.np	Method	AAT/NAP
Start	4161	End	9795
GI	6063554	Score	151
Exons	4161..4340, 4961..4991, 5640..5859, 9762..9795		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	454	Seq. ID	OJ990503_25.9922.C21
Gene No.	864	Strand	-
Start	4161	End	9795

Name	OJ990503_25.9922.C21.o3.np	Method	AAT/NAP
Start	6573	End	8521
GI	4680186	Score	185
Exons	6573..6771, 8481..8521		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	455	Seq. ID	OJ990503_25.9922.C22
Gene No.	865	Strand	+
Start	664	End	1045
Name	OJ990503_25.9922.C22.o1.gp	Method	AAT/GAP
Start	664	End	1045
GI	uC-osflcyp033a04b1	Score	655
Exons	664..1045		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	455	Seq. ID	OJ990503_25.9922.C22
Gene No.	866	Strand	+
Start	3666	End	4847
Name	OJ990503_25.9922.C22.o2.np	Method	AAT/NAP
Start	3666	End	4847
GI	6907087	Score	472
Exons	3666..4029, 4074..4847		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	455	Seq. ID	OJ990503_25.9922.C22
Gene No.	867	Strand	+
Start	4900	End	5771
Name	OJ990503_25.9922.C22.o2.gp	Method	AAT/GAP
Start	4900	End	5771
GI	4107138	Score	1367
Exons	4900..5771		
GI Descrip.	5852170/emb|AL117265.1|OST17804 1.0e-149 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804		

Seq. No.	455	Seq. ID	OJ990503_25.9922.C22
Gene No.	868	Strand	-
Start	1	End	6513
Name	OJ990503_25.9922.C22.o3.np	Method	AAT/NAP
Start	1	End	6513
GI	5852175	Score	94
Exons	1..42, 5025..5071, 5697..5807, 6364..6403, 6464..6513		
GI Descrip.	(AL117265) zhb0005.1 [Oryza sativa]		

Seq. No.	455	Seq. ID	OJ990503_25.9922.C22
Gene No.	868	Strand	-
Start	1	End	6513
Name	OJ990503_25.9922.C22.o1.gs	Method	GENSCAN
Start	581	End	5929
GI	none	Score	.68
Exons	581..797, 894..947, 3683..3782, 3859..4531, 4770..4899, 5369..5454, 5697..5798, 5888..5929		

Seq. No.	455	Seq. ID	OJ990503_25.9922.C22
Gene No.	868	Strand	-

Start	1	End	6513
Name	OJ990503_25.9922.C22.o1.np	Method	AAT/NAP
Start	597	End	1688
GI	4680186	Score	344
Exons	597..797, 1635..1688		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	456	Seq. ID	OJ990503_25.9922.C23
Gene No.	869	Strand	+
Start	715	End	7298
Name	OJ990503_25.9922.C23.o1.np	Method	AAT/NAP
Start	715	End	7298
GI	6175164	Score	570
Exons	715..926, 1279..1340, 3809..3881, 4199..4398, 5903..5942, 6072..6227, 6882..6974, 7137..7298		
GI Descrip.	(AC011437) putative tryptophanyl-tRNA synthetase [Arabidopsis thaliana]		

Seq. No.	456	Seq. ID	OJ990503_25.9922.C23
Gene No.	870	Strand	-
Start	25	End	1602
Name	OJ990503_25.9922.C23.o1.gs	Method	GENSCAN
Start	25	End	1602
GI	none	Score	.85
Exons	25..134, 140..476, 602..720, 1569..1602		

Seq. No.	456	Seq. ID	OJ990503_25.9922.C23
Gene No.	871	Strand	
Start	3821	End	7238
Name	OJ990503_25.9922.C23.o1.tm	Method	TBLASTX:Maize
Start	3821	End	7238
GI	none	Score	107
Exons	3821..3883, 3822..3881, 3823..3882, 4172..4237, 4196..4255, 4198..4269, 4245..4385, 4245..4385, 4246..4386, 4246..4386, 4247..4387, 6071..6187, 6078..6188, 6186..6242, 6189..6227, 6879..6974, 6880..6975, 6881..6967, 7099..7218, 7134..7238, 7136..7219		

Seq. No.	456	Seq. ID	OJ990503_25.9922.C23
Gene No.	871	Strand	
Start	3821	End	7238
Name	OJ990503_25.9922.C23.o1.ts	Method	TBLASTX:Soybean
Start	4196	End	4395
GI	none	Score	60
Exons	4196..4261, 4198..4251, 4246..4386, 4247..4387, 4252..4395		

Seq. No.	457	Seq. ID	OJ990503_25.9922.C24
Gene No.	872	Strand	+
Start	112	End	236
Name	OJ990503_25.9922.C24.o1.gs	Method	GENSCAN
Start	112	End	236
GI	none	Score	.42
Exons	112..236		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272

Name	OJ990503_25.9922.C26.o1.np	Method	AAT/NAP
Start	1	End	2272
GI	4680179	Score	2351
Exons	1..70, 680..2272		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o1.gs	Method	GENSCAN
Start	660	End	2247
GI	none	Score	.7
Exons	660..831, 964..2247		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o4.tw	Method	TBLASTX:Wheat
Start	691	End	830
GI	none	Score	79
Exons	691..804, 692..823, 692..829, 693..830		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o4.tm	Method	TBLASTX:Maize
Start	692	End	896
GI	none	Score	229
Exons	692..895, 693..896		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o2.tw	Method	TBLASTX:Wheat
Start	831	End	1256
GI	none	Score	580
Exons	831..1256, 833..1249, 906..1256		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o2.ts	Method	TBLASTX:Soybean
Start	840	End	1085
GI	none	Score	196
Exons	840..1085		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o2.tm	Method	TBLASTX:Maize
Start	903	End	1256
GI	none	Score	456
Exons	903..1256, 908..1171, 1217..1249		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272

Name	OJ990503_25.9922.C26.o1.tw	Method	TBLASTX:Wheat
Start	1287	End	1823
GI	none	Score	602
Exons	1287..1823, 1289..1822		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o3.tm	Method	TBLASTX:Maize
Start	1440	End	1787
GI	none	Score	267
Exons	1440..1703, 1473..1787, 1583..1786		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o1.ts	Method	TBLASTX:Soybean
Start	1611	End	1871
GI	none	Score	302
Exons	1611..1871, 1613..1870, 1614..1871		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o1.tm	Method	TBLASTX:Maize
Start	1788	End	2105
GI	none	Score	463
Exons	1788..2105, 1790..2098, 1803..2099		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o3.tw	Method	TBLASTX:Wheat
Start	1830	End	2272
GI	none	Score	532
Exons	1830..2267, 1832..2272		

Seq. No.	458	Seq. ID	OJ990503_25.9922.C26
Gene No.	873	Strand	+
Start	1	End	2272
Name	OJ990503_25.9922.C26.o5.tm	Method	TBLASTX:Maize
Start	2111	End	2267
GI	none	Score	191
Exons	2111..2266, 2112..2267		

Seq. No.	459	Seq. ID	OJ990503_25.9922.C27
Gene No.	874	Strand	+
Start	329	End	1967
Name	OJ990503_25.9922.C27.o1.np	Method	AAT/NAP
Start	329	End	1967
GI	6063554	Score	292
Exons	329..481, 598..848, 1796..1967		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	459	Seq. ID	OJ990503_25.9922.C27

Gene No.	875	Strand	+
Start	3095	End	5265
Name	OJ990503_25.9922.C27.o2.gs	Method	GENSCAN
Start	3095	End	5265
GI	none	Score	.81
Exons	3095..3169, 3839..3996, 4765..5265		

Seq. No.	459	Seq. ID	OJ990503_25.9922.C27
Gene No.	876	Strand	-
Start	594	End	935
Name	OJ990503_25.9922.C27.o1.gs	Method	GENSCAN
Start	594	End	935
GI	none	Score	.86
Exons	594..935		

Seq. No.	460	Seq. ID	OJ990503_25.9922.C28
Gene No.	877	Strand	-
Start	1813	End	2013
Name	OJ990503_25.9922.C28.o1.gs	Method	GENSCAN
Start	1813	End	2013
GI	none	Score	.82
Exons	1813..2013		

Seq. No.	460	Seq. ID	OJ990503_25.9922.C28
Gene No.	878	Strand	-
Start	3782	End	4590
Name	OJ990503_25.9922.C28.o2.gs	Method	GENSCAN
Start	3782	End	4590
GI	none	Score	.69
Exons	3782..3841, 4030..4315, 4441..4590		

Seq. No.	460	Seq. ID	OJ990503_25.9922.C28
Gene No.	878	Strand	-
Start	3782	End	4590
Name	OJ990503_25.9922.C28.o1.np	Method	AAT/NAP
Start	4030	End	4152
GI	5821432	Score	68
Exons	4030..4152		
GI Descrip.	(AB029060) F1F0-ATPase inhibitor protein [Oryza sativa]		

Seq. No.	460	Seq. ID	OJ990503_25.9922.C28
Gene No.	879	Strand	
Start	4797	End	5431
Name	OJ990503_25.9922.C28.o1.tm	Method	TBLASTX:Maize
Start	4797	End	5431
GI	none	Score	62
Exons	4797..4913, 4798..4917, 4798..4929, 4798..4917, 4806..4961, 4809..4958, 4813..4929, 4836..4928, 4844..4927, 4938..5069, 4955..5140, 4965..5216, 4968..5093, 4973..5107, 4973..5092, 4974..5096, 4976..5083, 4977..5084, 4977..5084, 4983..5069, 4997..5074, 5106..5228, 5109..5234, 5118..5246, 5123..5245, 5124..5246, 5127..5267, 5129..5245, 5129..5239, 5132..5239, 5254..5325, 5259..5330, 5261..5431, 5338..5418, 5348..5422		

Seq. No.	461	Seq. ID	OJ990503_25.9922.C29
Gene No.	880	Strand	+
Start	568	End	5056

Name	OJ990503_25.9922.C29.o1.gs	Method	GENSCAN
Start	568	End	5056
GI	none	Score	.55
Exons	568..683, 1254..1305, 1358..1793, 1884..2536, 2640..2798, 3023..3073, 3241..3475, 3971..4336, 4979..5056		

Seq. No.	461	Seq. ID	OJ990503_25.9922.C29
Gene No.	881	Strand	-
Start	1463	End	1881
Name	OJ990503_25.9922.C29.o1.np	Method	AAT/NAP
Start	1463	End	1881
GI	4558564	Score	143
Exons	1463..1881		
GI Descrip.	(AC007138) predicted protein of unknown function [Arabidopsis thaliana]		

Seq. No.	461	Seq. ID	OJ990503_25.9922.C29
Gene No.	882	Strand	
Start	3475	End	3984
Name	OJ990503_25.9922.C29.o1.tm	Method	TBLASTX:Maize
Start	3475	End	3984
GI	none	Score	65
Exons	3475..3555, 3511..3873, 3609..3869, 3622..3873, 3871..3948, 3885..3953, 3889..3951, 3946..3984		

Seq. No.	461	Seq. ID	OJ990503_25.9922.C29
Gene No.	883	Strand	
Start	4078	End	4394
Name	OJ990503_25.9922.C29.o2.tm	Method	TBLASTX:Maize
Start	4078	End	4394
GI	none	Score	94
Exons	4078..4158, 4147..4386, 4168..4392, 4173..4394		

Seq. No.	461	Seq. ID	OJ990503_25.9922.C29
Gene No.	884	Strand	
Start	4589	End	4946
Name	OJ990503_25.9922.C29.o3.tm	Method	TBLASTX:Maize
Start	4589	End	4946
GI	none	Score	101
Exons	4589..4801, 4590..4793, 4591..4944, 4609..4911, 4611..4946		

Seq. No.	462	Seq. ID	OJ990503_23.9927.C1
Gene No.	885	Strand	-
Start	1	End	623
Name	OJ990503_23.9927.C1.o1.np	Method	AAT/NAP
Start	1	End	623
GI	6691191	Score	443
Exons	1..623		
GI Descrip.	(AC007534) F7F22.15 [Arabidopsis thaliana]		

Seq. No.	462	Seq. ID	OJ990503_23.9927.C1
Gene No.	885	Strand	-
Start	1	End	623
Name	OJ990503_23.9927.C1.o1.tw	Method	TBLASTX:Wheat
Start	1	End	327
GI	none	Score	154
Exons	1..327, 41..310		

Seq. No.	462	Seq. ID	OJ990503_23.9927.C1
Gene No.	885	Strand	-
Start	1	End	623
Name	OJ990503_23.9927.C1.o1.ts	Method	TBLASTX:Soybean
Start	4	End	327
GI	none	Score	158
Exons	4..327, 53..301		

Seq. No.	462	Seq. ID	OJ990503_23.9927.C1
Gene No.	885	Strand	-
Start	1	End	623
Name	OJ990503_23.9927.C1.o1.gs	Method	GENSCAN
Start	202	End	582
GI	none	Score	.85
Exons	202..443, 516..582		

Seq. No.	463	Seq. ID	OJ990503_23.9927.C3
Gene No.	886	Strand	-
Start	1	End	698
Name	OJ990503_23.9927.C3.o1.np	Method	AAT/NAP
Start	1	End	698
GI	2498930	Score	760
Exons	1..417, 585..698		
GI Descrip.	DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]		

Seq. No.	463	Seq. ID	OJ990503_23.9927.C3
Gene No.	886	Strand	-
Start	1	End	698
Name	OJ990503_23.9927.C3.o1.gs	Method	GENSCAN
Start	23	End	644
GI	none	Score	1
Exons	23..417, 585..644		

Seq. No.	464	Seq. ID	OJ990503_23.9927.C5
Gene No.	887	Strand	+
Start	772	End	1063
Name	OJ990503_23.9927.C5.o1.gs	Method	GENSCAN
Start	772	End	1063
GI	none	Score	.49
Exons	772..875, 997..1063		

Seq. No.	464	Seq. ID	OJ990503_23.9927.C5
Gene No.	888	Strand	-
Start	347	End	438
Name	OJ990503_23.9927.C5.o1.gp	Method	AAT/GAP
Start	347	End	438
GI	uC-osflcyp088b12b1	Score	139
Exons	347..438		
GI Descrip.	'5257255/dbj|AP000364.1|AP000364 3.0e-36 Oryza sativa genomic DNA, chromosome 8, clone:P0026F07'		

Seq. No.	465	Seq. ID	OJ990503_23.9927.C6
Gene No.	889	Strand	+
Start	1	End	296
Name	OJ990503_23.9927.C6.o2.np	Method	AAT/NAP

Start	1	End	296
GI	4680183	Score	123
Exons	1..53, 207..296		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	465	Seq. ID	OJ990503_23.9927.C6
Gene No.	890	Strand	-
Start	1	End	174
Name	OJ990503_23.9927.C6.o1.np	Method	AAT/NAP
Start	1	End	174
GI	6721561	Score	143
Exons	1..174		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	466	Seq. ID	OJ990503_23.9927.C7
Gene No.	891	Strand	+
Start	1256	End	2682
Name	OJ990503_23.9927.C7.o1.gs	Method	GENSCAN
Start	1256	End	2682
GI	none	Score	.49
Exons	1256..1548, 2061..2682		

Seq. No.	466	Seq. ID	OJ990503_23.9927.C7
Gene No.	891	Strand	+
Start	1256	End	2682
Name	OJ990503_23.9927.C7.o2.np	Method	AAT/NAP
Start	2179	End	2664
GI	4263047	Score	309
Exons	2179..2664		
GI Descrip.	(AC005142) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	466	Seq. ID	OJ990503_23.9927.C7
Gene No.	892	Strand	+
Start	3328	End	4413
Name	OJ990503_23.9927.C7.o3.np	Method	AAT/NAP
Start	3328	End	4413
GI	5091513	Score	164
Exons	3328..3357, 4110..4413		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	466	Seq. ID	OJ990503_23.9927.C7
Gene No.	893	Strand	-
Start	1105	End	4375
Name	OJ990503_23.9927.C7.o1.np	Method	AAT/NAP
Start	1105	End	3514
GI	81286	Score	110
Exons	1105..1736, 2343..2457, 3494..3514		
GI Descrip.	extensin - Volvox carteri (fragment) gi|21992|emb|CAA46283| (X65165) extensin [Volvox carteri]		

Seq. No.	466	Seq. ID	OJ990503_23.9927.C7
Gene No.	893	Strand	-
Start	1105	End	4375

Name	OJ990503_23.9927.C7.o1.tm	Method	TBLASTX:Maize
Start	1363	End	2474
GI	none	Score	161
Exons	1363..1473, 2191..2316, 2193..2333, 2365..2469, 2379..2474		

Seq. No.	466	Seq. ID	OJ990503_23.9927.C7
Gene No.	893	Strand	-
Start	1105	End	4375
Name	OJ990503_23.9927.C7.o1.gp	Method	AAT/GAP
Start	2763	End	3212
GI	72524_1.R1084	Score	420
Exons	2763..2784, 2888..3212		
GI Descrip.	'5091496/dbj|AB023482.2|AB023482 3.0e-84 Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence'		

Seq. No.	466	Seq. ID	OJ990503_23.9927.C7
Gene No.	893	Strand	-
Start	1105	End	4375
Name	OJ990503_23.9927.C7.o2.gs	Method	GENSCAN
Start	3369	End	4375
GI	none	Score	.79
Exons	3369..3397, 3571..3748, 4307..4375		

Seq. No.	467	Seq. ID	OJ990503_23.9927.C8
Gene No.	894	Strand	+
Start	716	End	5982
Name	OJ990503_23.9927.C8.o1.gs	Method	GENSCAN
Start	716	End	3040
GI	none	Score	.78
Exons	716..1086, 1892..2365, 2541..2664, 2711..3040		

Seq. No.	467	Seq. ID	OJ990503_23.9927.C8
Gene No.	894	Strand	+
Start	716	End	5982
Name	OJ990503_23.9927.C8.o1.np	Method	AAT/NAP
Start	716	End	5982
GI	5091513	Score	888
Exons	716..919, 969..1210, 1954..2912, 3362..3435, 3532..3738, 5952..5982		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	467	Seq. ID	OJ990503_23.9927.C8
Gene No.	895	Strand	-
Start	238	End	550
Name	OJ990503_23.9927.C8.o1.gp	Method	AAT/GAP
Start	238	End	550
GI	72524_1.R1084	Score	424
Exons	238..550		
GI Descrip.	'5091496/dbj|AB023482.2|AB023482 3.0e-84 Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence'		

Seq. No.	467	Seq. ID	OJ990503_23.9927.C8
Gene No.	896	Strand	-
Start	4084	End	7969
Name	OJ990503_23.9927.C8.o2.np	Method	AAT/NAP
Start	4084	End	7322
GI	5852093	Score	46

Exons	4084..4177, 5795..5934, 7252..7322		
GI Descrip.	(AL117264) zwh16.1 [Oryza sativa]		
Seq. No.	467	Seq. ID	OJ990503_23.9927.C8
Gene No.	896	Strand	-
Start	4084	End	7969
Name	OJ990503_23.9927.C8.o3.gs	Method	GENSCAN
Start	4810	End	7969
GI	none	Score	.58
Exons	4810..4838, 5344..5505, 6127..6314, 7421..7590, 7868..7969		
Seq. No.	467	Seq. ID	OJ990503_23.9927.C8
Gene No.	896	Strand	-
Start	4084	End	7969
Name	OJ990503_23.9927.C8.o2.gp	Method	AAT/GAP
Start	5013	End	5325
GI	72524_1.R1084	Score	420
Exons	5013..5325		
GI Descrip.	'5091496/dbj|AB023482.2|AB023482 3.0e-84 Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence'		
Seq. No.	468	Seq. ID	OJ990503_23.9927.C9
Gene No.	897	Strand	
Start	675	End	1001
Name	OJ990503_23.9927.C9.o1.tw	Method	TBLASTX:Wheat
Start	675	End	1001
GI	none	Score	143
Exons	675..1001, 679..990		
Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	898	Strand	+
Start	1697	End	6753
Name	OJ990503_23.9927.C10.o3.np	Method	AAT/NAP
Start	1697	End	6753
GI	4680186	Score	362
Exons	1697..1786, 2907..2971, 5658..5712, 6551..6753		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		
Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	899	Strand	-
Start	1	End	6395
Name	OJ990503_23.9927.C10.o1.np	Method	AAT/NAP
Start	1	End	4368
GI	4680179	Score	5112
Exons	1..3252, 3286..4368		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		
Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	899	Strand	-
Start	1	End	6395
Name	OJ990503_23.9927.C10.o1.gs	Method	GENSCAN
Start	28	End	6395
GI	none	Score	.74
Exons	28..1002, 1135..1827, 1870..2174, 2289..4368, 4594..5415, 6351..6395		
Seq. No.	469	Seq. ID	OJ990503_23.9927.C10

Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o8.tw	Method	TBLASTX:Wheat
Start	1	End	229
GI	none	Score	127
Exons	1..228, 2..229		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o1.tm	Method	TBLASTX:Maize
Start	76	End	675
GI	none	Score	241
Exons	76..516, 92..514, 514..675, 521..643		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o1.tw	Method	TBLASTX:Wheat
Start	229	End	855
GI	none	Score	284
Exons	229..855, 230..799		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o4.tm	Method	TBLASTX:Maize
Start	724	End	1016
GI	none	Score	208
Exons	724..1014, 728..1015, 855..1016		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o2.ts	Method	TBLASTX:Soybean
Start	814	End	1050
GI	none	Score	149
Exons	814..1050, 815..1042		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o3.tw	Method	TBLASTX:Wheat
Start	862	End	1351
GI	none	Score	306
Exons	862..1350, 863..1351		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o2.tw	Method	TBLASTX:Wheat
Start	1351	End	1854
GI	none	Score	362
Exons	1351..1854, 1433..1822		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-

Start	6303	End	6686
Name	OJ990503_23.9927.C10.o2.tm	Method	TBLASTX:Maize
Start	1420	End	1783
GI	none	Score	163
Exons	1420..1782, 1429..1782, 1433..1783		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o3.ts	Method	TBLASTX:Soybean
Start	1603	End	1848
GI	none	Score	66
Exons	1603..1848, 1703..1831		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o3.tm	Method	TBLASTX:Maize
Start	1819	End	2319
GI	none	Score	50
Exons	1819..2133, 1862..1912, 1949..1993, 2140..2319		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o5.tw	Method	TBLASTX:Wheat
Start	1857	End	2157
GI	none	Score	259
Exons	1857..2003, 1861..2157, 1871..2155		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o1.ts	Method	TBLASTX:Soybean
Start	1870	End	2265
GI	none	Score	186
Exons	1870..2229, 1871..2161, 2192..2227, 2233..2265, 2234..2263		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o4.tw	Method	TBLASTX:Wheat
Start	2206	End	2688
GI	none	Score	213
Exons	2206..2583, 2249..2584, 2638..2688		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o5.tm	Method	TBLASTX:Maize
Start	2387	End	2676
GI	none	Score	143
Exons	2387..2578, 2389..2580, 2389..2676		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686

Name	OJ990503_23.9927.C10.o7.tw	Method	TBLASTX:Wheat
Start	2803	End	3225
GI	none	Score	69
Exons	2803..2970, 2858..2971, 3016..3225, 3017..3169		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o7.tm	Method	TBLASTX:Maize
Start	2908	End	3261
GI	none	Score	189
Exons	2908..3261		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o6.tw	Method	TBLASTX:Wheat
Start	3544	End	3895
GI	none	Score	99
Exons	3544..3894, 3701..3895		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o6.tm	Method	TBLASTX:Maize
Start	3589	End	3894
GI	none	Score	77
Exons	3589..3894, 3764..3880		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o9.tw	Method	TBLASTX:Wheat
Start	3929	End	4188
GI	none	Score	126
Exons	3929..4126, 3931..4128, 4141..4188		

Seq. No.	469	Seq. ID	OJ990503_23.9927.C10
Gene No.	900	Strand	-
Start	6303	End	6686
Name	OJ990503_23.9927.C10.o1.gp	Method	AAT/GAP
Start	6303	End	6686
GI	uC-osflcyp033a04b1	Score	659
Exons	6303..6686		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	470	Seq. ID	OJ990503_23.9927.C11
Gene No.	901	Strand	+
Start	1	End	6380
Name	OJ990503_23.9927.C11.o2.np	Method	AAT/NAP
Start	1	End	6380
GI	5852175	Score	134
Exons	1..73, 1596..1644, 2217..2320, 2940..2972, 6349..6380		
GI Descrip.	(AL117265) zhb0005.1 [Oryza sativa]		

Seq. No.	470	Seq. ID	OJ990503_23.9927.C11

Gene No.	901	Strand	+
Start	1	End	6380
Name	OJ990503_23.9927.C11.o1.gs	Method	GENSCAN
Start	359	End	4633
GI	none	Score	.52
Exons	359..773, 794..975, 1049..1109, 3111..3562, 4525..4633		

Seq. No.	470	Seq. ID	OJ990503_23.9927.C11
Gene No.	901	Strand	+
Start	1	End	6380
Name	OJ990503_23.9927.C11.o3.np	Method	AAT/NAP
Start	1035	End	6035
GI	5852180	Score	310
Exons	1035..1103, 3148..3564, 5967..6035		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	470	Seq. ID	OJ990503_23.9927.C11
Gene No.	901	Strand	+
Start	1	End	6380
Name	OJ990503_23.9927.C11.o2.gp	Method	AAT/GAP
Start	2832	End	3108
GI	61605_1.R1084	Score	454
Exons	2832..3108		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	470	Seq. ID	OJ990503_23.9927.C11
Gene No.	902	Strand	-
Start	1	End	2211
Name	OJ990503_23.9927.C11.o1.np	Method	AAT/NAP
Start	1	End	2211
GI	5852179	Score	272
Exons	1..19, 742..926, 1001..1200, 2191..2211		
GI Descrip.	(AL117265) zhb0009.1 [Oryza sativa]		

Seq. No.	471	Seq. ID	OJ990503_23.9927.C12
Gene No.	903	Strand	+
Start	142	End	823
Name	OJ990503_23.9927.C12.o1.gs	Method	GENSCAN
Start	142	End	823
GI	none	Score	.55
Exons	142..291, 695..823		

Seq. No.	471	Seq. ID	OJ990503_23.9927.C12
Gene No.	904	Strand	-
Start	690	End	941
Name	OJ990503_23.9927.C12.o1.np	Method	AAT/NAP
Start	690	End	941
GI	4680179	Score	364
Exons	690..941		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	472	Seq. ID	OJ990503_23.9927.C13
Gene No.	905	Strand	+
Start	1	End	515
Name	OJ990503_23.9927.C13.o1.np	Method	AAT/NAP
Start	1	End	515

GI	5091513	Score	638
Exons	1..515		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		
Seq. No.	472	Seq. ID	OJ990503_23.9927.C13
Gene No.	905	Strand	+
Start	1	End	515
Name	OJ990503_23.9927.C13.o1.gs	Method	GENSCAN
Start	74	End	490
GI	none	Score	.71
Exons	74..490		
Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o1.np	Method	AAT/NAP
Start	1	End	873
GI	6498436	Score	406
Exons	1..578, 666..873		
GI Descrip.	(AP000815) hypothetical protein [Oryza sativa]		
Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o1.gs	Method	GENSCAN
Start	627	End	1993
GI	none	Score	.79
Exons	627..795, 1130..1325, 1728..1993		
Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o2.np	Method	AAT/NAP
Start	823	End	2206
GI	6705984	Score	329
Exons	823..1325, 2135..2206		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		
Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o2.tm	Method	TBLASTX:Maize
Start	959	End	1210
GI	none	Score	116
Exons	959..1183, 977..1210		
Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o1.ts	Method	TBLASTX:Soybean
Start	980	End	1325
GI	none	Score	77
Exons	980..1138, 1127..1318, 1130..1291, 1134..1325		
Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206

Name	OJ990503_23.9927.C14.o2.tw	Method	TBLASTX:Wheat
Start	987	End	1324
GI	none	Score	88
Exons	987..1151, 992..1171, 1010..1162, 1096..1176, 1175..1318, 1176..1313, 1181..1324, 1227..1319		

Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o3.np	Method	AAT/NAP
Start	1736	End	2206
GI	4680179	Score	678
Exons	1736..2206		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o1.tw	Method	TBLASTX:Wheat
Start	1781	End	2203
GI	none	Score	186
Exons	1781..2203, 1845..2168		

Seq. No.	473	Seq. ID	OJ990503_23.9927.C14
Gene No.	906	Strand	-
Start	1	End	2206
Name	OJ990503_23.9927.C14.o1.tm	Method	TBLASTX:Maize
Start	1877	End	2138
GI	none	Score	180
Exons	1877..2137, 1878..2138		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	907	Strand	+
Start	3187	End	12469
Name	OJ990503_23.9927.C15.o3.np	Method	AAT/NAP
Start	3187	End	12469
GI	5852180	Score	784
Exons	3187..3209, 6778..6834, 7826..7944, 7996..8423, 12430..12469		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	907	Strand	+
Start	3187	End	12469
Name	OJ990503_23.9927.C15.o4.np	Method	AAT/NAP
Start	8108	End	12469
GI	5852181	Score	116
Exons	8108..8143, 11361..11509, 12445..12469		
GI Descrip.	(AL117265) zhb0011.1 [Oryza sativa]		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	907	Strand	+
Start	3187	End	12469
Name	OJ990503_23.9927.C15.o2.gs	Method	GENSCAN
Start	11658	End	12397
GI	none	Score	.51
Exons	11658..11769, 12011..12137, 12208..12397		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o1.gs	Method	GENSCAN
Start	225	End	9753
GI	none	Score	.52
Exons	225..1220, 1265..2742, 2790..4740, 4965..4993, 5134..5797, 6733..6778, 7850..8020, 8154..8691, 9276..9753		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o1.np	Method	AAT/NAP
Start	228	End	4743
GI	4680179	Score	5357
Exons	228..3624, 3658..4743		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o6.tw	Method	TBLASTX:Wheat
Start	273	End	606
GI	none	Score	124
Exons	273..605, 294..602, 337..606		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o1.tm	Method	TBLASTX:Maize
Start	453	End	1052
GI	none	Score	111
Exons	453..893, 468..731, 469..888, 891..1052, 898..1044		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o1.tw	Method	TBLASTX:Wheat
Start	606	End	1232
GI	none	Score	59
Exons	606..1232, 609..731, 718..1176		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o4.tm	Method	TBLASTX:Maize
Start	1101	End	1391
GI	none	Score	177
Exons	1101..1334, 1105..1326, 1298..1390, 1344..1391		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o2.ts	Method	TBLASTX:Soybean
Start	1191	End	1450
GI	none	Score	92
Exons	1191..1322, 1191..1343, 1192..1326, 1340..1450		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o3.tw	Method	TBLASTX:Wheat
Start	1239	End	1723
GI	none	Score	101
Exons	1239..1334, 1240..1326, 1243..1341, 1343..1627, 1362..1622, 1622..1699, 1625..1723		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o2.tw	Method	TBLASTX:Wheat
Start	1724	End	2227
GI	none	Score	231
Exons	1724..2227, 1802..2179, 1806..2195		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o2.tm	Method	TBLASTX:Maize
Start	1793	End	2156
GI	none	Score	162
Exons	1793..2155, 1802..2155, 1806..2156		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o3.ts	Method	TBLASTX:Soybean
Start	1976	End	2221
GI	none	Score	66
Exons	1976..2221, 2076..2204		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o3.tm	Method	TBLASTX:Maize
Start	2192	End	2692
GI	none	Score	50
Exons	2192..2506, 2235..2285, 2313..2366, 2513..2692, 2538..2684		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o5.tw	Method	TBLASTX:Wheat
Start	2228	End	2530
GI	none	Score	274
Exons	2228..2530, 2244..2528		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o1.ts	Method	TBLASTX:Soybean
Start	2243	End	2638
GI	none	Score	193
Exons	2243..2602, 2244..2534, 2562..2600, 2606..2638, 2607..2636		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o4.tw	Method	TBLASTX:Wheat
Start	2579	End	3064
GI	none	Score	91
Exons	2579..2743, 2622..2738, 2710..2946, 2740..2955, 2753..3064, 3010..3060		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o5.tm	Method	TBLASTX:Maize
Start	2759	End	3049
GI	none	Score	178
Exons	2759..3049, 2761..3048		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o8.tw	Method	TBLASTX:Wheat
Start	3175	End	3597
GI	none	Score	68
Exons	3175..3342, 3230..3343, 3391..3597, 3392..3541		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o7.tm	Method	TBLASTX:Maize
Start	3280	End	3633
GI	none	Score	194
Exons	3280..3633		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o6.tm	Method	TBLASTX:Maize
Start	3961	End	4266
GI	none	Score	87
Exons	3961..4266, 4088..4252		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o7.tw	Method	TBLASTX:Wheat
Start	4147	End	4509
GI	none	Score	143
Exons	4147..4509, 4148..4507		

Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o1.gp	Method	AAT/GAP
Start	5068	End	5522
GI	95437_1.R1084	Score	726
Exons	5068..5522		

GI Descrip.	'4512226/dbj|AB014738.1|AB014738 1.0e-134 Oryza sativa gypsy-type retrotransposon RIRE3 DNA, internal region, complete sequence'		
Seq. No.	474	Seq. ID	OJ990503_23.9927.C15
Gene No.	908	Strand	-
Start	225	End	9753
Name	OJ990503_23.9927.C15.o2.gp	Method	AAT/GAP
Start	6685	End	7070
GI	uC-osflcyp033a04b1	Score	669
Exons	6685..7070		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		
Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	909	Strand	+
Start	1	End	3832
Name	OJ990503_23.9927.C16.o1.np	Method	AAT/NAP
Start	1	End	3832
GI	6691191	Score	2202
Exons	1..1090, 2519..3832		
GI Descrip.	(AC007534) F7F22.15 [Arabidopsis thaliana]		
Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	909	Strand	+
Start	1	End	3832
Name	OJ990503_23.9927.C16.o1.gs	Method	GENSCAN
Start	133	End	1095
GI	none	Score	.76
Exons	133..650, 674..1095		
Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	909	Strand	+
Start	1	End	3832
Name	OJ990503_23.9927.C16.o2.gs	Method	GENSCAN
Start	2816	End	3727
GI	none	Score	.81
Exons	2816..3318, 3625..3727		
Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	910	Strand	+
Start	6953	End	8883
Name	OJ990503_23.9927.C16.o2.np	Method	AAT/NAP
Start	6953	End	8883
GI	5852180	Score	600
Exons	6953..7015, 7998..8115, 8167..8583, 8858..8883		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		
Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	911	Strand	-
Start	6864	End	7245
Name	OJ990503_23.9927.C16.o1.gp	Method	AAT/GAP
Start	6864	End	7245
GI	uC-osflcyp033a04b1	Score	695
Exons	6864..7245		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o1.tw	Method	TBLASTX:Wheat
Start	89	End	520
GI	none	Score	531
Exons	89..520, 91..417, 110..496		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o1.tm	Method	TBLASTX:Maize
Start	254	End	801
GI	none	Score	266
Exons	254..652, 658..801		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o3.ts	Method	TBLASTX:Soybean
Start	380	End	663
GI	none	Score	71
Exons	380..472, 446..652, 446..640, 457..663		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o3.tw	Method	TBLASTX:Wheat
Start	524	End	825
GI	none	Score	199
Exons	524..652, 524..652, 526..654, 655..825, 731..793		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o6.tw	Method	TBLASTX:Wheat
Start	838	End	1089
GI	none	Score	196
Exons	838..1038, 840..971, 841..1008, 1030..1089		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o4.ts	Method	TBLASTX:Soybean
Start	844	End	1038
GI	none	Score	201
Exons	844..978, 844..960, 858..965, 988..1038		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o1.tc	Method	TBLASTX:Cress
Start	2597	End	2899
GI	none	Score	257
Exons	2597..2899		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o4.tw	Method	TBLASTX:Wheat
Start	2621	End	2938
GI	none	Score	288
Exons	2621..2938, 2623..2937		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o2.ts	Method	TBLASTX:Soybean
Start	2920	End	3244
GI	none	Score	73
Exons	2920..2961, 2921..2962, 2959..3243, 2960..3244		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o5.tw	Method	TBLASTX:Wheat
Start	2938	End	3232
GI	none	Score	251
Exons	2938..3156, 2939..3232		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o1.ts	Method	TBLASTX:Soybean
Start	3245	End	3724
GI	none	Score	350
Exons	3245..3634, 3247..3633, 3644..3724		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o2.tw	Method	TBLASTX:Wheat
Start	3251	End	3637
GI	none	Score	365
Exons	3251..3610, 3257..3637, 3313..3636		

Seq. No.	475	Seq. ID	OJ990503_23.9927.C16
Gene No.	912	Strand	-
Start	7643	End	8562
Name	OJ990503_23.9927.C16.o4.gs	Method	GENSCAN
Start	7643	End	8562
GI	none	Score	.53
Exons	7643..7762, 8323..8562		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	913	Strand	+
Start	1156	End	6680
Name	OJ990503_23.9927.C17.o1.gs	Method	GENSCAN
Start	1156	End	6680
GI	none	Score	.49
Exons	1156..1293, 1535..1634, 2215..2495, 2752..2915, 2997..3404, 3473..3548, 3640..3698, 3929..4624, 4721..5320, 5357..5410, 5459..5598, 6452..6680		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	914	Strand	+
Start	12081	End	14078
Name	OJ990503_23.9927.C17.o4.gs	Method	GENSCAN
Start	12081	End	14078
GI	none	Score	.72
Exons	12081..12146, 12508..12558, 12682..12828, 13362..14078		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	915	Strand	+
Start	14154	End	23329
Name	OJ990503_23.9927.C17.o2.np	Method	AAT/NAP
Start	14154	End	17138
GI	6691191	Score	2770
Exons	14154..17138		
GI Descrip.	(AC007534) F7F22.15 [Arabidopsis thaliana]		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	915	Strand	+
Start	14154	End	23329
Name	OJ990503_23.9927.C17.o5.gs	Method	GENSCAN
Start	14637	End	23327
GI	none	Score	.5
Exons	14637..16048, 16101..16260, 16528..16916, 16937..17040, 17480..17722, 17724..18294, 18605..18706, 19786..20038, 20092..20265, 22534..22755, 22854..23327		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	915	Strand	+
Start	14154	End	23329
Name	OJ990503_23.9927.C17.o3.np	Method	AAT/NAP
Start	22534	End	23329
GI	4512231	Score	1252
Exons	22534..23329		
GI Descrip.	(AB014741) ORF0 protein [Oryza sativa]		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	916	Strand	+
Start	23554	End	26821
Name	OJ990503_23.9927.C17.o4.np	Method	AAT/NAP
Start	23554	End	26821
GI	4680179	Score	3760
Exons	23554..24612, 24640..26821		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	916	Strand	+
Start	23554	End	26821
Name	OJ990503_23.9927.C17.o6.gs	Method	GENSCAN
Start	23617	End	26810
GI	none	Score	.92
Exons	23617..23948, 23973..24150, 24247..26017, 26543..26810		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442

Name	OJ990503_23.9927.C17.o1.np	Method	AAT/NAP
Start	5298	End	8436
GI	4378066	Score	915
Exons	5298..5331, 7096..8436		
GI Descrip.	(AF098806) polyprotein [Sorghum bicolor] gi|4680208|gb|AAD27571.1|AF114171_12 (AF114171) polyprotein [Sorghum bicolor]		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o2.gs	Method	GENSCAN
Start	6944	End	7466
GI	none	Score	.68
Exons	6944..7181, 7228..7466		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o7.tw	Method	TBLASTX:Wheat
Start	7584	End	8151
GI	none	Score	67
Exons	7584..7724, 7585..7725, 7765..7884, 7767..7991, 8041..8151		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o3.gs	Method	GENSCAN
Start	7740	End	11563
GI	none	Score	.48
Exons	7740..8242, 8260..9130, 9204..9304, 9455..9708, 9731..9817, 9850..10022, 10248..10640, 10892..11155, 11228..11563		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o2.ts	Method	TBLASTX:Soybean
Start	8435	End	25494
GI	none	Score	392
Exons	8435..8629, 14403..14828, 14429..14668, 14700..14828, 14701..14829, 25360..25494		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o11.tw	Method	TBLASTX:Wheat
Start	8453	End	14693
GI	none	Score	231
Exons	8453..8620, 14403..14693, 14420..14689		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o15.tw	Method	TBLASTX:Wheat
Start	8873	End	9198
GI	none	Score	84
Exons	8873..9094, 8874..9095, 9151..9198		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o13.tw	Method	TBLASTX:Wheat
Start	10140	End	13230
GI	none	Score	199
Exons	10140..10256, 12877..13230		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o2.tm	Method	TBLASTX:Maize
Start	14691	End	25695
GI	none	Score	229
Exons	14691..15053, 25248..25490, 25252..25695		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o2.tw	Method	TBLASTX:Wheat
Start	14694	End	25665
GI	none	Score	222
Exons	14694..14999, 14703..14966, 25182..25622, 25183..25665, 25207..25662		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o1.ts	Method	TBLASTX:Soybean
Start	14994	End	26001
GI	none	Score	226
Exons	14994..15335, 25606..25638, 25606..25638, 25642..26001, 25644..25685, 25758..25895		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o3.tw	Method	TBLASTX:Wheat
Start	15000	End	26001
GI	none	Score	422
Exons	15000..15335, 15002..15325, 25753..26001		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o3.tm	Method	TBLASTX:Maize
Start	15093	End	26082
GI	none	Score	254
Exons	15093..15473, 15224..15472, 25747..26082, 25803..26081		

Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o10.tw	Method	TBLASTX:Wheat
Start	15335	End	15497
GI	none	Score	235

Exons	15335..15496, 15339..15497		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o4.ts	Method	TBLASTX:Soybean
Start	15335	End	26148
GI	none	Score	215
Exons	15335..15550, 15336..15548, 26005..26148		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o1.tm	Method	TBLASTX:Maize
Start	15474	End	26442
GI	none	Score	199
Exons	15474..15785, 15545..15772, 26089..26442, 26094..26435		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o1.tw	Method	TBLASTX:Wheat
Start	15507	End	26442
GI	none	Score	157
Exons	15507..15785, 26017..26442, 26019..26435, 26092..26442		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o5.ts	Method	TBLASTX:Soybean
Start	15660	End	26439
GI	none	Score	195
Exons	15660..15800, 15674..15799, 15788..15838, 15789..15854, 26314..26439		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o1.tc	Method	TBLASTX:Cress
Start	15837	End	16221
GI	none	Score	61
Exons	15837..15914, 15918..16220, 15963..16220, 15964..16221		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o8.tw	Method	TBLASTX:Wheat
Start	15882	End	16259
GI	none	Score	54
Exons	15882..15950, 15927..16259		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o6.ts	Method	TBLASTX:Soybean
Start	16215	End	16557
GI	none	Score	174

Exons	16215..16436, 16241..16426, 16513..16557		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o14.tw	Method	TBLASTX:Wheat
Start	16259	End	16563
GI	none	Score	145
Exons	16259..16426, 16260..16433, 16409..16531, 16513..16545, 16516..16563		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o3.ts	Method	TBLASTX:Soybean
Start	16559	End	17045
GI	none	Score	334
Exons	16559..16738, 16560..16886, 16561..16902, 16956..17045		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o4.tw	Method	TBLASTX:Wheat
Start	16569	End	16905
GI	none	Score	354
Exons	16569..16904, 16570..16905		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o12.tw	Method	TBLASTX:Wheat
Start	23763	End	23961
GI	none	Score	213
Exons	23763..23960, 23764..23961		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o4.tm	Method	TBLASTX:Maize
Start	24013	End	24351
GI	none	Score	235
Exons	24013..24351, 24013..24309		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o6.tw	Method	TBLASTX:Wheat
Start	24013	End	24363
GI	none	Score	305
Exons	24013..24363		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o9.tw	Method	TBLASTX:Wheat
Start	24697	End	25050
GI	none	Score	252

Exons	24697..25050, 24697..24975		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	917	Strand	-
Start	5298	End	26442
Name	OJ990503_23.9927.C17.o5.tm	Method	TBLASTX:Maize
Start	25084	End	25245
GI	none	Score	185
Exons	25084..25245, 25092..25199		
Seq. No.	476	Seq. ID	OJ990503_23.9927.C17
Gene No.	918	Strand	
Start	26470	End	26819
Name	OJ990503_23.9927.C17.o5.tw	Method	TBLASTX:Wheat
Start	26470	End	26819
GI	none	Score	321
Exons	26470..26814, 26475..26813, 26610..26819		
Seq. No.	477	Seq. ID	OJ990503_23.9927.C19
Gene No.	919	Strand	-
Start	1	End	567
Name	OJ990503_23.9927.C19.o1.np	Method	AAT/NAP
Start	1	End	567
GI	4680179	Score	854
Exons	1..567		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		
Seq. No.	477	Seq. ID	OJ990503_23.9927.C19
Gene No.	919	Strand	-
Start	1	End	567
Name	OJ990503_23.9927.C19.o1.tm	Method	TBLASTX:Maize
Start	3	End	408
GI	none	Score	44
Exons	3..89, 3..248, 118..249, 246..407, 253..408		
Seq. No.	477	Seq. ID	OJ990503_23.9927.C19
Gene No.	919	Strand	-
Start	1	End	567
Name	OJ990503_23.9927.C19.o1.tw	Method	TBLASTX:Wheat
Start	3	End	566
GI	none	Score	259
Exons	3..566, 82..534		
Seq. No.	477	Seq. ID	OJ990503_23.9927.C19
Gene No.	919	Strand	-
Start	1	End	567
Name	OJ990503_23.9927.C19.o1.gs	Method	GENSCAN
Start	120	End	416
GI	none	Score	.91
Exons	120..416		
Seq. No.	477	Seq. ID	OJ990503_23.9927.C19
Gene No.	919	Strand	-
Start	1	End	567
Name	OJ990503_23.9927.C19.o2.tm	Method	TBLASTX:Maize
Start	408	End	567
GI	none	Score	104

Exons	408..566, 411..566, 421..567		
Seq. No.	478	Seq. ID	OJ990503_23.9927.C20
Gene No.	920	Strand	+
Start	1	End	1967
Name	OJ990503_23.9927.C20.o1.np	Method	AAT/NAP
Start	1	End	1967
GI	5852181	Score	101
Exons	1..46, 1206..1496, 1918..1967		
GI Descrip.	(AL117265) zhb0011.1 [Oryza sativa]		
Seq. No.	478	Seq. ID	OJ990503_23.9927.C20
Gene No.	921	Strand	-
Start	1145	End	1537
Name	OJ990503_23.9927.C20.o1.gs	Method	GENSCAN
Start	1145	End	1537
GI	none	Score	.65
Exons	1145..1256, 1377..1537		
Seq. No.	479	Seq. ID	OJ990503_23.9927.C21
Gene No.	922	Strand	-
Start	65	End	646
Name	OJ990503_23.9927.C21.o1.gs	Method	GENSCAN
Start	65	End	646
GI	none	Score	.86
Exons	65..646		
Seq. No.	480	Seq. ID	OJ990503_23.9927.C23
Gene No.	923	Strand	+
Start	85	End	365
Name	OJ990503_23.9927.C23.o1.gs	Method	GENSCAN
Start	85	End	365
GI	none	Score	.43
Exons	85..198, 291..365		
Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	924	Strand	+
Start	1	End	30852
Name	OJ990503_28.9924.C1.o3.np	Method	AAT/NAP
Start	1	End	30852
GI	2135765	Score	221
Exons	1..56, 9732..9845, 9885..10001, 16394..16535, 24859..24888, 27872..28163, 28193..28586, 30818..30852		
GI Descrip.	mucin 2 precursor, intestinal - human (fragments)		
Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	924	Strand	+
Start	1	End	30852
Name	OJ990503_28.9924.C1.o1.gp	Method	AAT/GAP
Start	9205	End	11542
GI	32997_1.R1084	Score	1167
Exons	9205..9290, 9598..10007, 10111..10171, 11448..11542		
GI Descrip.	'2499819/sp|Q42456|APR1_ORYSA 8.0e-49 ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]'		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	924	Strand	+
Start	1	End	30852
Name	OJ990503_28.9924.C1.o1.np	Method	AAT/NAP
Start	9612	End	15420
GI	2499819	Score	1718
Exons	9612..9799, 9830..10007, 10111..10171, 11448..11542, 11633..11745, 12079..12247, 12342..12381, 12507..12571, 13249..13362, 13454..13518, 13791..13947, 14026..14145, 14935..15023, 15339..15420		
GI Descrip.	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR gi|2130068|pir||S66516 aspartic proteinase 1 precursor - rice gi|1030715|dbj|BAA06876.1| (D32165) aspartic protease [Oryza sativa] gi|1711289|dbj|BAA06875| (D32144) aspartic protease [Oryza sativa]		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	924	Strand	+
Start	1	End	30852
Name	OJ990503_28.9924.C1.o2.gs	Method	GENSCAN
Start	9612	End	15423
GI	none	Score	.87
Exons	9612..10007, 10111..10144, 11448..11542, 11633..11745, 13791..13947, 14026..14145, 14935..15023, 15339..15423		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	924	Strand	+
Start	1	End	30852
Name	OJ990503_28.9924.C1.o2.gp	Method	AAT/GAP
Start	11696	End	15699
GI	31243_3.R1084	Score	2230
Exons	11696..11745, 12079..12247, 12342..12381, 12507..12571, 13249..13362, 13454..13518, 13791..13947, 14026..14145, 14935..15023, 15339..15699		
GI Descrip.	'2499819/sp|Q42456|APR1_ORYSA 1.0e-152 ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]'		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	924	Strand	+
Start	1	End	30852
Name	OJ990503_28.9924.C1.o3.gp	Method	AAT/GAP
Start	15792	End	16306
GI	none	Score	994
Exons	15792..16306		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	924	Strand	+
Start	1	End	30852
Name	OJ990503_28.9924.C1.o5.gs	Method	GENSCAN
Start	26779	End	29675
GI	none	Score	.55
Exons	26779..26814, 27749..27896, 28232..28477, 28483..28626, 28687..28758, 28852..28990, 29244..29332, 29611..29675		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	925	Strand	-
Start	16108	End	19506
Name	OJ990503_28.9924.C1.o3.gs	Method	GENSCAN
Start	16108	End	19506
GI	none	Score	.49
Exons	16108..16528, 16649..16980, 18642..18836, 19156..19506		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	925	Strand	-
Start	16108	End	19506
Name	OJ990503_28.9924.C1.o2.np	Method	AAT/NAP
Start	16147	End	19488
GI	6630541	Score	981
Exons	16147..16528, 16649..16980, 18642..18836, 19156..19488		
GI Descrip.	(AC011708) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	925	Strand	-
Start	16108	End	19506
Name	OJ990503_28.9924.C1.o4.gp	Method	AAT/GAP
Start	16745	End	16992
GI	62412_1.R1084	Score	475
Exons	16745..16992		
GI Descrip.	'4454480/gb|AAD20927| 7.0e-26 (AC006234) putative (1-4)-beta-mannan endohydrolase [Arabidopsis thaliana]'		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o2.tm	Method	TBLASTX:Maize
Start	9696	End	15423
GI	none	Score	99
Exons	9696..9797, 9696..9782, 9861..10010, 9867..10043, 10099..10173, 10110..10172, 11447..11548, 11448..11543, 11629..11754, 11631..11735, 11633..11746, 12077..12244, 12079..12246, 12080..12256, 12333..12383, 12341..12382, 12499..12570, 12500..12571, 13172..13198, 13234..13353, 13248..13361, 13249..13362, 13420..13557, 13451..13516, 13784..13852, 13788..13853, 13789..13851, 13831..13953, 13834..13953, 13836..13958, 14018..14125, 14020..14145, 14024..14125, 14025..14144, 14926..15024, 14933..14998, 14934..15023, 15326..15418, 15339..15422, 15339..15419, 15340..15423		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o2.tc	Method	TBLASTX:Cress
Start	9861	End	13489
GI	none	Score	221
Exons	9861..10010, 9869..10009, 10098..10172, 10099..10173, 11435..11548, 11447..11542, 11629..11778, 11633..11746, 12079..12252, 12080..12256, 12333..12383, 12341..12382, 12496..12570, 12500..12571, 13249..13362, 13451..13489		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o3.tw	Method	TBLASTX:Wheat
Start	9861	End	10173
GI	none	Score	207
Exons	9861..10022, 9869..10006, 10099..10173, 10110..10172		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o2.ts	Method	TBLASTX:Soybean
Start	9867	End	15423
GI	none	Score	213
Exons	9867..10010, 9869..9997, 9873..10004, 10099..10173, 10112..10141, 10113..10172, 11447..11542, 11461..11544, 11466..11543, 11629..11787, 11633..11746, 12080..12256, 12082..12282, 12333..12383, 12347..12382, 12496..12570, 12497..12571, 13252..13353, 13275..13346, 13278..13364, 13420..13491, 13445..13492, 13849..13953, 14020..14145, 14025..14144, 14926..15024, 14934..15023, 15339..15419, 15340..15423		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o4.tw	Method	TBLASTX:Wheat
Start	12101	End	12571
GI	none	Score	218
Exons	12101..12256, 12103..12246, 12333..12383, 12482..12571, 12505..12570		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o1.tw	Method	TBLASTX:Wheat
Start	13248	End	15423
GI	none	Score	144
Exons	13248..13361, 13249..13362, 13249..13362, 13289..13363, 13420..13518, 13451..13516, 13758..13925, 13780..13947, 13781..13942, 13789..13953, 13791..13961, 14020..14145, 14025..14141, 14050..14145, 14926..15024, 14933..15037, 14934..15023, 15319..15417, 15332..15418, 15339..15419, 15340..15423		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o4.tc	Method	TBLASTX:Cress
Start	13780	End	15423
GI	none	Score	143
Exons	13780..13953, 13789..13953, 14020..14145, 14025..14141, 14926..15024, 14934..15023, 15337..15414, 15339..15419, 15340..15423		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-

Start	30085	End	30245
Name	OJ990503_28.9924.C1.o1.tm	Method	TBLASTX:Maize
Start	16136	End	16698
GI	none	Score	286
Exons	16136..16522, 16180..16527, 16189..16530, 16648..16698, 16649..16693		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o1.ts	Method	TBLASTX:Soybean
Start	16189	End	19398
GI	none	Score	168
Exons	16189..16527, 16223..16438, 16648..16731, 16649..16726, 16762..16983, 16763..16978, 18628..18837, 18630..18839, 18642..18839, 19139..19213, 19156..19212, 19210..19398, 19211..19249, 19298..19396		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o1.tc	Method	TBLASTX:Cress
Start	16642	End	18800
GI	none	Score	66
Exons	16642..16743, 16646..16726, 16756..16983, 16763..16981, 18639..18800		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o2.tw	Method	TBLASTX:Wheat
Start	16642	End	16954
GI	none	Score	55
Exons	16642..16722, 16655..16723, 16738..16953, 16739..16954		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o3.tm	Method	TBLASTX:Maize
Start	16705	End	17005
GI	none	Score	53
Exons	16705..16749, 16706..16762, 16750..16983, 16766..17005		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o4.tm	Method	TBLASTX:Maize
Start	18744	End	19609
GI	none	Score	120
Exons	18744..18839, 18744..18839, 19145..19216, 19156..19215, 19189..19398, 19205..19249, 19228..19314, 19301..19396, 19550..19609		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o3.tc	Method	TBLASTX:Cress

Start	19142	End	19398
GI	none	Score	36
Exons	19142..19213, 19156..19212, 19210..19398, 19211..19246, 19298..19396		

Seq. No.	481	Seq. ID	OJ990503_28.9924.C1
Gene No.	926	Strand	-
Start	30085	End	30245
Name	OJ990503_28.9924.C1.o4.np	Method	AAT/NAP
Start	30085	End	30245
GI	4680183	Score	138
Exons	30085..30245		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	482	Seq. ID	OJ990503_28.9924.C2
Gene No.	927	Strand	+
Start	6294	End	7724
Name	OJ990503_28.9924.C2.o1.gp	Method	AAT/GAP
Start	6294	End	7724
GI	LIB3432-060-P1-K1-G9	Score	689
Exons	6294..6591, 7638..7724		
GI Descrip.	'5091604/gb|AAD39593.1|AC007858_7 6.0e-17 (AC007858) 10A19I.8 [Oryza sativa]'		

Seq. No.	482	Seq. ID	OJ990503_28.9924.C2
Gene No.	927	Strand	+
Start	6294	End	7724
Name	OJ990503_28.9924.C2.o1.tm	Method	TBLASTX:Maize
Start	6326	End	6589
GI	none	Score	100
Exons	6326..6499, 6358..6582, 6367..6588, 6386..6589		

Seq. No.	482	Seq. ID	OJ990503_28.9924.C2
Gene No.	927	Strand	+
Start	6294	End	7724
Name	OJ990503_28.9924.C2.o1.np	Method	AAT/NAP
Start	6349	End	6566
GI	5091604	Score	170
Exons	6349..6566		
GI Descrip.	(AC007858) 10A19I.8 [Oryza sativa]		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	928	Strand	+
Start	1984	End	2818
Name	OJ990503_28.9924.C3.o1.np	Method	AAT/NAP
Start	1984	End	2818
GI	4006901	Score	176
Exons	1984..2107, 2135..2307, 2469..2818		
GI Descrip.	(Z99708) transcription factor like protein [Arabidopsis thaliana]		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	929	Strand	+
Start	4203	End	7433
Name	OJ990503_28.9924.C3.o1.gp	Method	AAT/GAP
Start	4161	End	4883
GI	uC-osroM202020c02b1	Score	844

Exons	4161..4451, 4640..4762, 4854..4883		
GI Descrip.	'2462733 2.0e-32 (AC002292) Putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana]'		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	929	Strand	+
Start	4203	End	7433
Name	OJ990503_28.9924.C3.o2.np	Method	AAT/NAP
Start	4185	End	7430
GI	2462733	Score	970
Exons	4185..4451, 4640..4762, 4854..4955, 5395..5472, 5526..5627, 6616..6667, 6718..6781, 6809..6920, 7022..7144, 7317..7430		
GI Descrip.	(AC002292) Putative enoyl-CoA hydratase/isomerase [Arabidopsis thaliana]		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	929	Strand	+
Start	4203	End	7433
Name	OJ990503_28.9924.C3.o2.gs	Method	GENSCAN
Start	4203	End	7433
GI	none	Score	.93
Exons	4203..4451, 4640..4762, 4854..4955, 5529..5627, 6616..6663, 6825..6920, 7022..7144, 7317..7433		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	930	Strand	+
Start	8353	End	11193
Name	OJ990503_28.9924.C3.o3.gs	Method	GENSCAN
Start	8353	End	10916
GI	none	Score	.88
Exons	8353..8466, 8593..8665, 9993..10047, 10769..10916		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	930	Strand	+
Start	8353	End	11193
Name	OJ990503_28.9924.C3.o3.np	Method	AAT/NAP
Start	8374	End	10907
GI	2832672	Score	326
Exons	8374..8665, 9993..10047, 10769..10907		
GI Descrip.	(AL021712) nifU-like protein [Arabidopsis thaliana]		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	930	Strand	+
Start	8353	End	11193
Name	OJ990503_28.9924.C3.o2.gp	Method	AAT/GAP
Start	8580	End	11193
GI	1671_1.R1084	Score	1038
Exons	8580..8665, 9993..10047, 10769..11193		
GI Descrip.	'2832672/emb|CAA16772.1| 4.0e-59 (AL021712) nifU-like protein [Arabidopsis thaliana]'		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o3.tm	Method	TBLASTX:Maize
Start	4172	End	4454
GI	none	Score	65

Exons	4172..4252, 4194..4244, 4322..4450, 4323..4454		
Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o1.ts	Method	TBLASTX:Soybean
Start	4205	End	4949
GI	none	Score	64
Exons	4205..4258, 4323..4376, 4331..4357, 4374..4454, 4631..4768, 4639..4767, 4833..4949, 4847..4948		
Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o2.tm	Method	TBLASTX:Maize
Start	4661	End	5587
GI	none	Score	157
Exons	4661..4768, 4663..4776, 4833..4958, 4847..4957, 4853..4987, 5356..5436, 5382..5435, 5517..5585, 5527..5583, 5528..5587		
Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o1.tw	Method	TBLASTX:Wheat
Start	8607	End	11122
GI	none	Score	92
Exons	8607..8663, 8608..8664, 9976..10047, 9992..10048, 9992..10054, 9999..10055, 10765..10812, 10766..10819, 10767..10859, 10767..10859, 10769..10918, 10894..10923, 10994..11044, 11015..11041, 11044..11109, 11048..11122		
Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o3.gp	Method	AAT/GAP
Start	16062	End	16495
GI	760_1.R1084	Score	837
Exons	16062..16495		
GI Descrip.	'4176424/dbj|BAA37171| 2.0e-46 (AB022674) ribosomal protein L12 [Oryza sativa]'		
Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o1.tm	Method	TBLASTX:Maize
Start	16191	End	16494
GI	none	Score	72
Exons	16191..16286, 16193..16261, 16263..16343, 16264..16494, 16265..16486, 16426..16491		
Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o1.tc	Method	TBLASTX:Cress
Start	16297	End	16495
GI	none	Score	98
Exons	16297..16494, 16301..16495		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o2.ts	Method	TBLASTX:Soybean
Start	16297	End	16495
GI	none	Score	38
Exons	16297..16494, 16302..16340, 16388..16495		

Seq. No.	483	Seq. ID	OJ990503_28.9924.C3
Gene No.	931	Strand	-
Start	16062	End	16495
Name	OJ990503_28.9924.C3.o4.np	Method	AAT/NAP
Start	16300	End	16495
GI	4176424	Score	276
Exons	16300..16495		
GI Descrip.	(AB022674) ribosomal protein L12 [Oryza sativa]		

Seq. No.	484	Seq. ID	OJ990503_28.9924.C4
Gene No.	932	Strand	-
Start	1	End	102
Name	OJ990503_28.9924.C4.o1.gp	Method	AAT/GAP
Start	1	End	102
GI	760_1.R1084	Score	183
Exons	1..102		
GI Descrip.	'4176424/dbj|BAA37171| 2.0e-46 (AB022674) ribosomal protein L12 [Oryza sativa]'		

Seq. No.	485	Seq. ID	OJ990503_28.9924.C6
Gene No.	933	Strand	+
Start	266	End	4051
Name	OJ990503_28.9924.C6.o1.gs	Method	GENSCAN
Start	266	End	4051
GI	none	Score	.43
Exons	266..447, 2705..2796, 3232..3329, 3563..4051		

Seq. No.	485	Seq. ID	OJ990503_28.9924.C6
Gene No.	933	Strand	+
Start	266	End	4051
Name	OJ990503_28.9924.C6.o1.gp	Method	AAT/GAP
Start	978	End	1406
GI	94945_1.R1084	Score	560
Exons	978..1406		
GI Descrip.	'4521194/dbj|AB013613.1|AB013613 1.0e-132 Oryza sativa DNA, centromere sequence RCB11'		

Seq. No.	485	Seq. ID	OJ990503_28.9924.C6
Gene No.	934	Strand	+
Start	4350	End	8536
Name	OJ990503_28.9924.C6.o1.np	Method	AAT/NAP
Start	4350	End	8536
GI	6815052	Score	470
Exons	4350..4424, 7718..7981, 8063..8137, 8418..8536		
GI Descrip.	(AP001080) hypothetical protein [Oryza sativa]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	935	Strand	+

Start	3115	End	3542
Name	OJ990503_28.9924.C7.o1.gp	Method	AAT/GAP
Start	3115	End	3542
GI	LIB3479-006-Q6-K1-B11	Score	582
Exons	3115..3542		
GI Descrip.	'5734616/dbj|AP000391.1|AP000391 1.0e-110 Oryza sativa genomic DNA, chromosome 6, clone:P0538C01'		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	936	Strand	+
Start	7322	End	9209
Name	OJ990503_28.9924.C7.o3.np	Method	AAT/NAP
Start	7322	End	9209
GI	6016711	Score	121
Exons	7322..7604, 9175..9209		
GI Descrip.	(AC009325) unknown protein [Arabidopsis thaliana]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	937	Strand	+
Start	11469	End	11965
Name	OJ990503_28.9924.C7.o3.gp	Method	AAT/GAP
Start	11469	End	11965
GI	11905_1.R1084	Score	881
Exons	11469..11965		
GI Descrip.	'4432848/gb|AAD20696| 1.0e-35 (AC006300) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	938	Strand	+
Start	23161	End	25611
Name	OJ990503_28.9924.C7.o4.gs	Method	GENSCAN
Start	23161	End	25549
GI	none	Score	.42
Exons	23161..23307, 23538..23747, 23752..25549		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	938	Strand	+
Start	23161	End	25611
Name	OJ990503_28.9924.C7.o6.np	Method	AAT/NAP
Start	23161	End	25611
GI	5042454	Score	2427
Exons	23161..23311, 23641..23747, 23803..25216, 25441..25611		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	939	Strand	-
Start	2908	End	3322
Name	OJ990503_28.9924.C7.o1.np	Method	AAT/NAP
Start	2908	End	3322
GI	6539570	Score	135
Exons	2908..2974, 3128..3322		
GI Descrip.	(AP000836) hypothetical protein [Oryza sativa]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	940	Strand	-
Start	3458	End	4415
Name	OJ990503_28.9924.C7.o2.np	Method	AAT/NAP

Start	3458	End	4415
GI	6630699	Score	106
Exons	3458..3551, 4172..4415		
GI Descrip.	(AP000969) hypothetical protein [Oryza sativa] gi|6721536|dbj|BAA89566.1| (AP001073) hypothetical protein [Oryza sativa]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o2.tm	Method	TBLASTX:Maize
Start	11331	End	11597
GI	none	Score	92
Exons	11331..11384, 11354..11383, 11378..11443, 11379..11597		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o1.tm	Method	TBLASTX:Maize
Start	13981	End	15385
GI	none	Score	209
Exons	13981..14199, 14009..14200, 14022..14192, 14316..14372, 14317..14370, 15094..15156, 15096..15161, 15331..15384, 15335..15385		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o1.ts	Method	TBLASTX:Soybean
Start	14027	End	15592
GI	none	Score	56
Exons	14027..14206, 14028..14105, 14111..14203, 14316..14372, 14326..14367, 15096..15161, 15115..15165, 15331..15420, 15542..15592		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o4.np	Method	AAT/NAP
Start	14027	End	17951
GI	6573732	Score	360
Exons	14027..14223, 14268..14382, 15088..15173, 15259..15405, 15542..15612, 17883..17951		
GI Descrip.	(AC009398) F20B24.2 [Arabidopsis thaliana]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o2.tw	Method	TBLASTX:Wheat
Start	14027	End	14366
GI	none	Score	135
Exons	14027..14191, 14028..14198, 14313..14366		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o3.gs	Method	GENSCAN

Start	14955	End	21822
GI	none	Score	.78
Exons	14955..14963, 15099..15161, 15542..15604, 15715..15804, 15907..16226, 16887..16931, 17007..17046, 17690..17764, 18103..18205, 19178..19253, 19483..19555, 20124..20216, 20461..20517, 21031..21117, 21226..21380, 21395..21488, 21790..21822		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o5.tm	Method	TBLASTX:Maize
Start	15776	End	16344
GI	none	Score	45
Exons	15776..15805, 15907..16089, 15908..16078, 15908..16096, 16150..16215, 16291..16344		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o4.gp	Method	AAT/GAP
Start	15985	End	16976
GI	426194	Score	658
Exons	15985..16213, 16301..16341, 16887..16976		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o3.tm	Method	TBLASTX:Maize
Start	18798	End	19108
GI	none	Score	144
Exons	18798..18920, 18800..18925, 18800..18868, 18805..18924, 18805..18867, 19000..19101, 19005..19100, 19007..19108, 19009..19101		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o2.ts	Method	TBLASTX:Soybean
Start	18805	End	19224
GI	none	Score	72
Exons	18805..18924, 18817..18924, 19009..19104, 19010..19114, 19183..19224, 19203..19223		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o5.np	Method	AAT/NAP
Start	18805	End	20517
GI	6598555	Score	357
Exons	18805..18924, 19012..19102, 19178..19259, 20105..20216, 20461..20517		
GI Descrip.	(AC006300) unknown protein [Arabidopsis thaliana]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822

Name	OJ990503_28.9924.C7.o5.gp	Method	AAT/GAP
Start	19184	End	21303
GI	2427446	Score	744
Exons	19184..19253, 19483..19555, 20124..20216, 20461..20517, 21031..21117, 21226..21303		
GI Descrip.	4432848/gb|AAD20696| 1.0e-35 (AC006300) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	941	Strand	-
Start	14027	End	21822
Name	OJ990503_28.9924.C7.o4.tm	Method	TBLASTX:Maize
Start	19198	End	21448
GI	none	Score	65
Exons	19198..19254, 19201..19254, 19484..19558, 19485..19556, 20121..20216, 20125..20214, 20461..20517, 20461..20520, 21017..21118, 21031..21120, 21032..21121, 21226..21300, 21230..21301, 21390..21446, 21392..21448		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	942	Strand	
Start	24475	End	24867
Name	OJ990503_28.9924.C7.o1.tw	Method	TBLASTX:Wheat
Start	24475	End	24867
GI	none	Score	57
Exons	24475..24522, 24529..24627, 24546..24626, 24594..24833, 24610..24867		

Seq. No.	486	Seq. ID	OJ990503_28.9924.C7
Gene No.	942	Strand	
Start	24475	End	24867
Name	OJ990503_28.9924.C7.o6.tm	Method	TBLASTX:Maize
Start	24480	End	24765
GI	none	Score	193
Exons	24480..24764, 24517..24765		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o1.np	Method	AAT/NAP
Start	1	End	2919
GI	6498441	Score	3329
Exons	1..335, 519..654, 829..1149, 1342..1743, 1915..2919		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o1.tw	Method	TBLASTX:Wheat
Start	1	End	432
GI	none	Score	534
Exons	1..432, 6..425		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+

Start	1	End	2919
Name	OJ990503_28.9924.C8.o3.ts	Method	TBLASTX:Soybean
Start	19	End	375
GI	none	Score	101
Exons	19..234, 241..375		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o1.gs	Method	GENSCAN
Start	25	End	2772
GI	none	Score	.94
Exons	25..2772		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o1.tm	Method	TBLASTX:Maize
Start	100	End	456
GI	none	Score	392
Exons	100..456, 135..446, 151..456		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o2.tm	Method	TBLASTX:Maize
Start	483	End	867
GI	none	Score	358
Exons	483..848, 484..867		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o2.tw	Method	TBLASTX:Wheat
Start	540	End	965
GI	none	Score	496
Exons	540..965, 541..960		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o1.ts	Method	TBLASTX:Soybean
Start	619	End	990
GI	none	Score	279
Exons	619..990, 636..779		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o3.tw	Method	TBLASTX:Wheat
Start	1591	End	2049
GI	none	Score	234
Exons	1591..1839, 1615..1839, 1680..1853, 1900..2049, 1911..2048		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919

Name	OJ990503_28.9924.C8.o2.ts	Method	TBLASTX:Soybean
Start	1738	End	2304
GI	5666795	Score	68
Exons	1738..1836, 1912..2049, 2104..2304		
GI Descrip.	4206306 2.0e-10 (AF049110) prpol [Zea mays]		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o5.tw	Method	TBLASTX:Wheat
Start	2052	End	2364
GI	none	Score	192
Exons	2052..2228, 2104..2364		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o3.tm	Method	TBLASTX:Maize
Start	2557	End	2874
GI	none	Score	356
Exons	2557..2874, 2586..2867		

Seq. No.	487	Seq. ID	OJ990503_28.9924.C8
Gene No.	943	Strand	+
Start	1	End	2919
Name	OJ990503_28.9924.C8.o4.tw	Method	TBLASTX:Wheat
Start	2560	End	2877
GI	none	Score	311
Exons	2560..2877, 2583..2876		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	944	Strand	+
Start	315	End	778
Name	OJ990503_28.9924.C9.o1.gp	Method	AAT/GAP
Start	315	End	778
GI	2428323	Score	806
Exons	315..778		
GI Descrip.	5803242/dbj|AP000399.1|AP000399 0.0e+00 Oryza sativa genomic DNA, chromosome 6, clone:P0535G04		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	945	Strand	+
Start	3993	End	8022
Name	OJ990503_28.9924.C9.o2.gs	Method	GENSCAN
Start	3993	End	8022
GI	none	Score	.64
Exons	3993..4129, 5710..5832, 7103..7283, 7348..8022		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	946	Strand	-
Start	28	End	6541
Name	OJ990503_28.9924.C9.o1.gs	Method	GENSCAN
Start	28	End	3829
GI	none	Score	.68
Exons	28..150, 836..1117, 1141..1705, 1809..2727, 2823..3829		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9

Gene No.	946	Strand	-
Start	28	End	6541
Name	OJ990503_28.9924.C9.o1.np	Method	AAT/NAP
Start	789	End	4084
GI	5803259	Score	4989
Exons	789..2455, 2498..2727, 2823..4084		
GI Descrip.	(AP000399) hypothetical protein [Oryza sativa]		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	946	Strand	-
Start	28	End	6541
Name	OJ990503_28.9924.C9.o2.np	Method	AAT/NAP
Start	3451	End	6541
GI	5922623	Score	72
Exons	3451..3467, 4900..4975, 5143..5221, 6500..6541		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016856|dbj|BAA85199.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o3.np	Method	AAT/NAP
Start	8242	End	13258
GI	4680179	Score	5698
Exons	8242..12666, 13213..13258		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o6.tw	Method	TBLASTX:Wheat
Start	8287	End	8620
GI	none	Score	146
Exons	8287..8619, 8339..8620		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o1.tm	Method	TBLASTX:Maize
Start	8482	End	9067
GI	none	Score	104
Exons	8482..8907, 8483..8680, 8744..8908, 8905..9066, 8912..9067		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o1.tw	Method	TBLASTX:Wheat
Start	8620	End	9246
GI	none	Score	44
Exons	8620..9246, 8621..8680, 8741..9187		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o3.tm	Method	TBLASTX:Maize
Start	9115	End	9406

GI	none	Score	296
Exons	9115..9405, 9119..9406		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o2.ts	Method	TBLASTX:Soybean
Start	9205	End	9465
GI	none	Score	185
Exons	9205..9465, 9206..9454		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o1.tc	Method	TBLASTX:Cress
Start	9229	End	9555
GI	none	Score	87
Exons	9229..9372, 9230..9370, 9373..9555		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o2.tw	Method	TBLASTX:Wheat
Start	9252	End	9792
GI	none	Score	141
Exons	9252..9533, 9253..9792, 9257..9610		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o2.tm	Method	TBLASTX:Maize
Start	9820	End	10173
GI	none	Score	209
Exons	9820..10173, 9827..10168		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o3.tw	Method	TBLASTX:Wheat
Start	9820	End	10245
GI	none	Score	194
Exons	9820..10170, 9820..10245, 9827..10243		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o3.ts	Method	TBLASTX:Soybean
Start	9991	End	10236
GI	none	Score	204
Exons	9991..10236		

Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o5.tm	Method	TBLASTX:Maize
Start	10180	End	10512
GI	none	Score	144

Exons	10180..10512, 10181..10459		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o5.tw	Method	TBLASTX:Wheat
Start	10246	End	10509
GI	none	Score	245
Exons	10246..10509, 10247..10507		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o1.ts	Method	TBLASTX:Soybean
Start	10261	End	10656
GI	none	Score	189
Exons	10261..10512, 10271..10504, 10567..10620, 10577..10618, 10624..10656, 10624..10656		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o4.tm	Method	TBLASTX:Maize
Start	10567	End	11014
GI	none	Score	113
Exons	10567..11010, 10577..11014		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o4.tw	Method	TBLASTX:Wheat
Start	10596	End	11080
GI	none	Score	219
Exons	10596..10970, 10597..11079, 10600..11076, 10640..11080		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o4.ts	Method	TBLASTX:Soybean
Start	10729	End	11043
GI	none	Score	198
Exons	10729..11043		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o7.tm	Method	TBLASTX:Maize
Start	11015	End	11208
GI	none	Score	156
Exons	11015..11170, 11017..11208		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o8.tw	Method	TBLASTX:Wheat
Start	11212	End	11565
GI	none	Score	256

Exons	11212..11565		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o7.tw	Method	TBLASTX:Wheat
Start	11899	End	12249
GI	none	Score	312
Exons	11899..12249		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o6.tm	Method	TBLASTX:Maize
Start	11944	End	12249
GI	none	Score	246
Exons	11944..12249		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o9.tw	Method	TBLASTX:Wheat
Start	12301	End	12499
GI	none	Score	136
Exons	12301..12498, 12302..12499		
Seq. No.	488	Seq. ID	OJ990503_28.9924.C9
Gene No.	947	Strand	-
Start	8242	End	13649
Name	OJ990503_28.9924.C9.o4.np	Method	AAT/NAP
Start	12937	End	13649
GI	4512231	Score	1120
Exons	12937..13649		
GI Descrip.	(AB014741) ORF0 protein [Oryza sativa]		
Seq. No.	489	Seq. ID	OJ990503_28.9924.C11
Gene No.	948	Strand	+
Start	1	End	1132
Name	OJ990503_28.9924.C11.o1.np	Method	AAT/NAP
Start	1	End	1132
GI	6907089	Score	1635
Exons	1..960, 1060..1132		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		
Seq. No.	489	Seq. ID	OJ990503_28.9924.C11
Gene No.	948	Strand	+
Start	1	End	1132
Name	OJ990503_28.9924.C11.o1.gs	Method	GENSCAN
Start	14	End	960
GI	none	Score	.71
Exons	14..960		
Seq. No.	490	Seq. ID	OJ990503_28.9924.C12
Gene No.	949	Strand	+
Start	1	End	831
Name	OJ990503_28.9924.C12.o1.np	Method	AAT/NAP
Start	1	End	831

GI	6498441	Score	1345
Exons	1..831		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	490	Seq. ID	OJ990503_28.9924.C12
Gene No.	949	Strand	+
Start	1	End	831
Name	OJ990503_28.9924.C12.o1.gs	Method	GENSCAN
Start	118	End	762
GI	none	Score	.41
Exons	118..762		

Seq. No.	490	Seq. ID	OJ990503_28.9924.C12
Gene No.	949	Strand	+
Start	1	End	831
Name	OJ990503_28.9924.C12.o1.tm	Method	TBLASTX:Maize
Start	189	End	551
GI	none	Score	364
Exons	189..512, 218..499, 504..551		

Seq. No.	490	Seq. ID	OJ990503_28.9924.C12
Gene No.	949	Strand	+
Start	1	End	831
Name	OJ990503_28.9924.C12.o1.tw	Method	TBLASTX:Wheat
Start	326	End	707
GI	none	Score	378
Exons	326..382, 327..707, 423..668, 428..676		

Seq. No.	491	Seq. ID	OJ990503_28.9924.C13
Gene No.	950	Strand	+
Start	206	End	300
Name	OJ990503_28.9924.C13.o1.gs	Method	GENSCAN
Start	206	End	300
GI	none	Score	.99
Exons	206..300		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	951	Strand	+
Start	1	End	8099
Name	OJ990503_28.9924.C14.o1.np	Method	AAT/NAP
Start	1	End	8099
GI	5042454	Score	139
Exons	1..49, 378..471, 2827..2949, 3042..3236, 7797..8099		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	951	Strand	+
Start	1	End	8099
Name	OJ990503_28.9924.C14.o1.gs	Method	GENSCAN
Start	275	End	1619
GI	none	Score	.64
Exons	275..448, 1491..1619		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	952	Strand	-

Start	1679	End	8038
Name	OJ990503_28.9924.C14.o2.np	Method	AAT/NAP
Start	1679	End	7025
GI	4510344	Score	203
Exons	1679..1835, 2612..2709, 2847..3058, 3341..3646, 6962..7025		
GI Descrip.	(AC006921) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	952	Strand	-
Start	1679	End	8038
Name	OJ990503_28.9924.C14.o2.gs	Method	GENSCAN
Start	2290	End	8038
GI	none	Score	.69
Exons	2290..2306, 2752..3357, 6181..6206, 6402..6616, 7347..7428, 7578..8038		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	952	Strand	-
Start	1679	End	8038
Name	OJ990503_28.9924.C14.o2.ts	Method	TBLASTX:Soybean
Start	2616	End	2953
GI	none	Score	62
Exons	2616..2753, 2616..2753, 2846..2953, 2847..2942		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	952	Strand	-
Start	1679	End	8038
Name	OJ990503_28.9924.C14.o2.gp	Method	AAT/GAP
Start	3195	End	3598
GI	LIB3474-004-P1-K1-D11	Score	741
Exons	3195..3598		
GI Descrip.	'5803242/dbj|AP000399.1|AP000399 0.0e+00 Oryza sativa genomic DNA, chromosome 6, clone:P0535G04'		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	952	Strand	-
Start	1679	End	8038
Name	OJ990503_28.9924.C14.o1.ts	Method	TBLASTX:Soybean
Start	6398	End	7780
GI	none	Score	187
Exons	6398..6616, 6399..6617, 6401..6562, 7341..7430, 7345..7437, 7556..7669, 7727..7780		

Seq. No.	492	Seq. ID	OJ990503_28.9924.C14
Gene No.	952	Strand	-
Start	1679	End	8038
Name	OJ990503_28.9924.C14.o1.tm	Method	TBLASTX:Maize
Start	7619	End	7864
GI	none	Score	80
Exons	7619..7762, 7646..7696, 7751..7864, 7752..7850		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	953	Strand	+
Start	129	End	260
Name	OJ990503_28.9924.C15.o1.gs	Method	GENSCAN
Start	129	End	260
GI	none	Score	.85

Exons	129..260		
Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	954	Strand	+
Start	1256	End	2843
Name	OJ990503_28.9924.C15.o2.gs	Method	GENSCAN
Start	1256	End	2843
GI	none	Score	.81
Exons	1256..1284, 1810..1865, 2221..2843		
Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	955	Strand	+
Start	5471	End	11126
Name	OJ990503_28.9924.C15.o1.np	Method	AAT/NAP
Start	5471	End	11126
GI	6498441	Score	6896
Exons	5471..6543, 6874..7337, 7401..7774, 7958..8092, 8267..8607, 8800..9182, 9354..10751, 10845..11126		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		
Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	956	Strand	+
Start	14722	End	16680
Name	OJ990503_28.9924.C15.o3.np	Method	AAT/NAP
Start	14722	End	16680
GI	4680186	Score	163
Exons	14722..14747, 16475..16680		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		
Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	957	Strand	-
Start	11776	End	15011
Name	OJ990503_28.9924.C15.o4.gs	Method	GENSCAN
Start	11776	End	15011
GI	none	Score	.63
Exons	11776..13157, 13268..13650, 13750..14815, 14882..15011		
Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	957	Strand	-
Start	11776	End	15011
Name	OJ990503_28.9924.C15.o2.np	Method	AAT/NAP
Start	11779	End	15011
GI	5803259	Score	4325
Exons	11779..13650, 13750..15011		
GI Descrip.	(AP000399) hypothetical protein [Oryza sativa]		
Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	958	Strand	-
Start	15725	End	16233
Name	OJ990503_28.9924.C15.o5.gs	Method	GENSCAN
Start	15725	End	16233
GI	none	Score	.79
Exons	15725..15791, 16157..16233		
Seq. No.	493	Seq. ID	OJ990503_28.9924.C15

Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o1.tm	Method	TBLASTX:Maize
Start	2262	End	2903
GI	none	Score	110
Exons	2262..2378, 2270..2377, 2367..2483, 2370..2849, 2381..2848, 2550..2903		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o1.ts	Method	TBLASTX:Soybean
Start	2415	End	2831
GI	none	Score	363
Exons	2415..2483, 2426..2800, 2427..2831, 2550..2831		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o6.tw	Method	TBLASTX:Wheat
Start	5620	End	6012
GI	none	Score	58
Exons	5620..5667, 5674..5772, 5679..5771, 5739..5978, 5755..6012		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o5.tm	Method	TBLASTX:Maize
Start	5625	End	5910
GI	none	Score	197
Exons	5625..5909, 5662..5910		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o5.tw	Method	TBLASTX:Wheat
Start	6020	End	9488
GI	none	Score	235
Exons	6020..6073, 9053..9295, 9054..9305, 9339..9488, 9350..9487		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o3.tw	Method	TBLASTX:Wheat
Start	6758	End	7217
GI	none	Score	405
Exons	6758..6895, 6759..7217, 6953..7213		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o1.tw	Method	TBLASTX:Wheat
Start	7409	End	7871
GI	none	Score	587
Exons	7409..7864, 7410..7871, 7410..7865		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15

Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o3.ts	Method	TBLASTX:Soybean
Start	7449	End	7814
GI	none	Score	117
Exons	7449..7673, 7680..7814		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o2.tm	Method	TBLASTX:Maize
Start	7539	End	7895
GI	none	Score	392
Exons	7539..7895, 7574..7885, 7590..7895		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o3.tm	Method	TBLASTX:Maize
Start	7922	End	8306
GI	none	Score	363
Exons	7922..8287, 7923..8306		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o2.tw	Method	TBLASTX:Wheat
Start	7979	End	8399
GI	none	Score	493
Exons	7979..8392, 7980..8399		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o2.ts	Method	TBLASTX:Soybean
Start	8058	End	8429
GI	none	Score	279
Exons	8058..8429, 8075..8218		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o8.tw	Method	TBLASTX:Wheat
Start	9491	End	9803
GI	none	Score	189
Exons	9491..9667, 9543..9803		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o4.tm	Method	TBLASTX:Maize
Start	9996	End	10319
GI	none	Score	362
Exons	9996..10319, 10025..10306		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-

Start	17074	End	18979
Name	OJ990503_28.9924.C15.o4.tw	Method	TBLASTX:Wheat
Start	10133	End	10514
GI	none	Score	375
Exons	10133..10189, 10134..10514, 10137..10388, 10235..10483		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o7.tw	Method	TBLASTX:Wheat
Start	10515	End	11117
GI	none	Score	266
Exons	10515..10805, 10520..10798, 10991..11113, 10992..11117		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o6.gs	Method	GENSCAN
Start	17074	End	18979
GI	none	Score	.81
Exons	17074..17178, 17729..18349, 18359..18979		

Seq. No.	493	Seq. ID	OJ990503_28.9924.C15
Gene No.	959	Strand	-
Start	17074	End	18979
Name	OJ990503_28.9924.C15.o4.np	Method	AAT/NAP
Start	17077	End	18979
GI	6907087	Score	1100
Exons	17077..17178, 17729..18392, 18602..18979		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	494	Seq. ID	OJ990503_28.9924.C16
Gene No.	960	Strand	+
Start	413	End	597
Name	OJ990503_28.9924.C16.o1.gs	Method	GENSCAN
Start	413	End	597
GI	none	Score	.55
Exons	413..597		

Seq. No.	494	Seq. ID	OJ990503_28.9924.C16
Gene No.	961	Strand	-
Start	1	End	2568
Name	OJ990503_28.9924.C16.o1.np	Method	AAT/NAP
Start	1	End	2568
GI	4680179	Score	587
Exons	1..41, 1308..1542, 1711..2568		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	494	Seq. ID	OJ990503_28.9924.C16
Gene No.	961	Strand	-
Start	1	End	2568
Name	OJ990503_28.9924.C16.o2.gs	Method	GENSCAN
Start	1198	End	2547
GI	none	Score	.62
Exons	1198..2547		

Seq. No.	494	Seq. ID	OJ990503_28.9924.C16
Gene No.	961	Strand	-
Start	1	End	2568
Name	OJ990503_28.9924.C16.o1.tm	Method	TBLASTX:Maize
Start	1786	End	2085
GI	none	Score	71
Exons	1786..2085, 1982..2071		

Seq. No.	494	Seq. ID	OJ990503_28.9924.C16
Gene No.	961	Strand	-
Start	1	End	2568
Name	OJ990503_28.9924.C16.o1.tw	Method	TBLASTX:Wheat
Start	1966	End	2325
GI	none	Score	150
Exons	1966..2325, 1970..2323		

Seq. No.	495	Seq. ID	OJ990503_28.9924.C17
Gene No.	962	Strand	+
Start	144	End	219
Name	OJ990503_28.9924.C17.o1.gs	Method	GENSCAN
Start	144	End	219
GI	none	Score	.47
Exons	144..219		

Seq. No.	495	Seq. ID	OJ990503_28.9924.C17
Gene No.	963	Strand	-
Start	263	End	350
Name	OJ990503_28.9924.C17.o1.np	Method	AAT/NAP
Start	263	End	350
GI	2832672	Score	87
Exons	263..350		
GI Descrip.	(AL021712) nifU-like protein [Arabidopsis thaliana]		

Seq. No.	495	Seq. ID	OJ990503_28.9924.C17
Gene No.	964	Strand	-
Start	263	End	350
Name	OJ990503_28.9924.C17.o1.gp	Method	AAT/GAP
Start	263	End	350
GI	1671_1.R1084	Score	155
Exons	263..350		
GI Descrip.	'2832672/emb|CAA16772.1| 4.0e-59 (AL021712) nifU-like protein [Arabidopsis thaliana]'		

Seq. No.	496	Seq. ID	OJ990323_25.9923.C1
Gene No.	965	Strand	+
Start	2598	End	9080
Name	OJ990323_25.9923.C1.o1.gs	Method	GENSCAN
Start	2598	End	9080
GI	none	Score	.44
Exons	2598..2642, 5458..5623, 5969..6091, 6903..7028, 7218..7369, 7444..7618, 8956..9080		

Seq. No.	496	Seq. ID	OJ990323_25.9923.C1
Gene No.	966	Strand	-
Start	10933	End	12303
Name	OJ990323_25.9923.C1.o1.tm	Method	TBLASTX:Maize

Start	10931	End	11088
GI	none	Score	198
Exons	10931..10990, 10954..11088, 10955..11086, 10960..11088		

Seq. No.	496	Seq. ID	OJ990323_25.9923.C1
Gene No.	966	Strand	-
Start	10933	End	12303
Name	OJ990323_25.9923.C1.o2.gs	Method	GENSCAN
Start	10933	End	12297
GI	none	Score	.99
Exons	10933..11200, 11207..12297		

Seq. No.	496	Seq. ID	OJ990323_25.9923.C1
Gene No.	966	Strand	-
Start	10933	End	12303
Name	OJ990323_25.9923.C1.o1.np	Method	AAT/NAP
Start	10936	End	12303
GI	4115384	Score	1580
Exons	10936..12122, 12165..12303		
GI Descrip.	(AC005967) unknown protein [Arabidopsis thaliana]		

Seq. No.	496	Seq. ID	OJ990323_25.9923.C1
Gene No.	966	Strand	-
Start	10933	End	12303
Name	OJ990323_25.9923.C1.o2.ts	Method	TBLASTX:Soybean
Start	11128	End	11446
GI	none	Score	51
Exons	11128..11163, 11161..11226, 11170..11211, 11218..11445, 11219..11446		

Seq. No.	496	Seq. ID	OJ990323_25.9923.C1
Gene No.	966	Strand	-
Start	10933	End	12303
Name	OJ990323_25.9923.C1.o1.ts	Method	TBLASTX:Soybean
Start	11462	End	12279
GI	none	Score	150
Exons	11462..11623, 11464..11739, 11464..12108, 11672..11923, 12016..12108, 12169..12279, 12170..12277		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	967	Strand	+
Start	1	End	19670
Name	OJ990323_25.9923.C2.o3.np	Method	AAT/NAP
Start	1	End	19646
GI	2980767	Score	506
Exons	1..86, 17771..17940, 17974..18037, 19327..19646		
GI Descrip.	(AL022198) putative protein [Arabidopsis thaliana]		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	967	Strand	+
Start	1	End	19670
Name	OJ990323_25.9923.C2.o2.gs	Method	GENSCAN
Start	8569	End	16039
GI	none	Score	.69
Exons	8569..8582, 9340..9554, 9655..9730, 9810..9873, 10534..10668, 10757..10888, 11198..11281, 11722..11813, 12010..12082, 12206..12358, 12918..13001, 13161..13235, 13315..13458,		

13746..13853, 14070..14189, 14639..15029, 15852..16039

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	967	Strand	+
Start	1	End	19670
Name	OJ990323_25.9923.C2.o3.gp	Method	AAT/GAP
Start	13780	End	14802
GI	none	Score	642
Exons	13780..13853, 13928..13990, 14070..14144, 14639..14802		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	967	Strand	+
Start	1	End	19670
Name	OJ990323_25.9923.C2.o4.gp	Method	AAT/GAP
Start	17655	End	17947
GI	569219	Score	476
Exons	17655..17947		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	967	Strand	+
Start	1	End	19670
Name	OJ990323_25.9923.C2.o3.gs	Method	GENSCAN
Start	17791	End	19670
GI	none	Score	.69
Exons	17791..18034, 18072..18134, 19327..19670		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	968	Strand	+
Start	25158	End	25715
Name	OJ990323_25.9923.C2.o6.gs	Method	GENSCAN
Start	25158	End	25715
GI	none	Score	.58
Exons	25158..25715		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	969	Strand	+
Start	26228	End	37094
Name	OJ990323_25.9923.C2.o7.gs	Method	GENSCAN
Start	26228	End	37094
GI	none	Score	.68
Exons	26228..26563, 27328..27414, 27590..27683, 28614..29158, 29768..29968, 30073..30255, 30705..30814, 31047..31106, 31350..31641, 32626..32726, 33005..33879, 34576..35535, 35755..35964, 36585..36655, 36906..37094		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	969	Strand	+
Start	26228	End	37094
Name	OJ990323_25.9923.C2.o5.gp	Method	AAT/GAP
Start	28610	End	28986
GI	none	Score	526
Exons	28610..28986		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	969	Strand	+
Start	26228	End	37094
Name	OJ990323_25.9923.C2.o6.gp	Method	AAT/GAP

Start	35964	End	36137
GI	6025123	Score	296
Exons	35964..36137		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	970	Strand	+
Start	52409	End	58824
Name	OJ990323_25.9923.C2.o8.np	Method	AAT/NAP
Start	52409	End	58824
GI	6063554	Score	328
Exons	52409..52436, 56875..57155, 57260..57465, 57987..58014, 58650..58824		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	971	Strand	-
Start	1	End	334
Name	OJ990323_25.9923.C2.o1.gp	Method	AAT/GAP
Start	1	End	334
GI	3767832	Score	650
Exons	1..334		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	972	Strand	-
Start	238	End	6586
Name	OJ990323_25.9923.C2.o1.gs	Method	GENSCAN
Start	238	End	6586
GI	none	Score	.98
Exons	238..742, 1427..1461, 1532..1600, 1720..1771, 2171..2253, 2352..2453, 2877..3611, 3689..3739, 4519..4710, 4793..4943, 5739..5920, 6056..6259, 6479..6586		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	972	Strand	-
Start	238	End	6586
Name	OJ990323_25.9923.C2.o2.np	Method	AAT/NAP
Start	253	End	6580
GI	4584527	Score	543
Exons	253..825, 1532..1600, 1720..1771, 2171..2238, 2877..3748, 4406..4710, 4815..4943, 5739..5920, 6056..6259, 6479..6580		
GI Descrip.	(AL049607) putative protein [Arabidopsis thaliana]		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	972	Strand	-
Start	238	End	6586
Name	OJ990323_25.9923.C2.o2.gp	Method	AAT/GAP
Start	1513	End	3356
GI	none	Score	1383
Exons	1513..1600, 1720..1771, 2171..2253, 2352..2453, 2877..3356		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	973	Strand	-
Start	20756	End	22589
Name	OJ990323_25.9923.C2.o4.gs	Method	GENSCAN
Start	20756	End	22589

GI	none	Score	.85
Exons	20756..21330, 21388..21469, 21598..21636, 22141..22236, 22326..22589		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	973	Strand	-
Start	20756	End	22589
Name	OJ990323_25.9923.C2.o4.np	Method	AAT/NAP
Start	20759	End	21456
GI	6728965	Score	62
Exons	20759..20859, 21100..21285, 21388..21456		
GI Descrip.	(AC018363) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	974	Strand	-
Start	23476	End	23769
Name	OJ990323_25.9923.C2.o5.gs	Method	GENSCAN
Start	23476	End	23769
GI	none	Score	.9
Exons	23476..23769		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	975	Strand	-
Start	38038	End	40031
Name	OJ990323_25.9923.C2.o5.np	Method	AAT/NAP
Start	38038	End	39524
GI	133866	Score	622
Exons	38038..38128, 38320..38409, 38498..38642, 39284..39384, 39472..39524		
GI Descrip.	40S RIBOSOMAL PROTEIN S11-ALPHA gi|81659|pir||C35542 ribosomal protein S11 - Arabidopsis thaliana gi|454808 (L28828) ribosomal protein S11 [Arabidopsis thaliana] gi|6522573|emb|CAB62017.1| (AL132967) cytosolic ribosomal protein S11 [Arabidopsis thaliana]		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	975	Strand	-
Start	38038	End	40031
Name	OJ990323_25.9923.C2.o7.gp	Method	AAT/GAP
Start	38332	End	40031
GI	30446_1.R1084	Score	786
Exons	38332..38409, 38498..38642, 39284..39384, 39472..39512, 39907..40031		
GI Descrip.	'5708091/emb|CAA18213.2| 8.0e-22 (AL022198) ribosomal protein S11-like [Arabidopsis thaliana]'		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	976	Strand	-
Start	46419	End	50300
Name	OJ990323_25.9923.C2.o6.np	Method	AAT/NAP
Start	46419	End	50300
GI	6539553	Score	6458
Exons	46419..50300		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	977	Strand	-
Start	51551	End	54107
Name	OJ990323_25.9923.C2.o7.np	Method	AAT/NAP
Start	51551	End	54107
GI	6815109	Score	165
Exons	51551..51577, 53944..54107		
GI Descrip.	(AP001081) hypothetical protein [Oryza sativa]		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	978	Strand	-
Start	56871	End	57606
Name	OJ990323_25.9923.C2.o9.gs	Method	GENSCAN
Start	56871	End	57606
GI	none	Score	1
Exons	56871..57365, 57385..57606		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o12.tm	Method	TBLASTX:Maize
Start	180	End	887
GI	none	Score	56
Exons	180..287, 181..288, 282..380, 309..374, 334..546, 397..591, 408..473, 486..527, 542..619, 581..640, 639..722, 646..726, 647..727, 822..878, 825..887		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o15.tm	Method	TBLASTX:Maize
Start	3015	End	3409
GI	none	Score	119
Exons	3015..3149, 3016..3150, 3102..3287, 3152..3253, 3153..3287, 3273..3404, 3277..3372, 3320..3409		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o5.tc	Method	TBLASTX:Cress
Start	4841	End	6248
GI	none	Score	59
Exons	4841..4951, 5726..5845, 5741..5944, 5820..5936, 6054..6248, 6056..6244		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o12.ts	Method	TBLASTX:Soybean
Start	6054	End	6271
GI	none	Score	119
Exons	6054..6254, 6056..6271		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448

Name	OJ990323_25.9923.C2.o14.tm	Method	TBLASTX:Maize
Start	6077	End	6589
GI	none	Score	193
Exons	6077..6265, 6078..6269, 6479..6589		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o6.tc	Method	TBLASTX:Cress
Start	9497	End	10840
GI	none	Score	88
Exons	9497..9556, 9498..9554, 10528..10668, 10532..10669, 10533..10664, 10751..10840, 10753..10836		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o13.ts	Method	TBLASTX:Soybean
Start	12003	End	12352
GI	none	Score	117
Exons	12003..12083, 12011..12082, 12202..12351, 12206..12352, 12260..12352		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o3.tm	Method	TBLASTX:Maize
Start	12195	End	15058
GI	none	Score	37
Exons	12195..12230, 12206..12232, 12231..12362, 12235..12360, 12236..12367, 12444..12569, 12447..12566, 12451..12627, 12655..12708, 12656..12709, 12890..13000, 12915..13001, 12916..12999, 12918..13001, 13155..13271, 13159..13236, 13160..13246, 13287..13367, 13314..13367, 13315..13371, 13370..13459, 13371..13460, 13372..13461, 13531..13659, 13531..13659, 13533..13664, 13533..13664, 13737..13874, 13751..13867, 13916..13996, 13923..14033, 13925..13993, 13927..14052, 14068..14142, 14068..14142, 14069..14182, 14638..14838, 14639..14833, 14923..15033, 14924..15055, 14924..15058		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o6.ts	Method	TBLASTX:Soybean
Start	12917	End	13954
GI	none	Score	125
Exons	12917..12997, 12918..13001, 13155..13259, 13157..13237, 13390..13461, 13395..13460, 13527..13658, 13528..13659, 13533..13649, 13737..13856, 13751..13855, 13925..13954		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o11.ts	Method	TBLASTX:Soybean
Start	17839	End	19640
GI	none	Score	97

Exons	17839..17907, 17995..18036, 19332..19511, 19345..19518, 19460..19636, 19590..19640		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o13.tm	Method	TBLASTX:Maize
Start	19353	End	19762
GI	none	Score	260
Exons	19353..19511, 19355..19639, 19357..19650, 19357..19638, 19460..19645, 19545..19649, 19679..19762, 19691..19744		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o2.tc	Method	TBLASTX:Cress
Start	28667	End	29059
GI	none	Score	71
Exons	28667..28729, 28730..29059, 28822..29058		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o4.tm	Method	TBLASTX:Maize
Start	30207	End	32811
GI	none	Score	86
Exons	30207..30257, 30207..30257, 30208..30258, 30703..30813, 30705..30815, 30728..30814, 31044..31112, 31045..31107, 31321..31629, 31341..31643, 31341..31643, 32534..32776, 32536..32781, 32536..32775, 32537..32776, 32777..32809, 32779..32811, 32782..32811		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o5.ts	Method	TBLASTX:Soybean
Start	30705	End	31614
GI	none	Score	84
Exons	30705..30791, 31045..31107, 31306..31602, 31321..31614, 31329..31607		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o10.ts	Method	TBLASTX:Soybean
Start	32594	End	32818
GI	none	Score	245
Exons	32594..32818, 32596..32817		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o16.tm	Method	TBLASTX:Maize
Start	33150	End	33283
GI	none	Score	218
Exons	33150..33281, 33150..33281, 33152..33283, 33152..33283		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o2.ts	Method	TBLASTX:Soybean
Start	33282	End	33596
GI	none	Score	120
Exons	33282..33494, 33284..33595, 33284..33595, 33285..33596		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o1.tm	Method	TBLASTX:Maize
Start	33284	End	33881
GI	none	Score	940
Exons	33284..33880, 33285..33881		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o1.ts	Method	TBLASTX:Soybean
Start	33743	End	35133
GI	none	Score	136
Exons	33743..33799, 33788..33880, 34581..34709, 34613..34708, 34790..34864, 34794..35132, 34907..34927, 34964..35089, 34966..35133		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o2.tm	Method	TBLASTX:Maize
Start	34696	End	35408
GI	none	Score	68
Exons	34696..34752, 34698..34751, 34785..34949, 34785..34865, 34953..35342, 34955..35350, 35373..35408, 35373..35408		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o3.tc	Method	TBLASTX:Cress
Start	35130	End	35542
GI	none	Score	228
Exons	35130..35333, 35138..35302, 35139..35303, 35382..35537, 35382..35537, 35383..35541, 35402..35542		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o9.ts	Method	TBLASTX:Soybean
Start	35201	End	35975
GI	none	Score	122
Exons	35201..35302, 35202..35306, 35348..35551, 35382..35537, 35383..35544, 35753..35971, 35754..35975		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o9.tm	Method	TBLASTX:Maize

Start	35408	End	36048
GI	none	Score	219
Exons	35408..35551, 35409..35537, 35744..35971, 35751..36002, 35754..35990, 35755..36000, 36028..36048		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o5.tw	Method	TBLASTX:Wheat
Start	35798	End	36142
GI	none	Score	291
Exons	35798..35971, 35799..35990, 35803..35976, 36019..36060, 36029..36061, 36066..36104, 36068..36142		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o6.tm	Method	TBLASTX:Maize
Start	38003	End	39516
GI	none	Score	41
Exons	38003..38065, 38035..38070, 38056..38130, 38075..38131, 38319..38411, 38319..38411, 38320..38412, 38320..38412, 38494..38640, 38497..38643, 38498..38656, 38498..38644, 39283..39336, 39283..39369, 39284..39367, 39474..39515, 39475..39516		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o3.ts	Method	TBLASTX:Soybean
Start	38056	End	39516
GI	none	Score	94
Exons	38056..38130, 38057..38131, 38318..38410, 38319..38411, 38319..38411, 38320..38412, 38494..38643, 38497..38643, 38498..38656, 38498..38644, 39280..39378, 39282..39380, 39474..39515, 39475..39516		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o1.tc	Method	TBLASTX:Cress
Start	38068	End	39515
GI	none	Score	84
Exons	38068..38130, 38078..38131, 38315..38404, 38319..38408, 38319..38411, 38320..38409, 38494..38643, 38497..38643, 38504..38659, 38505..38648, 39283..39333, 39285..39341, 39289..39363, 39474..39515		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o1.tw	Method	TBLASTX:Wheat
Start	46542	End	47007
GI	none	Score	323
Exons	46542..46916, 46555..46917, 46564..46917, 46932..47006, 46936..47007		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o14.ts	Method	TBLASTX:Soybean
Start	46644	End	47012
GI	none	Score	104
Exons	46644..46868, 46887..47012		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o11.tm	Method	TBLASTX:Maize
Start	46863	End	47203
GI	none	Score	164
Exons	46863..47093, 46864..47082, 46990..47112, 47083..47202, 47090..47203		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o7.ts	Method	TBLASTX:Soybean
Start	47013	End	47359
GI	none	Score	119
Exons	47013..47063, 47080..47358, 47159..47359		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o3.tw	Method	TBLASTX:Wheat
Start	47212	End	47742
GI	none	Score	314
Exons	47212..47418, 47413..47742		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o8.tm	Method	TBLASTX:Maize
Start	47293	End	47751
GI	none	Score	138
Exons	47293..47751, 47396..47743		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o4.ts	Method	TBLASTX:Soybean
Start	47428	End	47892
GI	5509260	Score	52
Exons	47428..47892, 47447..47506, 47573..47797		
GI Descrip.	-		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o4.tc	Method	TBLASTX:Cress
Start	47539	End	47799
GI	none	Score	100
Exons	47539..47799, 47627..47797		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o2.tw	Method	TBLASTX:Wheat
Start	47812	End	48566
GI	none	Score	204
Exons	47812..48060, 47812..48000, 47829..48059, 48065..48289, 48118..48354, 48276..48566, 48287..48430, 48289..48558		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o8.ts	Method	TBLASTX:Soybean
Start	48217	End	48614
GI	none	Score	38
Exons	48217..48291, 48273..48389, 48343..48381, 48390..48614, 48405..48599, 48436..48606		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o10.tm	Method	TBLASTX:Maize
Start	48402	End	48836
GI	none	Score	84
Exons	48402..48836, 48427..48627		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o6.tw	Method	TBLASTX:Wheat
Start	48567	End	48905
GI	none	Score	77
Exons	48567..48905, 48588..48773		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o15.ts	Method	TBLASTX:Soybean
Start	48624	End	49010
GI	none	Score	87
Exons	48624..48848, 48855..49010		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o5.tm	Method	TBLASTX:Maize
Start	49037	End	49359
GI	none	Score	392
Exons	49037..49204, 49038..49343, 49039..49338, 49105..49359		

Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o7.tm	Method	TBLASTX:Maize
Start	49858	End	50171
GI	none	Score	296

Exons	49858..50163, 49860..50171		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o4.tw	Method	TBLASTX:Wheat
Start	49920	End	50306
GI	none	Score	242
Exons	49920..50306, 49921..50295		
Seq. No.	497	Seq. ID	OJ990323_25.9923.C2
Gene No.	979	Strand	-
Start	59192	End	59448
Name	OJ990323_25.9923.C2.o9.gp	Method	AAT/GAP
Start	59192	End	59448
GI	61605_3.R1084	Score	434
Exons	59192..59448		
GI Descrip.	'1402920/emb|CAA66965| 2.0e-20 (X98321) peroxidase [Arabidopsis thaliana]'		
Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	980	Strand	+
Start	1	End	6411
Name	OJ990323_25.9923.C3.o1.gp	Method	AAT/GAP
Start	1	End	417
GI	700148	Score	742
Exons	1..417		
GI Descrip.	6091732/gb|AAF03444.1|AC010797_20 3.0e-14 (AC010797) unknown protein [Arabidopsis thaliana]		
Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	980	Strand	+
Start	1	End	6411
Name	OJ990323_25.9923.C3.o1.np	Method	AAT/NAP
Start	1	End	4590
GI	6730730	Score	1349
Exons	1..241, 2823..3733, 4110..4590		
GI Descrip.	(AC018849) nodulin-like protein [Arabidopsis thaliana]		
Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	980	Strand	+
Start	1	End	6411
Name	OJ990323_25.9923.C3.o2.gs	Method	GENSCAN
Start	2892	End	6411
GI	none	Score	.76
Exons	2892..3705, 4358..4501, 4679..4841, 5447..5499, 5865..6001, 6154..6411		
Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	980	Strand	+
Start	1	End	6411
Name	OJ990323_25.9923.C3.o2.gp	Method	AAT/GAP
Start	4503	End	4977
GI	none	Score	804
Exons	4503..4977		
Seq. No.	498	Seq. ID	OJ990323_25.9923.C3

Gene No.	981	Strand	+
Start	8596	End	13147
Name	OJ990323_25.9923.C3.o3.gs	Method	GENSCAN
Start	8596	End	13147
GI	none	Score	.86
Exons	8596..8908, 9442..9509, 9598..9821, 10069..10152, 10733..10946, 11392..11568, 11666..11785, 12005..12219, 12244..12270, 12354..12401, 12685..13147		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	981	Strand	+
Start	8596	End	13147
Name	OJ990323_25.9923.C3.o2.np	Method	AAT/NAP
Start	9418	End	12202
GI	2827631	Score	1021
Exons	9418..9509, 9598..9821, 10069..10152, 10733..10946, 11392..11568, 11666..11785, 12005..12202		
GI Descrip.	(AL021636) putative protein [Arabidopsis thaliana]		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	981	Strand	+
Start	8596	End	13147
Name	OJ990323_25.9923.C3.o3.gp	Method	AAT/GAP
Start	10676	End	12497
GI	25650_1.R1084	Score	1629
Exons	10676..10946, 11392..11568, 11666..11785, 12005..12270, 12354..12497		
GI Descrip.	'2827631/emb|CAA16584.1| 2.0e-67 (AL021636) putative protein [Arabidopsis thaliana]'		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	982	Strand	+
Start	20071	End	24329
Name	OJ990323_25.9923.C3.o6.np	Method	AAT/NAP
Start	20071	End	24329
GI	4567305	Score	182
Exons	20071..20122, 22285..22999, 24309..24329		
GI Descrip.	(AC005956) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	982	Strand	+
Start	20071	End	24329
Name	OJ990323_25.9923.C3.o4.np	Method	AAT/NAP
Start	20832	End	21049
GI	6572240	Score	55
Exons	20832..21049		
GI Descrip.	(Z95115) bK445C9.5 (novel protein, ortholog of mouse tuftelin-interacting protein 10 (similar to worm C07E3.1A)) [Homo sapiens]		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	982	Strand	+
Start	20071	End	24329
Name	OJ990323_25.9923.C3.o5.gs	Method	GENSCAN
Start	20876	End	22945
GI	none	Score	.63
Exons	20876..21235, 21642..21775, 21801..21950, 21959..22354,		

22753..22945

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	982	Strand	+
Start	20071	End	24329
Name	OJ990323_25.9923.C3.o4.gp	Method	AAT/GAP
Start	21235	End	21486
GI	LIB3475-004-P1-K2-A5	Score	409
Exons	21235..21486		
GI Descrip.	'5777612/emb|AJ245900.1|OSA245900 1.0e-94 Oryza sativa chromosome 4 BAC q3037-207F1 complete genome'		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	982	Strand	+
Start	20071	End	24329
Name	OJ990323_25.9923.C3.o5.np	Method	AAT/NAP
Start	21362	End	21526
GI	4539658	Score	91
Exons	21362..21526		
GI Descrip.	(AF061282) serine carboxypeptidase-like protein [Sorghum bicolor]		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	983	Strand	+
Start	31754	End	36594
Name	OJ990323_25.9923.C3.o7.gs	Method	GENSCAN
Start	31754	End	36594
GI	none	Score	.49
Exons	31754..31817, 31835..31896, 33831..33896, 34961..35084, 36129..36308, 36515..36594		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	984	Strand	+
Start	39401	End	41666
Name	OJ990323_25.9923.C3.o9.gs	Method	GENSCAN
Start	39401	End	41327
GI	none	Score	.83
Exons	39401..39473, 39607..39860, 40279..40444, 40519..40608, 41068..41327		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	984	Strand	+
Start	39401	End	41666
Name	OJ990323_25.9923.C3.o7.np	Method	AAT/NAP
Start	39690	End	41666
GI	4699942	Score	718
Exons	39690..39860, 40279..40444, 40519..40608, 41068..41370, 41591..41666		
GI Descrip.	(AC007166) putative protein kinase [Arabidopsis thaliana]		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	985	Strand	-
Start	8	End	681
Name	OJ990323_25.9923.C3.o1.gs	Method	GENSCAN
Start	8	End	681
GI	none	Score	.81
Exons	8..396, 660..681		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	986	Strand	-
Start	13808	End	20764
Name	OJ990323_25.9923.C3.o4.gs	Method	GENSCAN
Start	13808	End	20764
GI	none	Score	.71
Exons	13808..14616, 14651..14756, 14935..15182, 15255..15539, 16298..16496, 16517..16653, 17074..17320, 17831..17943, 18799..18971, 19275..19303, 19318..19497, 19580..19702, 20330..20764		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	986	Strand	-
Start	13808	End	20764
Name	OJ990323_25.9923.C3.o3.np	Method	AAT/NAP
Start	17810	End	19515
GI	6063536	Score	415
Exons	17810..17943, 18555..18710, 18799..18877, 18908..18971, 19275..19515		
GI Descrip.	(AP000615) ESTs C22369(C12239),C22370(C12239), AU057852(S21844),AU057853(S21844) correspond to a region of the predicted gene.; similar to calcium dependent protein kinase. (AF048691) [Oryza sativa]		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	987	Strand	-
Start	23634	End	31701
Name	OJ990323_25.9923.C3.o6.gs	Method	GENSCAN
Start	23634	End	30912
GI	none	Score	.76
Exons	23634..23783, 23906..24062, 24149..24400, 24451..24631, 24713..24859, 25221..25292, 25650..25793, 25934..26005, 26486..26557, 27022..27093, 27423..27602, 28021..28041, 28712..28783, 29117..29191, 29467..29613, 29741..29948, 30504..30632, 30706..30912		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	987	Strand	-
Start	23634	End	31701
Name	OJ990323_25.9923.C3.o5.gp	Method	AAT/GAP
Start	28972	End	29957
GI	none	Score	861
Exons	28972..29024, 29117..29191, 29467..29613, 29741..29957		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	987	Strand	-
Start	23634	End	31701
Name	OJ990323_25.9923.C3.o6.gp	Method	AAT/GAP
Start	30513	End	31701
GI	74226_1.R1084	Score	1152
Exons	30513..30632, 30706..31063, 31567..31701		
GI Descrip.	'5257279/dbj|BAA81778.1| 0.0e+00 (AP000364) Similar to Transposon MAGGY gag and pol gene homologues. (L35053) [Oryza sativa]'		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3

Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o5.tc	Method	TBLASTX:Cress
Start	10	End	3002
GI	none	Score	231
Exons	10..84, 11..226, 130..219, 2813..2917, 2823..3002, 2829..2999		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o7.ts	Method	TBLASTX:Soybean
Start	14	End	205
GI	none	Score	216
Exons	14..205, 23..205		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o7.tm	Method	TBLASTX:Maize
Start	2850	End	3113
GI	none	Score	287
Exons	2850..3113, 2850..3113		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o9.ts	Method	TBLASTX:Soybean
Start	2916	End	3170
GI	none	Score	154
Exons	2916..3101, 2922..3083, 2969..3085, 3099..3170, 3122..3166		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o2.tm	Method	TBLASTX:Maize
Start	3423	End	4235
GI	none	Score	503
Exons	3423..3737, 3425..3736, 3682..3738, 4097..4234, 4107..4235, 4108..4233		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o6.tc	Method	TBLASTX:Cress
Start	3458	End	3740
GI	none	Score	228
Exons	3458..3739, 3486..3740		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o3.ts	Method	TBLASTX:Soybean
Start	3495	End	4209
GI	none	Score	317
Exons	3495..3737, 3500..3733, 4108..4209		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3

Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o1.tc	Method	TBLASTX:Cress
Start	4104	End	4566
GI	none	Score	144
Exons	4104..4250, 4108..4251, 4260..4382, 4261..4386, 4425..4562, 4426..4566		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o2.ts	Method	TBLASTX:Soybean
Start	4224	End	4578
GI	none	Score	221
Exons	4224..4427, 4225..4401, 4429..4578, 4434..4571		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o1.tm	Method	TBLASTX:Maize
Start	4236	End	4588
GI	none	Score	183
Exons	4236..4451, 4236..4583, 4237..4584, 4237..4584, 4280..4588		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o1.tw	Method	TBLASTX:Wheat
Start	4336	End	4596
GI	none	Score	418
Exons	4336..4596, 4338..4595, 4369..4596		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o2.tc	Method	TBLASTX:Cress
Start	9441	End	11478
GI	none	Score	102
Exons	9441..9509, 9452..9508, 9463..9510, 9579..9833, 9586..9834, 9598..9837, 10061..10162, 10069..10158, 10081..10167, 10721..10822, 10727..10813, 10728..10952, 10728..10949, 11389..11478		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o5.tm	Method	TBLASTX:Maize
Start	9441	End	9836
GI	none	Score	100
Exons	9441..9509, 9450..9509, 9591..9836, 9592..9822		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o5.ts	Method	TBLASTX:Soybean
Start	9598	End	10117
GI	none	Score	302

Exons 9598..9837, 9600..9833, 10061..10117, 10069..10113

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o4.tm	Method	TBLASTX:Maize
Start	10100	End	12217
GI	none	Score	79

Exons 10100..10153, 10100..10153, 10733..10951, 10733..10951, 10737..10952, 11384..11470, 11389..11568, 11390..11569, 11660..11785, 11664..11786, 11665..11787, 11666..11788, 12004..12207, 12005..12217

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o4.ts	Method	TBLASTX:Soybean
Start	10731	End	12234
GI	none	Score	118

Exons 10731..10949, 10733..10942, 10734..10952, 11362..11568, 11403..11573, 11665..11778, 11666..11788, 12004..12234, 12005..12169

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o8.tc	Method	TBLASTX:Cress
Start	17864	End	19515
GI	none	Score	61

Exons 17864..17941, 18068..18112, 18581..18643, 18651..18722, 18653..18721, 18800..18877, 18801..18878, 18912..18962, 18917..18964, 19267..19293, 19348..19380, 19381..19515

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o9.tm	Method	TBLASTX:Maize
Start	17864	End	19515
GI	none	Score	58

Exons 17864..17941, 18653..18721, 18660..18722, 18771..18878, 18800..18910, 18801..18878, 18917..18964, 18921..18965, 18924..18965, 19267..19293, 19348..19380, 19381..19515

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o8.ts	Method	TBLASTX:Soybean
Start	17864	End	19549
GI	none	Score	35

Exons 17864..17941, 18581..18643, 18588..18644, 18653..18721, 18660..18722, 18800..18868, 18800..18877, 18908..18964, 18921..18965, 19267..19293, 19295..19327, 19348..19380, 19381..19515, 19391..19549

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499

Name	OJ990323_25.9923.C3.o6.tm	Method	TBLASTX:Maize
Start	24429	End	28776
GI	none	Score	105
Exons	24429..24641, 24447..24632, 24448..24633, 24681..24857, 24715..24858, 24718..24858, 24719..24859, 24759..24875, 25220..25291, 25222..25290, 25225..25293, 25642..25797, 25648..25785, 25652..25807, 25920..26006, 25921..26007, 26484..26576, 26485..26565, 26485..26577, 27016..27099, 27023..27094, 27024..27101, 27413..27508, 27421..27507, 28701..28775, 28702..28776		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o3.tw	Method	TBLASTX:Wheat
Start	24437	End	24633
GI	none	Score	64
Exons	24437..24619, 24444..24632, 24448..24633		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o4.tc	Method	TBLASTX:Cress
Start	24437	End	25797
GI	none	Score	64
Exons	24437..24619, 24444..24641, 24447..24632, 24448..24633, 24681..24869, 24715..24858, 25222..25290, 25232..25291, 25642..25785, 25652..25783, 25666..25797		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o6.ts	Method	TBLASTX:Soybean
Start	24705	End	30852
GI	none	Score	117
Exons	24705..24866, 29525..29617, 29739..29951, 29755..29940, 30504..30635, 30706..30747, 30778..30852		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o3.tm	Method	TBLASTX:Maize
Start	29109	End	30932
GI	none	Score	128
Exons	29109..29189, 29463..29615, 29466..29573, 29468..29617, 29739..29951, 29740..29949, 29742..29879, 30493..30633, 30504..30635, 30705..30791, 30712..30789, 30879..30932		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o7.tc	Method	TBLASTX:Cress
Start	29468	End	30918
GI	none	Score	87
Exons	29468..29539, 29829..29879, 29862..29951, 30504..30635, 30504..30635, 30706..30747, 30772..30852, 30868..30918		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	988	Strand	-
Start	38041	End	38499
Name	OJ990323_25.9923.C3.o8.gs	Method	GENSCAN
Start	38041	End	38499
GI	none	Score	.76
Exons	38041..38161, 38396..38499		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	989	Strand	
Start	39636	End	41387
Name	OJ990323_25.9923.C3.o1.ts	Method	TBLASTX:Soybean
Start	39636	End	41380
GI	none	Score	37
Exons	39636..39854, 39639..39662, 39683..39862, 39738..39869, 40276..40446, 40276..40446, 40278..40448, 40509..40607, 40511..40606, 40525..40614, 40526..40615, 41050..41160, 41066..41365, 41067..41366, 41204..41380		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	989	Strand	
Start	39636	End	41387
Name	OJ990323_25.9923.C3.o8.tm	Method	TBLASTX:Maize
Start	40303	End	41366
GI	none	Score	93
Exons	40303..40440, 41054..41167, 41067..41168, 41177..41353, 41178..41366		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	989	Strand	
Start	39636	End	41387
Name	OJ990323_25.9923.C3.o3.tc	Method	TBLASTX:Cress
Start	40348	End	41387
GI	none	Score	95
Exons	40348..40449, 40350..40451, 40509..40604, 40550..40603, 41067..41168, 41072..41167, 41184..41381, 41186..41365, 41208..41387		

Seq. No.	498	Seq. ID	OJ990323_25.9923.C3
Gene No.	989	Strand	
Start	39636	End	41387
Name	OJ990323_25.9923.C3.o2.tw	Method	TBLASTX:Wheat
Start	40383	End	41267
GI	none	Score	100
Exons	40383..40445, 40384..40449, 40385..40450, 40509..40607, 40511..40606, 40520..40615, 40522..40614, 41065..41217, 41066..41266, 41067..41267		

Seq. No.	499	Seq. ID	OJ990323_25.9923.C5
Gene No.	990	Strand	+
Start	147	End	185
Name	OJ990323_25.9923.C5.o1.gs	Method	GENSCAN
Start	147	End	185
GI	none	Score	.55
Exons	147..185		

Seq. No.	500	Seq. ID	OJ990503_22.9919.C1

Gene No.	991	Strand	-
Start	88	End	315
Name	OJ990503_22.9919.C1.o1.gs	Method	GENSCAN
Start	88	End	315
GI	none	Score	.87
Exons	88..315		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	992	Strand	+
Start	1	End	5931
Name	OJ990503_22.9919.C2.o3.np	Method	AAT/NAP
Start	1	End	5456
GI	5734728	Score	804
Exons	1..52, 3385..3497, 3594..3804, 3901..4138, 4742..4852, 5141..5456		
GI Descrip.	(AC007259) Very similar to receptor-like protein kinases [Arabidopsis thaliana]		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	992	Strand	+
Start	1	End	5931
Name	OJ990503_22.9919.C2.o2.np	Method	AAT/NAP
Start	1181	End	1280
GI	5922634	Score	118
Exons	1181..1280		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016867|dbj|BAA85210.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	992	Strand	+
Start	1	End	5931
Name	OJ990503_22.9919.C2.o1.gs	Method	GENSCAN
Start	1406	End	5931
GI	none	Score	.8
Exons	1406..2291, 3319..3497, 3594..3804, 5906..5931		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	993	Strand	-
Start	1	End	984
Name	OJ990503_22.9919.C2.o1.np	Method	AAT/NAP
Start	1	End	984
GI	3875904	Score	54
Exons	1..82, 798..984		
GI Descrip.	(Z70207) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65905 comes from this gene; cDNA EST EMBL:D65858 comes from this gene; cDNA EST EMBL:D69306 comes from this gene; cDNA EST EMBL:D65755 comes from this g...		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	994	Strand	
Start	2033	End	5471
Name	OJ990503_22.9919.C2.o1.tc	Method	TBLASTX:Cress
Start	2033	End	5401
GI	none	Score	88
Exons	2033..2095, 3390..3503, 3434..3535, 3591..3803, 3593..3817, 3899..4078, 3900..4136, 3920..4138, 4746..4862, 4746..4862,		

4754..4870, 5160..5372, 5258..5401

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	994	Strand	
Start	2033	End	5471
Name	OJ990503_22.9919.C2.o1.ts	Method	TBLASTX:Soybean
Start	3390	End	5372
GI	none	Score	104
Exons	3390..3497, 3434..3490, 3591..3803, 3593..3817, 3921..4136, 3926..4138, 4742..4858, 4743..4892, 5151..5372		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	994	Strand	
Start	2033	End	5471
Name	OJ990503_22.9919.C2.o1.tm	Method	TBLASTX:Maize
Start	3591	End	4136
GI	none	Score	291
Exons	3591..3803, 3593..3802, 3863..4135, 3900..4136		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	994	Strand	
Start	2033	End	5471
Name	OJ990503_22.9919.C2.o1.tw	Method	TBLASTX:Wheat
Start	3719	End	4130
GI	none	Score	54
Exons	3719..3802, 3722..3802, 3726..3803, 3726..3803, 3727..3807, 3899..4102, 3900..4130, 3918..4115		

Seq. No.	501	Seq. ID	OJ990503_22.9919.C2
Gene No.	994	Strand	
Start	2033	End	5471
Name	OJ990503_22.9919.C2.o2.tm	Method	TBLASTX:Maize
Start	4732	End	5471
GI	none	Score	68
Exons	4732..4878, 4741..4842, 4742..4852, 4743..4892, 4746..4892, 5159..5215, 5160..5420, 5224..5322, 5258..5410, 5406..5471		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	995	Strand	+
Start	796	End	4858
Name	OJ990503_22.9919.C3.o1.gs	Method	GENSCAN
Start	796	End	4858
GI	none	Score	.56
Exons	796..912, 3958..4102, 4346..4538, 4855..4858		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	996	Strand	+
Start	15882	End	20175
Name	OJ990503_22.9919.C3.o2.np	Method	AAT/NAP
Start	15882	End	20175
GI	6498441	Score	4696
Exons	15882..16946, 17277..17740, 17804..18177, 18361..18495, 18670..19084, 19277..19585, 19757..20175		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	997	Strand	+
Start	20467	End	23141
Name	OJ990503_22.9919.C3.o5.gs	Method	GENSCAN
Start	20467	End	23141
GI	none	Score	.76
Exons	20467..20521, 21283..21474, 21566..21733, 21738..21845, 22334..22479, 22757..22810, 22959..23141		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	998	Strand	-
Start	5038	End	10722
Name	OJ990503_22.9919.C3.o2.gs	Method	GENSCAN
Start	5038	End	10722
GI	none	Score	.49
Exons	5038..5479, 6767..6922, 7019..8207, 8358..8618, 8763..9314, 9525..9580, 9701..9881, 10641..10722		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	998	Strand	-
Start	5038	End	10722
Name	OJ990503_22.9919.C3.o1.np	Method	AAT/NAP
Start	6947	End	8865
GI	479357	Score	1023
Exons	6947..8589, 8657..8865		
GI Descrip.	hypothetical protein 612 - maize transposon MuA2 gi|22375|emb|CAA44165| (X62251) ORF [Zea mays]		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423
Name	OJ990503_22.9919.C3.o5.tw	Method	TBLASTX:Wheat
Start	3319	End	16423
GI	none	Score	57
Exons	3319..3402, 16031..16078, 16085..16183, 16090..16182, 16150..16389, 16166..16423		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423
Name	OJ990503_22.9919.C3.o1.tm	Method	TBLASTX:Maize
Start	7588	End	8211
GI	none	Score	80
Exons	7588..7863, 7601..7858, 7871..7936, 7873..7935, 7964..8206, 7966..8211		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423
Name	OJ990503_22.9919.C3.o3.gs	Method	GENSCAN
Start	11239	End	12699
GI	none	Score	1
Exons	11239..12699		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423

Name	OJ990503_22.9919.C3.o1.tc	Method	TBLASTX:Cress
Start	11291	End	12676
GI	none	Score	34
Exons	11291..11332, 11392..11628, 11393..11596, 11692..11886, 11714..11827, 11911..12081, 12193..12342, 12221..12343, 12382..12516, 12431..12517, 12550..12675, 12569..12676		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423
Name	OJ990503_22.9919.C3.o4.tm	Method	TBLASTX:Maize
Start	11324	End	11869
GI	none	Score	196
Exons	11324..11629, 11392..11628, 11689..11853, 11692..11853, 11714..11869		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423
Name	OJ990503_22.9919.C3.o1.ts	Method	TBLASTX:Soybean
Start	11393	End	12675
GI	none	Score	143
Exons	11393..11623, 11395..11628, 11707..11886, 11714..11887, 11923..12081, 12193..12378, 12242..12361, 12437..12517, 12478..12516, 12550..12675		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423
Name	OJ990503_22.9919.C3.o6.tw	Method	TBLASTX:Wheat
Start	11456	End	11853
GI	none	Score	158
Exons	11456..11629, 11461..11634, 11464..11634, 11701..11853, 11716..11820, 11717..11848		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	999	Strand	-
Start	11239	End	16423
Name	OJ990503_22.9919.C3.o5.tm	Method	TBLASTX:Maize
Start	16036	End	16321
GI	none	Score	197
Exons	16036..16320, 16073..16321		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1000	Strand	
Start	17161	End	17647
Name	OJ990503_22.9919.C3.o3.tw	Method	TBLASTX:Wheat
Start	17161	End	17647
GI	none	Score	408
Exons	17161..17298, 17162..17647, 17162..17323, 17356..17616, 17381..17620		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1001	Strand	
Start	17811	End	18298
Name	OJ990503_22.9919.C3.o1.tw	Method	TBLASTX:Wheat
Start	17811	End	18274

GI	none	Score	199
Exons	17811..18254, 17812..18267, 17813..18274, 17813..18268		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1001	Strand	
Start	17811	End	18298
Name	OJ990503_22.9919.C3.o3.ts	Method	TBLASTX:Soybean
Start	17852	End	18217
GI	none	Score	119
Exons	17852..18076, 18083..18217		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1001	Strand	
Start	17811	End	18298
Name	OJ990503_22.9919.C3.o2.tm	Method	TBLASTX:Maize
Start	17942	End	18298
GI	none	Score	392
Exons	17942..18298, 17977..18288, 17993..18298		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1002	Strand	
Start	18325	End	18832
Name	OJ990503_22.9919.C3.o3.tm	Method	TBLASTX:Maize
Start	18325	End	18709
GI	none	Score	359
Exons	18325..18690, 18326..18709		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1002	Strand	
Start	18325	End	18832
Name	OJ990503_22.9919.C3.o2.tw	Method	TBLASTX:Wheat
Start	18382	End	18802
GI	none	Score	485
Exons	18382..18795, 18383..18802		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1002	Strand	
Start	18325	End	18832
Name	OJ990503_22.9919.C3.o2.ts	Method	TBLASTX:Soybean
Start	18461	End	18832
GI	none	Score	278
Exons	18461..18832, 18478..18621		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1003	Strand	
Start	19457	End	20170
Name	OJ990503_22.9919.C3.o4.tw	Method	TBLASTX:Wheat
Start	19457	End	19891
GI	none	Score	233
Exons	19457..19708, 19457..19681, 19522..19698, 19742..19891, 19760..19888, 19768..19890		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1003	Strand	
Start	19457	End	20170
Name	OJ990503_22.9919.C3.o4.ts	Method	TBLASTX:Soybean
Start	19580	End	20146

GI	5666795	Score	64
Exons	19580..19678, 19757..19891, 19931..20146		
GI Descrip.	4206306 2.0e-10 (AF049110) prpol [Zea mays]		

Seq. No.	502	Seq. ID	OJ990503_22.9919.C3
Gene No.	1003	Strand	
Start	19457	End	20170
Name	OJ990503_22.9919.C3.o7.tw	Method	TBLASTX:Wheat
Start	19894	End	20170
GI	none	Score	179
Exons	19894..20070, 19907..20095, 19931..20170		

Seq. No.	503	Seq. ID	OJ990503_22.9919.C5
Gene No.	1004	Strand	+
Start	369	End	3004
Name	OJ990503_22.9919.C5.o1.gs	Method	GENSCAN
Start	369	End	3004
GI	none	Score	.85
Exons	369..587, 1064..1192, 2891..3004		

Seq. No.	503	Seq. ID	OJ990503_22.9919.C5
Gene No.	1005	Strand	+
Start	3899	End	5170
Name	OJ990503_22.9919.C5.o1.np	Method	AAT/NAP
Start	3899	End	5170
GI	3261518	Score	61
Exons	3899..4436, 5126..5170		
GI Descrip.	(AL021841) PE_PGRS [Mycobacterium tuberculosis]		

Seq. No.	503	Seq. ID	OJ990503_22.9919.C5
Gene No.	1006	Strand	-
Start	3823	End	4335
Name	OJ990503_22.9919.C5.o2.gs	Method	GENSCAN
Start	3823	End	4335
GI	none	Score	.56
Exons	3823..4014, 4161..4335		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1007	Strand	+
Start	11173	End	11723
Name	OJ990503_22.9919.C6.o3.gs	Method	GENSCAN
Start	11173	End	11723
GI	none	Score	.62
Exons	11173..11354, 11518..11600, 11608..11723		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1008	Strand	-
Start	1992	End	5527
Name	OJ990503_22.9919.C6.o1.gs	Method	GENSCAN
Start	1992	End	5527
GI	none	Score	.89
Exons	1992..2068, 3772..4026, 5377..5527		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1009	Strand	-
Start	6863	End	7126
Name	OJ990503_22.9919.C6.o2.gs	Method	GENSCAN

Start	6863	End	7126
GI	none	Score	.78
Exons	6863..7126		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o1.np	Method	AAT/NAP
Start	11166	End	18361
GI	5257279	Score	6893
Exons	11166..11390, 12787..13387, 13502..13660, 13877..16595, 17232..17467, 17816..18361		
GI Descrip.	(AP000364) Similar to Transposon MAGGY gag and pol gene homologues. (L35053) [Oryza sativa]		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o6.tw	Method	TBLASTX:Wheat
Start	12424	End	12755
GI	none	Score	76
Exons	12424..12588, 12617..12754, 12639..12755		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o4.gs	Method	GENSCAN
Start	12584	End	18160
GI	none	Score	.45
Exons	12584..12865, 12887..13273, 13502..14248, 14300..15684, 15712..16755, 17118..17315, 17332..17437, 17504..18160		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o1.tm	Method	TBLASTX:Maize
Start	12614	End	13198
GI	none	Score	247
Exons	12614..13042, 12627..13043, 12684..13043, 12901..13047, 12902..13102, 13036..13170, 13040..13198, 13044..13196		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o1.tw	Method	TBLASTX:Wheat
Start	12755	End	13366
GI	none	Score	313
Exons	12755..13366, 12756..13325		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o4.tm	Method	TBLASTX:Maize
Start	13250	End	13541
GI	none	Score	235
Exons	13250..13540, 13254..13541		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o2.ts	Method	TBLASTX:Soybean
Start	13343	End	13589
GI	none	Score	107
Exons	13343..13588, 13344..13589		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o1.tc	Method	TBLASTX:Cress
Start	13365	End	13681
GI	none	Score	95
Exons	13365..13505, 13397..13507, 13508..13681, 13560..13673		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o3.tw	Method	TBLASTX:Wheat
Start	13397	End	13877
GI	none	Score	300
Exons	13397..13876, 13401..13877		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o2.tw	Method	TBLASTX:Wheat
Start	13877	End	14380
GI	none	Score	258
Exons	13877..14380, 13968..14345, 14122..14352		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o1.gp	Method	AAT/GAP
Start	14044	End	15405
GI	4107139	Score	2536
Exons	14044..15405		
GI Descrip.	5257279/dbj|BAA81778.1| 0.0e+00 (AP000364) Similar to Transposon MAGGY gag and pol gene homologues. (L35053) [Oryza sativa]		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o2.tm	Method	TBLASTX:Maize
Start	14069	End	14510
GI	none	Score	213
Exons	14069..14509, 14082..14510		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o3.ts	Method	TBLASTX:Soybean
Start	14129	End	14374
GI	none	Score	199
Exons	14129..14374		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o5.tw	Method	TBLASTX:Wheat
Start	14381	End	14683
GI	none	Score	269
Exons	14381..14683, 14397..14681, 14447..14683		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o1.ts	Method	TBLASTX:Soybean
Start	14396	End	14791
GI	none	Score	245
Exons	14396..14755, 14397..14753, 14426..14761, 14602..14760, 14759..14791		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o6.tm	Method	TBLASTX:Maize
Start	14514	End	14677
GI	none	Score	132
Exons	14514..14672, 14516..14677, 14522..14677		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o3.tm	Method	TBLASTX:Maize
Start	14678	End	15148
GI	none	Score	401
Exons	14678..15148		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o4.tw	Method	TBLASTX:Wheat
Start	14732	End	15214
GI	none	Score	88
Exons	14732..15214, 14736..14879, 14765..15154, 14907..15203		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o7.tm	Method	TBLASTX:Maize
Start	15149	End	15311
GI	none	Score	153
Exons	15149..15310, 15150..15311		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o7.tw	Method	TBLASTX:Wheat
Start	15386	End	15764
GI	none	Score	95
Exons	15386..15508, 15387..15497, 15392..15544, 15542..15763,		

15642..15764

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o5.tm	Method	TBLASTX:Maize
Start	15444	End	15769
GI	none	Score	61
Exons	15444..15578, 15446..15769, 15621..15722		

Seq. No.	504	Seq. ID	OJ990503_22.9919.C6
Gene No.	1010	Strand	-
Start	11166	End	18361
Name	OJ990503_22.9919.C6.o8.tw	Method	TBLASTX:Wheat
Start	16316	End	16702
GI	none	Score	105
Exons	16316..16462, 16487..16702, 16497..16658, 16642..16680		

Seq. No.	505	Seq. ID	OJ990503_29.9919.C1
Gene No.	1011	Strand	-
Start	64	End	195
Name	OJ990503_29.9919.C1.o1.gs	Method	GENSCAN
Start	64	End	195
GI	none	Score	.86
Exons	64..195		

Seq. No.	505	Seq. ID	OJ990503_29.9919.C1
Gene No.	1012	Strand	-
Start	142	End	480
Name	OJ990503_29.9919.C1.o1.np	Method	AAT/NAP
Start	142	End	480
GI	5042454	Score	68
Exons	142..195, 434..480		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	506	Seq. ID	OJ990503_29.9919.C2
Gene No.	1013	Strand	-
Start	329	End	660
Name	OJ990503_29.9919.C2.o1.np	Method	AAT/NAP
Start	329	End	660
GI	5042454	Score	69
Exons	329..382, 638..660		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	507	Seq. ID	OJ990503_29.9919.C4
Gene No.	1014	Strand	-
Start	259	End	733
Name	OJ990503_29.9919.C4.o1.gp	Method	AAT/GAP
Start	259	End	733
GI	none	Score	829
Exons	259..733		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o1.gs	Method	GENSCAN
Start	1203	End	5567

GI	none	Score	.84
Exons	1203..1457, 1752..1848, 3934..4140, 4244..4476, 4587..4747, 4832..4922, 5009..5158, 5331..5567		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o1.ts	Method	TBLASTX:Soybean
Start	1233	End	4928
GI	none	Score	77
Exons	1233..1355, 1289..1354, 1582..1650, 1773..1847, 3936..4145, 3938..4144, 4242..4340, 4243..4344, 4362..4418, 4363..4512, 4626..4748, 4835..4927, 4836..4928		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o1.np	Method	AAT/NAP
Start	1243	End	5579
GI	4973431	Score	1345
Exons	1243..1457, 1582..1650, 1752..1848, 3934..4144, 4248..4476, 4587..4747, 4832..4922, 5009..5158, 5331..5579		
GI Descrip.	(AF148877) putative aldehyde dehydrogenase OS-ALDH [Oryza sativa subsp. indica]		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o3.tm	Method	TBLASTX:Maize
Start	1295	End	1840
GI	none	Score	50
Exons	1295..1333, 1296..1334, 1334..1459, 1425..1472, 1579..1650, 1582..1650, 1584..1652, 1749..1838, 1749..1838, 1751..1840		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o1.tm	Method	TBLASTX:Maize
Start	3965	End	4609
GI	none	Score	221
Exons	3965..4144, 3990..4145, 4173..4349, 4242..4340, 4243..4356, 4243..4353, 4350..4418, 4351..4470, 4586..4609		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o1.gp	Method	AAT/GAP
Start	4668	End	5855
GI	80420_1:R1084	Score	1474
Exons	4668..4747, 4832..4922, 5009..5158, 5331..5855		
GI Descrip.	'4973431/gb|AAD35089.1|AF148877_1 1.0e-64 (AF148877) putative aldehyde dehydrogenase OS-ALDH [Oryza sativa subsp. indica]'		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o2.tm	Method	TBLASTX:Maize

Start	4831	End	5566
GI	none	Score	150
Exons	4831..4923, 4832..4951, 4836..4925, 4836..4952, 4990..5100, 4994..5101, 5012..5101, 5101..5187, 5102..5191, 5325..5528, 5327..5566, 5399..5560		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o1.tc	Method	TBLASTX:Cress
Start	4836	End	5483
GI	none	Score	132
Exons	4836..4925, 4838..4924, 4994..5191, 5023..5145, 5325..5483, 5330..5428		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o3.ts	Method	TBLASTX:Soybean
Start	4993	End	5179
GI	none	Score	192
Exons	4993..5157, 4994..5179		

Seq. No.	508	Seq. ID	OJ990503_29.9919.C5
Gene No.	1015	Strand	+
Start	1203	End	5855
Name	OJ990503_29.9919.C5.o2.ts	Method	TBLASTX:Soybean
Start	5324	End	5531
GI	none	Score	207
Exons	5324..5479, 5325..5531		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1016	Strand	+
Start	2019	End	2452
Name	OJ990503_29.9919.C6.o1.gp	Method	AAT/GAP
Start	2019	End	2452
GI	LIB3432-022-P1-K1-A8	Score	825
Exons	2019..2452		
GI Descrip.	'6015437/dbj|AB008112.1|AB008112 6.0e-10 Homo sapiens PEX1 mRNA, complete cds'		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1017	Strand	+
Start	16735	End	26748
Name	OJ990503_29.9919.C6.o5.gs	Method	GENSCAN
Start	16735	End	26748
GI	none	Score	.64
Exons	16735..16890, 17556..17651, 18023..18139, 18662..18739, 18859..18969, 19176..19269, 19275..19372, 20315..20434, 20523..20592, 20706..20857, 21037..21138, 21740..21940, 22231..22386, 22492..22566, 22709..22807, 23250..23327, 23965..24096, 24308..24441, 26598..26748		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1017	Strand	+
Start	16735	End	26748
Name	OJ990503_29.9919.C6.o3.np	Method	AAT/NAP

Start	19319	End	22880
GI	3096935	Score	814
Exons	19319..19372, 20309..20434, 20523..20592, 20706..20857, 21037..21138, 21740..21965, 22036..22109, 22231..22412, 22518..22566, 22716..22880		
GI Descrip.	(AL023094) putative protein [Arabidopsis thaliana]		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1017	Strand	+
Start	16735	End	26748
Name	OJ990503_29.9919.C6.o3.gp	Method	AAT/GAP
Start	22249	End	22956
GI	2276033	Score	824
Exons	22249..22386, 22492..22566, 22709..22956		
GI Descrip.	4539321/emb|CAB38822.1| 6.0e-17 (AL035679) putative protein [Arabidopsis thaliana]		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1018	Strand	-
Start	165	End	5844
Name	OJ990503_29.9919.C6.o1.gs	Method	GENSCAN
Start	165	End	5835
GI	none	Score	.59
Exons	165..247, 3116..3249, 3867..4113, 4197..4465, 4484..4688, 4817..5282, 5557..5633, 5775..5835		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1018	Strand	-
Start	165	End	5844
Name	OJ990503_29.9919.C6.o1.np	Method	AAT/NAP
Start	3860	End	5844
GI	2160169	Score	929
Exons	3860..4113, 4194..4465, 4576..4719, 4894..5282, 5452..5680, 5792..5844		
GI Descrip.	(AC000132) No definition line found [Arabidopsis thaliana]		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1019	Strand	-
Start	6163	End	7779
Name	OJ990503_29.9919.C6.o2.gs	Method	GENSCAN
Start	6163	End	7779
GI	none	Score	.81
Exons	6163..6341, 7161..7218, 7286..7511, 7658..7779		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1020	Strand	-
Start	8204	End	11374
Name	OJ990503_29.9919.C6.o3.gs	Method	GENSCAN
Start	8204	End	11186
GI	none	Score	.81
Exons	8204..8263, 9029..9167, 9578..9693, 10536..10892, 10986..11186		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1020	Strand	-
Start	8204	End	11374
Name	OJ990503_29.9919.C6.o2.np	Method	AAT/NAP
Start	9454	End	11186

GI	4539326	Score	350
Exons	9454..9481, 10630..10889, 10986..11186		
GI Descrip.	(AL035679) putative zinc finger protein [Arabidopsis thaliana]		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1020	Strand	-
Start	8204	End	11374
Name	OJ990503_29.9919.C6.o2.gp	Method	AAT/GAP
Start	10804	End	11374
GI	48654_1.R1084	Score	880
Exons	10804..10892, 10986..11374		
GI Descrip.	'3618312/dbj|BAA33202| 2.0e-18 (AB001884) zinc finger protein [Oryza sativa]'		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1021	Strand	-
Start	25462	End	25520
Name	OJ990503_29.9919.C6.o4.gp	Method	AAT/GAP
Start	25462	End	25520
GI	2312838	Score	64
Exons	25462..25520		
GI Descrip.	1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o1.tc	Method	TBLASTX:Cress
Start	3848	End	5246
GI	none	Score	87
Exons	3848..4057, 3891..4058, 4055..4114, 4072..4116, 4195..4443, 4214..4405, 4552..4575, 4600..4719, 4623..4742, 4847..4867, 4971..5123, 4972..5124, 5082..5246, 5149..5235		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o3.ts	Method	TBLASTX:Soybean
Start	3854	End	4054
GI	none	Score	102
Exons	3854..4054, 3891..4052		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o1.tm	Method	TBLASTX:Maize
Start	3905	End	5637
GI	none	Score	100
Exons	3905..4054, 3905..4057, 3906..4061, 4049..4114, 4050..4112, 4061..4150, 4204..4416, 4205..4405, 4597..4719, 4623..4742, 4971..5123, 5029..5124, 5082..5279, 5149..5298, 5584..5637		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o2.ts	Method	TBLASTX:Soybean
Start	4055	End	4416

GI	none	Score	126
Exons	4055..4132, 4195..4416, 4217..4405		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919:C6.o2.tw	Method	TBLASTX:Wheat
Start	4282	End	4416
GI	none	Score	116
Exons	4282..4416, 4283..4405		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o4.ts	Method	TBLASTX:Soybean
Start	5031	End	5294
GI	4260377	Score	79
Exons	5031..5123, 5032..5124, 5082..5294, 5149..5277		
GI Descrip.	2160169 3.0e-26 (AC000132) No definition line found [Arabidopsis thaliana]		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o3.tm	Method	TBLASTX:Maize
Start	10779	End	11196
GI	none	Score	133
Exons	10779..10877, 10806..10895, 10820..10894, 10990..11031, 11020..11196, 11052..11195		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o2.tm	Method	TBLASTX:Maize
Start	19315	End	21138
GI	none	Score	90
Exons	19315..19368, 19316..19372, 20311..20334, 20341..20433, 20342..20452, 20512..20583, 20517..20591, 20520..20594, 20522..20593, 20691..20858, 20698..20871, 20702..20860, 21027..21134, 21028..21138, 21034..21138		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o1.ts	Method	TBLASTX:Soybean
Start	20342	End	21943
GI	none	Score	106
Exons	20342..20452, 20344..20427, 20508..20594, 20516..20617, 20517..20594, 20698..20859, 20702..20860, 20703..20861, 21025..21138, 21027..21137, 21034..21138, 21715..21942, 21740..21943		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o1.tw	Method	TBLASTX:Wheat
Start	21849	End	22774

GI	none	Score	69
Exons	21849..21941, 21851..21958, 21851..21940, 22011..22103, 22030..22104, 22031..22108, 22044..22121, 22230..22397, 22230..22400, 22231..22413, 22477..22569, 22489..22569, 22490..22582, 22706..22774, 22708..22767		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o4.tm	Method	TBLASTX:Maize
Start	22353	End	22836
GI	none	Score	50
Exons	22353..22397, 22356..22406, 22489..22569, 22490..22561, 22706..22831, 22708..22836, 22708..22830		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o5.ts	Method	TBLASTX:Soybean
Start	22489	End	22831
GI	none	Score	78
Exons	22489..22569, 22694..22831, 22717..22809		

Seq. No.	509	Seq. ID	OJ990503_29.9919.C6
Gene No.	1022	Strand	-
Start	27536	End	31102
Name	OJ990503_29.9919.C6.o6.gs	Method	GENSCAN
Start	27536	End	31102
GI	none	Score	.74
Exons	27536..27595, 27834..27860, 30637..30649, 30894..31102		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1023	Strand	+
Start	2320	End	3265
Name	OJ990503_29.9919.C7.o2.gs	Method	GENSCAN
Start	2320	End	3265
GI	none	Score	.57
Exons	2320..2328, 2624..2749, 2887..3059, 3166..3265		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1024	Strand	+
Start	5715	End	6079
Name	OJ990503_29.9919.C7.o3.gp	Method	AAT/GAP
Start	5715	End	6079
GI	3761807	Score	700
Exons	5715..6079		
GI Descrip.	984926/gb|U35137|XXU35137 1.0e-57 Plasmid pBSL99 cloning vector, complete sequence		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1025	Strand	+
Start	17664	End	20804
Name	OJ990503_29.9919.C7.o2.np	Method	AAT/NAP
Start	17598	End	20804
GI	5731998	Score	430
Exons	17598..17982, 18196..18408, 20768..20804		
GI Descrip.	(AF139532) aldehyde 5-hydroxylase [Liquidambar styraciflua]		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1025	Strand	+
Start	17664	End	20804
Name	OJ990503_29.9919.C7.o5.gs	Method	GENSCAN
Start	17664	End	18602
GI	none	Score	.41
Exons	17664..18037, 18161..18602		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1025	Strand	+
Start	17664	End	20804
Name	OJ990503_29.9919.C7.o3.np	Method	AAT/NAP
Start	18408	End	18602
GI	1845567	Score	146
Exons	18408..18602		
GI Descrip.	(D89435) cytochrome P450 [Glycyrrhiza echinata]		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1025	Strand	+
Start	17664	End	20804
Name	OJ990503_29.9919.C7.o6.gs	Method	GENSCAN
Start	19503	End	20707
GI	none	Score	.79
Exons	19503..19581, 20368..20442, 20484..20707		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1026	Strand	+
Start	24840	End	35217
Name	OJ990503_29.9919.C7.o8.gs	Method	GENSCAN
Start	24840	End	28016
GI	none	Score	.88
Exons	24840..25451, 26077..26305, 27378..27454, 27939..28016		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1026	Strand	+
Start	24840	End	35217
Name	OJ990503_29.9919.C7.o4.gp	Method	AAT/GAP
Start	25317	End	26226
GI	428764	Score	550
Exons	25317..25451, 26077..26226		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1026	Strand	+
Start	24840	End	35217
Name	OJ990503_29.9919.C7.o5.np	Method	AAT/NAP
Start	27183	End	35217
GI	135574	Score	44
Exons	27183..27231, 29157..29475, 35198..35217		
GI Descrip.	LARGE TEGUMENT PROTEIN gi|73929|pir||QQBE8 BPLF1 protein - human herpesvirus 4 (strain B95-8) gi|1334853|emb|CAA24839.1| (V01555) BPLF1 reading frame, 1 NXT/S, analogous to VZV RF22 [Human herpesvirus 4] gi|225109|prf||1208408E gene BPLF1 [Human herpesvirus 4]		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1026	Strand	+

Start	24840	End	35217
Name	OJ990503_29.9919.C7.o5.gp	Method	AAT/GAP
Start	27381	End	28312
GI	3767920	Score	848
Exons	27381..27454, 27939..28312		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1027	Strand	-
Start	1095	End	2417
Name	OJ990503_29.9919.C7.o1.np	Method	AAT/NAP
Start	931	End	2417
GI	5852093	Score	63
Exons	931..1035, 2379..2417		
GI Descrip.	(AL117264) zwh16.1 [Oryza sativa]		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1027	Strand	-
Start	1095	End	2417
Name	OJ990503_29.9919.C7.o1.gs	Method	GENSCAN
Start	1095	End	1455
GI	none	Score	.74
Exons	1095..1118, 1396..1455		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1028	Strand	-
Start	3332	End	3850
Name	OJ990503_29.9919.C7.o1.gp	Method	AAT/GAP
Start	3332	End	3850
GI	87034_1.R1084	Score	994
Exons	3332..3850		
GI Descrip.	'984926/gb|U35137|XXU35137 1.0e-57 Plasmid pBSL99 cloning vector, complete sequence'		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1029	Strand	-
Start	4520	End	8883
Name	OJ990503_29.9919.C7.o2.gp	Method	AAT/GAP
Start	4176	End	4445
GI	3762907	Score	488
Exons	4176..4445		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1029	Strand	-
Start	4520	End	8883
Name	OJ990503_29.9919.C7.o3.gs	Method	GENSCAN
Start	4520	End	8883
GI	none	Score	.64
Exons	4520..5356, 5480..5899, 5981..6063, 7447..7499, 7833..7964, 8816..8883		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1030	Strand	-
Start	9441	End	11480
Name	OJ990503_29.9919.C7.o4.gs	Method	GENSCAN
Start	9441	End	11480
GI	none	Score	.73
Exons	9441..9572, 9890..10011, 10130..10286, 11050..11278,		

11284..11308, 11345..11480

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1031	Strand	-
Start	22362	End	23462
Name	OJ990503_29.9919.C7.o7.gs	Method	GENSCAN
Start	22362	End	23462
GI	none	Score	.62
Exons	22362..22675, 23023..23106, 23273..23294, 23349..23462		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1032	Strand	-
Start	26138	End	29664
Name	OJ990503_29.9919.C7.o4.np	Method	AAT/NAP
Start	26138	End	29664
GI	4467098	Score	451
Exons	26138..26204, 28657..28827, 28892..29335, 29567..29664		
GI Descrip.	(AL035538) putative protein [Arabidopsis thaliana]		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1032	Strand	-
Start	26138	End	29664
Name	OJ990503_29.9919.C7.o9.gs	Method	GENSCAN
Start	28648	End	29464
GI	none	Score	1
Exons	28648..28824, 28979..29464		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o1.tc	Method	TBLASTX:Cress
Start	4566	End	4786
GI	none	Score	187
Exons	4566..4772, 4568..4786		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o2.ts	Method	TBLASTX:Soybean
Start	4566	End	4787
GI	none	Score	229
Exons	4566..4787, 4577..4786		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o2.tm	Method	TBLASTX:Maize
Start	4577	End	4793
GI	none	Score	239
Exons	4577..4786, 4578..4793		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o4.tm	Method	TBLASTX:Maize
Start	5308	End	6029
GI	none	Score	82

Exons	5308..5370, 5309..5371, 5309..5371, 5479..5568, 5481..5513, 5522..5695, 5541..5693, 5796..5837, 5967..5996, 5984..6028, 5988..6029		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o2.tc	Method	TBLASTX:Cress
Start	17751	End	26386
GI	none	Score	208
Exons	17751..17993, 17852..17995, 18197..18349, 18198..18386, 18414..18497, 18513..18590, 26300..26386		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o4.ts	Method	TBLASTX:Soybean
Start	17751	End	18346
GI	none	Score	200
Exons	17751..17993, 17852..18019, 18197..18346, 18198..18344		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o3.tm	Method	TBLASTX:Maize
Start	24720	End	25097
GI	none	Score	220
Exons	24720..24743, 24833..24997, 24834..24998, 25014..25097, 25016..25066		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o1.tm	Method	TBLASTX:Maize
Start	28645	End	29233
GI	none	Score	188
Exons	28645..28827, 28646..28825, 28977..29021, 28979..29233, 29016..29201		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o1.ts	Method	TBLASTX:Soybean
Start	28675	End	29230
GI	none	Score	109
Exons	28675..28827, 28712..28825, 28979..29230, 29013..29201		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o4.tc	Method	TBLASTX:Cress
Start	29054	End	29252
GI	none	Score	74
Exons	29054..29182, 29085..29252		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-

Start	30530	End	33318
Name	OJ990503_29.9919.C7.o6.np	Method	AAT/NAP
Start	30521	End	31298
GI	5103836	Score	286
Exons	30521..30766, 30858..30978, 31144..31298		
GI Descrip.	(AC007591) Is a member of the PF|00903 gyloxalase family. ESTs gb|T44721, gb|T21844 and gb|AA395404 come from this gene. [Arabidopsis thaliana]		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o10.gs	Method	GENSCAN
Start	30530	End	33318
GI	none	Score	.75
Exons	30530..30766, 30858..30978, 31144..31494, 33278..33318		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o3.tc	Method	TBLASTX:Cress
Start	30594	End	30980
GI	none	Score	92
Exons	30594..30758, 30596..30772, 30599..30679, 30600..30767, 30858..30893, 30945..30980		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o3.ts	Method	TBLASTX:Soybean
Start	30599	End	31274
GI	none	Score	122
Exons	30599..30772, 30603..30767, 30852..30890, 30942..30977, 31135..31257, 31143..31274		

Seq. No.	510	Seq. ID	OJ990503_29.9919.C7
Gene No.	1033	Strand	-
Start	30530	End	33318
Name	OJ990503_29.9919.C7.o5.tm	Method	TBLASTX:Maize
Start	30599	End	31316
GI	none	Score	122
Exons	30599..30772, 30603..30767, 30858..30890, 30859..30894, 30927..30977, 30928..30978, 31143..31316, 31143..31274		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1034	Strand	+
Start	1126	End	18008
Name	OJ990503_29.9919.C8.o1.gs	Method	GENSCAN
Start	1126	End	18008
GI	none	Score	.47
Exons	1126..1298, 1763..1912, 2579..2624, 2725..2797, 3061..3179, 3758..3881, 4699..4799, 4900..4956, 5103..5184, 5455..5473, 5834..6161, 6338..6451, 6531..7403, 7605..7906, 7999..8170, 8973..9405, 10850..10970, 11040..11985, 12992..13125, 15911..15989, 16232..16264, 17194..17271, 17431..17600, 17727..17883, 17976..18008		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1034	Strand	+
Start	1126	End	18008
Name	OJ990503_29.9919.C8.o1.np	Method	AAT/NAP
Start	3831	End	8320
GI	4539314	Score	1528
Exons	3831..4017, 4505..4596, 4701..4799, 4900..5013, 5103..5186, 5230..5347, 5603..5727, 5834..6161, 6338..6477, 6577..6617, 6669..6974, 7122..7451, 7698..7906, 7999..8320		
GI Descrip.	(AL035679) kinesin like protein [Arabidopsis thaliana]		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1034	Strand	+
Start	1126	End	18008
Name	OJ990503_29.9919.C8.o1.gp	Method	AAT/GAP
Start	5831	End	6842
GI	26184_1.R1084	Score	1462
Exons	5831..6161, 6338..6451, 6531..6842		
GI Descrip.	'5668645/emb|CAB51660.1| 5.0e-51 (AL109619) putative protein [Arabidopsis thaliana]'		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1034	Strand	+
Start	1126	End	18008
Name	OJ990503_29.9919.C8.o2.np	Method	AAT/NAP
Start	11035	End	13779
GI	6561959	Score	217
Exons	11035..11854, 13729..13779		
GI Descrip.	(AL132964) putative protein [Arabidopsis thaliana]		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1034	Strand	+
Start	1126	End	18008
Name	OJ990503_29.9919.C8.o4.gp	Method	AAT/GAP
Start	12094	End	16254
GI	none	Score	1029
Exons	12094..12168, 12992..13125, 15911..16254		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1035	Strand	+
Start	20481	End	23649
Name	OJ990503_29.9919.C8.o3.gs	Method	GENSCAN
Start	20481	End	23649
GI	none	Score	.78
Exons	20481..20610, 20677..21742, 21843..23406, 23425..23649		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1035	Strand	+
Start	20481	End	23649
Name	OJ990503_29.9919.C8.o3.np	Method	AAT/NAP
Start	20481	End	23646
GI	6907089	Score	4163
Exons	20481..21742, 21843..23646		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1036	Strand	-

Start	8018	End	8483
Name	OJ990503_29.9919.C8.o2.gp	Method	AAT/GAP
Start	8018	End	8483
GI	uC-osflcyp082f04a1	Score	900
Exons	8018..8483		
GI Descrip.	'4539314/emb|CAB38815.1| 4.0e-19 (AL035679) kinesin like protein [Arabidopsis thaliana]'		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1037	Strand	-
Start	8718	End	9015
Name	OJ990503_29.9919.C8.o3.gp	Method	AAT/GAP
Start	8718	End	9015
GI	none	Score	596
Exons	8718..9015		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1038	Strand	-
Start	18740	End	20199
Name	OJ990503_29.9919.C8.o2.gs	Method	GENSCAN
Start	18740	End	20199
GI	none	Score	.76
Exons	18740..18871, 19104..19274, 19553..19610, 20096..20199		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o10.tm	Method	TBLASTX:Maize
Start	3767	End	4001
GI	none	Score	80
Exons	3767..3835, 3848..3985, 3852..4001, 3866..4000		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o2.ts	Method	TBLASTX:Soybean
Start	4549	End	5150
GI	none	Score	60
Exons	4549..4596, 4554..4595, 4667..4792, 4680..4799, 4697..4780, 4704..4790, 4897..5025, 4899..5024, 5088..5150		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o3.tm	Method	TBLASTX:Maize
Start	4554	End	5488
GI	none	Score	61
Exons	4554..4589, 4674..4799, 4675..4794, 4680..4799, 4897..5022, 4897..5013, 5100..5183, 5101..5190, 5102..5182, 5268..5339, 5278..5343, 5279..5344, 5450..5488, 5454..5486		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o8.tm	Method	TBLASTX:Maize
Start	5490	End	5939
GI	none	Score	41

Exons	5490..5516, 5491..5517, 5596..5727, 5603..5719, 5607..5726, 5608..5727, 5814..5939, 5827..5937, 5831..5938		
Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o1.ts	Method	TBLASTX:Soybean
Start	5650	End	6154
GI	none	Score	113
Exons	5650..5727, 5651..5722, 5814..6098, 5831..6094, 5841..6095, 5842..6105, 6128..6154		
Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o1.tm	Method	TBLASTX:Maize
Start	5969	End	7452
GI	none	Score	84
Exons	5969..6019, 5970..6020, 5970..6026, 5977..6024, 6016..6162, 6020..6160, 6021..6167, 6333..6425, 6335..6427, 6532..6585, 6534..6572, 6574..6756, 6598..7062, 6600..7337, 6624..7328, 7334..7399, 7334..7399, 7335..7403, 7399..7452		
Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o2.tm	Method	TBLASTX:Maize
Start	7601	End	8374
GI	none	Score	429
Exons	7601..7867, 7602..7874, 7981..8346, 7990..8370, 7997..8374		
Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o5.ts	Method	TBLASTX:Soybean
Start	7677	End	7868
GI	none	Score	228
Exons	7677..7868, 7679..7867		
Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o3.ts	Method	TBLASTX:Soybean
Start	7996	End	8262
GI	none	Score	271
Exons	7996..8262, 7997..8260		
Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o9.tm	Method	TBLASTX:Maize
Start	11407	End	11631
GI	none	Score	137
Exons	11407..11502, 11407..11469, 11485..11631, 11502..11630, 11521..11631		
Seq. No.	511	Seq. ID	OJ990503_29.9919.C8

Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o6.ts	Method	TBLASTX:Soybean
Start	11512	End	11787
GI	none	Score	219
Exons	11512..11787, 11517..11786		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o7.tm	Method	TBLASTX:Maize
Start	15909	End	16485
GI	none	Score	268
Exons	15909..16217, 15909..16109, 15910..16224, 15910..16218, 16316..16363, 16317..16364, 16318..16371, 16423..16485		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o4.gs	Method	GENSCAN
Start	24271	End	32982
GI	none	Score	.47
Exons	24271..25266, 25408..26292, 26416..27030, 27240..28073, 28137..28576, 28734..30516, 30572..30783, 30988..31186, 32692..32982		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o4.np	Method	AAT/NAP
Start	24274	End	29993
GI	6498441	Score	7075
Exons	24274..24555, 24649..26046, 26218..26568, 26836..27208, 27382..27516, 27700..28073, 28137..28600, 28929..29993		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o7.tw	Method	TBLASTX:Wheat
Start	24283	End	24885
GI	none	Score	75
Exons	24283..24408, 24287..24409, 24575..24883, 24601..24885, 24602..24880		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o4.tw	Method	TBLASTX:Wheat
Start	24886	End	25267
GI	none	Score	224
Exons	24886..25266, 24917..25267		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-

Start	24271	End	34016
Name	OJ990503_29.9919.C8.o5.tm	Method	TBLASTX:Maize
Start	25061	End	25404
GI	none	Score	219
Exons	25061..25210, 25081..25404, 25094..25375		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o8.tw	Method	TBLASTX:Wheat
Start	25597	End	25909
GI	none	Score	64
Exons	25597..25857, 25733..25909		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o7.ts	Method	TBLASTX:Soybean
Start	25657	End	26223
GI	5666795	Score	67
Exons	25657..25857, 25912..26049, 26125..26223		
GI Descrip.	4206306 2.0e-10 (AF049110) prpol [Zea mays]		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o5.tw	Method	TBLASTX:Wheat
Start	25912	End	26370
GI	none	Score	88
Exons	25912..26061, 25913..26050, 25915..26052, 26095..26346, 26105..26281, 26122..26370		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o4.ts	Method	TBLASTX:Soybean
Start	27046	End	27416
GI	none	Score	83
Exons	27046..27276, 27273..27416, 27274..27399		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o2.tw	Method	TBLASTX:Wheat
Start	27076	End	27495
GI	none	Score	96
Exons	27076..27282, 27101..27256, 27264..27494, 27265..27495		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o6.tm	Method	TBLASTX:Maize
Start	27169	End	27552
GI	none	Score	204
Exons	27169..27279, 27267..27551, 27268..27552		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8

Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o4.tm	Method	TBLASTX:Maize
Start	27579	End	27935
GI	none	Score	73
Exons	27579..27695, 27579..27935, 27589..27900		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o1.tw	Method	TBLASTX:Wheat
Start	27603	End	28066
GI	none	Score	213
Exons	27603..28064, 27609..28064, 27610..28065, 27623..28066		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o3.tw	Method	TBLASTX:Wheat
Start	28230	End	28665
GI	none	Score	163
Exons	28230..28664, 28261..28521, 28543..28665		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o6.tw	Method	TBLASTX:Wheat
Start	29452	End	29841
GI	none	Score	95
Exons	29452..29709, 29486..29725, 29692..29790, 29693..29773, 29797..29841		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o11.tm	Method	TBLASTX:Maize
Start	29554	End	29838
GI	none	Score	101
Exons	29554..29802, 29555..29800, 29566..29838		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o5.np	Method	AAT/NAP
Start	30730	End	34016
GI	5042454	Score	171
Exons	30730..30790, 31147..31362, 32963..33046, 33988..34016		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	511	Seq. ID	OJ990503_29.9919.C8
Gene No.	1039	Strand	-
Start	24271	End	34016
Name	OJ990503_29.9919.C8.o5.gs	Method	GENSCAN
Start	33718	End	33893
GI	none	Score	.98
Exons	33718..33893		

Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1040	Strand	+
Start	4437	End	5231
Name	OJ990503_29.9919.C9.o2.gs	Method	GENSCAN
Start	4437	End	5231
GI	none	Score	.63
Exons	4437..5231		

Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1040	Strand	+
Start	4437	End	5231
Name	OJ990503_29.9919.C9.o1.np	Method	AAT/NAP
Start	4594	End	5204
GI	6143895	Score	459
Exons	4594..5204		
GI Descrip.	(AC010718) nodulin-like protein [Arabidopsis thaliana]		

Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1041	Strand	+
Start	10620	End	11007
Name	OJ990503_29.9919.C9.o1.gp	Method	AAT/GAP
Start	10540	End	11007
GI	none	Score	928
Exons	10540..11007		

Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1041	Strand	+
Start	10620	End	11007
Name	OJ990503_29.9919.C9.o4.gs	Method	GENSCAN
Start	10620	End	10961
GI	none	Score	.98
Exons	10620..10961		

Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1042	Strand	+
Start	13266	End	16658
Name	OJ990503_29.9919.C9.o2.np	Method	AAT/NAP
Start	13266	End	16658
GI	6630460	Score	432
Exons	13266..13334, 13744..13937, 16265..16658		
GI Descrip.	(AC007190) F23N19.11 [Arabidopsis thaliana]		

Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1043	Strand	-
Start	11994	End	15357
Name	OJ990503_29.9919.C9.o2.ts	Method	TBLASTX:Soybean
Start	4632	End	5195
GI	none	Score	280
Exons	4632..4769, 4656..4874, 4676..4867, 4929..5045, 4931..5023, 5112..5195, 5112..5159		

Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1043	Strand	-
Start	11994	End	15357
Name	OJ990503_29.9919.C9.o1.tc	Method	TBLASTX:Cress
Start	4656	End	4862
GI	none	Score	264

Exons	4656..4862, 4676..4861		
Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1043	Strand	-
Start	11994	End	15357
Name	OJ990503_29.9919.C9.o2.tm	Method	TBLASTX:Maize
Start	4667	End	5015
GI	none	Score	252
Exons	4667..4867, 4668..4874, 4929..5015		
Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1043	Strand	-
Start	11994	End	15357
Name	OJ990503_29.9919.C9.o5.gs	Method	GENSCAN
Start	11994	End	15357
GI	none	Score	.76
Exons	11994..12003, 12955..13125, 13131..13367, 14341..14534, 14948..15044, 15281..15357		
Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1044	Strand	
Start	16256	End	16658
Name	OJ990503_29.9919.C9.o1.ts	Method	TBLASTX:Soybean
Start	16256	End	16658
GI	none	Score	84
Exons	16256..16399, 16257..16400, 16261..16401, 16264..16404, 16265..16405, 16476..16658, 16526..16657, 16533..16658		
Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1044	Strand	
Start	16256	End	16658
Name	OJ990503_29.9919.C9.o2.tc	Method	TBLASTX:Cress
Start	16262	End	16405
GI	none	Score	216
Exons	16262..16402, 16264..16404, 16265..16405		
Seq. No.	512	Seq. ID	OJ990503_29.9919.C9
Gene No.	1044	Strand	
Start	16256	End	16658
Name	OJ990503_29.9919.C9.o1.tm	Method	TBLASTX:Maize
Start	16327	End	16658
GI	none	Score	118
Exons	16327..16404, 16328..16405, 16476..16658, 16478..16657		
Seq. No.	513	Seq. ID	OJ990503_29.9919.C10
Gene No.	1045	Strand	+
Start	1	End	583
Name	OJ990503_29.9919.C10.o1.np	Method	AAT/NAP
Start	1	End	583
GI	6630460	Score	805
Exons	1..583		
GI Descrip.	(AC007190) F23N19.11 [Arabidopsis thaliana]		
Seq. No.	513	Seq. ID	OJ990503_29.9919.C10
Gene No.	1045	Strand	+
Start	1	End	583
Name	OJ990503_29.9919.C10.o1.gs	Method	GENSCAN

Start	3	End	474
GI	none	Score	.78
Exons	3..474		

Seq. No.	513	Seq. ID	OJ990503_29.9919.C10
Gene No.	1045	Strand	+
Start	1	End	583
Name	OJ990503_29.9919.C10.o1.tc	Method	TBLASTX:Cress
Start	3	End	583
GI	none	Score	91
Exons	3..98, 3..86, 95..205, 96..431, 219..419, 284..433, 356..583, 432..581, 473..583		

Seq. No.	513	Seq. ID	OJ990503_29.9919.C10
Gene No.	1045	Strand	+
Start	1	End	583
Name	OJ990503_29.9919.C10.o1.gp	Method	AAT/GAP
Start	79	End	583
GI	9108_1.R1084	Score	949
Exons	79..583		
GI Descrip.	'402753/emb|CAA50573| 0.0e+00 (X71439) translation elongation factor EF-G [Glycine max]'		

Seq. No.	513	Seq. ID	OJ990503_29.9919.C10
Gene No.	1045	Strand	+
Start	1	End	583
Name	OJ990503_29.9919.C10.o1.ts	Method	TBLASTX:Soybean
Start	80	End	583
GI	none	Score	716
Exons	80..583, 84..581, 488..583		

Seq. No.	513	Seq. ID	OJ990503_29.9919.C10
Gene No.	1045	Strand	+
Start	1	End	583
Name	OJ990503_29.9919.C10.o1.tm	Method	TBLASTX:Maize
Start	141	End	575
GI	none	Score	680
Exons	141..575, 145..435, 147..575		

Seq. No.	513	Seq. ID	OJ990503_29.9919.C10
Gene No.	1045	Strand	+
Start	1	End	583
Name	OJ990503_29.9919.C10.o1.tw	Method	TBLASTX:Wheat
Start	305	End	583
GI	none	Score	254
Exons	305..583, 315..581		

Seq. No.	514	Seq. ID	OJ990503_11.9921.C3
Gene No.	1046	Strand	-
Start	341	End	703
Name	OJ990503_11.9921.C3.o1.gs	Method	GENSCAN
Start	341	End	564
GI	none	Score	.99
Exons	341..427, 514..564		

Seq. No.	514	Seq. ID	OJ990503_11.9921.C3
Gene No.	1046	Strand	-

Start	341	End	703
Name	OJ990503_11.9921.C3.o1.np	Method	AAT/NAP
Start	350	End	703
GI	3297812	Score	191
Exons	350..427, 514..579, 677..703		
GI Descrip.	(AL031032) putative protein [Arabidopsis thaliana]		

Seq. No.	515	Seq. ID	OJ990503_11.9921.C4
Gene No.	1047	Strand	+
Start	1	End	2636
Name	OJ990503_11.9921.C4.o1.np	Method	AAT/NAP
Start	1	End	447
GI	6539553	Score	745
Exons	1..447		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	515	Seq. ID	OJ990503_11.9921.C4
Gene No.	1047	Strand	+
Start	1	End	2636
Name	OJ990503_11.9921.C4.o1.tw	Method	TBLASTX:Wheat
Start	1	End	311
GI	none	Score	409
Exons	1..273, 3..311		

Seq. No.	515	Seq. ID	OJ990503_11.9921.C4
Gene No.	1047	Strand	+
Start	1	End	2636
Name	OJ990503_11.9921.C4.o1.gs	Method	GENSCAN
Start	109	End	2601
GI	none	Score	.52
Exons	109..446, 1329..1385, 1581..1816, 2101..2601		

Seq. No.	515	Seq. ID	OJ990503_11.9921.C4
Gene No.	1047	Strand	+
Start	1	End	2636
Name	OJ990503_11.9921.C4.o2.tw	Method	TBLASTX:Wheat
Start	2004	End	2391
GI	none	Score	349
Exons	2004..2390, 2015..2389, 2128..2391		

Seq. No.	515	Seq. ID	OJ990503_11.9921.C4
Gene No.	1047	Strand	+
Start	1	End	2636
Name	OJ990503_11.9921.C4.o2.np	Method	AAT/NAP
Start	2010	End	2636
GI	6539553	Score	1072
Exons	2010..2636		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	515	Seq. ID	OJ990503_11.9921.C4
Gene No.	1047	Strand	+

Start	1	End	2636
Name	OJ990503_11.9921.C4.o1.tm	Method	TBLASTX:Maize
Start	2139	End	2452
GI	none	Score	361
Exons	2139..2450, 2147..2452		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o1.np	Method	AAT/NAP
Start	1	End	1424
GI	6539553	Score	2495
Exons	1..1424		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o2.ts	Method	TBLASTX:Soybean
Start	161	End	547
GI	none	Score	88
Exons	161..316, 299..547		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o1.gs	Method	GENSCAN
Start	224	End	1415
GI	none	Score	.59
Exons	224..1415		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o1.tm	Method	TBLASTX:Maize
Start	335	End	769
GI	none	Score	299
Exons	335..769, 544..696		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o2.tw	Method	TBLASTX:Wheat
Start	413	End	604
GI	none	Score	275
Exons	413..604, 413..604		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o1.ts	Method	TBLASTX:Soybean
Start	557	End	955
GI	none	Score	193
Exons	557..781, 565..735, 782..955, 790..828		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o1.tc	Method	TBLASTX:Cress
Start	590	End	979
GI	none	Score	108
Exons	590..772, 785..979		

Seq. No.	516	Seq. ID	OJ990503_11.9921.C5
Gene No.	1048	Strand	+
Start	1	End	1424
Name	OJ990503_11.9921.C5.o1.tw	Method	TBLASTX:Wheat
Start	605	End	1360
GI	none	Score	639
Exons	605..1069, 612..1061, 613..1092, 1113..1343, 1121..1360, 1143..1340, 1201..1359		

Seq. No.	517	Seq. ID	OJ990503_11.9921.C6
Gene No.	1049	Strand	+
Start	1	End	842
Name	OJ990503_11.9921.C6.o1.np	Method	AAT/NAP
Start	1	End	842
GI	6539553	Score	1284
Exons	1..842		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	517	Seq. ID	OJ990503_11.9921.C6
Gene No.	1049	Strand	+
Start	1	End	842
Name	OJ990503_11.9921.C6.o1.gs	Method	GENSCAN
Start	124	End	585
GI	none	Score	.77
Exons	124..132, 315..585		

Seq. No.	517	Seq. ID	OJ990503_11.9921.C6
Gene No.	1049	Strand	+
Start	1	End	842
Name	OJ990503_11.9921.C6.o1.ts	Method	TBLASTX:Soybean
Start	140	End	485
GI	none	Score	314
Exons	140..340, 141..485		

Seq. No.	517	Seq. ID	OJ990503_11.9921.C6
Gene No.	1049	Strand	+
Start	1	End	842
Name	OJ990503_11.9921.C6.o1.tm	Method	TBLASTX:Maize
Start	296	End	635
GI	none	Score	318
Exons	296..634, 297..635		

Seq. No.	517	Seq. ID	OJ990503_11.9921.C6
Gene No.	1049	Strand	+
Start	1	End	842

Name	OJ990503_11.9921.C6.o1.tw	Method	TBLASTX:Wheat
Start	491	End	776
GI	none	Score	101
Exons	491..562, 492..566, 493..564, 582..776	581..775, 581..775, 582..776,	

Seq. No.	517	Seq. ID	OJ990503_11.9921.C6
Gene No.	1049	Strand	+
Start	1	End	842
Name	OJ990503_11.9921.C6.o2.ts	Method	TBLASTX:Soybean
Start	498	End	776
GI	none	Score	91
Exons	498..611, 524..604, 630..776,	635..775	

Seq. No.	518	Seq. ID	OJ990503_11.9921.C8
Gene No.	1050	Strand	-
Start	1	End	262
Name	OJ990503_11.9921.C8.o1.np	Method	AAT/NAP
Start	1	End	262
GI	6539588	Score	138
Exons	1..262		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	519	Seq. ID	OJ990503_11.9921.C9
Gene No.	1051	Strand	+
Start	9411	End	13084
Name	OJ990503_11.9921.C9.o3.gs	Method	GENSCAN
Start	9411	End	13084
GI	none	Score	.7
Exons	9411..9485, 11719..11916, 12138..12216, 12318..13084		

Seq. No.	519	Seq. ID	OJ990503_11.9921.C9
Gene No.	1052	Strand	+
Start	12991	End	13242
Name	OJ990503_11.9921.C9.o2.gp	Method	AAT/GAP
Start	12991	End	13242
GI	5004669	Score	478
Exons	12991..13242		

Seq. No.	519	Seq. ID	OJ990503_11.9921.C9
Gene No.	1053	Strand	-
Start	838	End	3133
Name	OJ990503_11.9921.C9.o1.gs	Method	GENSCAN
Start	838	End	3133
GI	none	Score	.88
Exons	838..956, 1319..1430, 2320..2432, 3113..3133		

Seq. No.	519	Seq. ID	OJ990503_11.9921.C9
Gene No.	1054	Strand	-
Start	5524	End	5596
Name	OJ990503_11.9921.C9.o1.gp	Method	AAT/GAP
Start	5524	End	5596
GI	LIB3477-003-P1-K1-E9	Score	100
Exons	5524..5596		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		

Seq. No.	519	Seq. ID	OJ990503_11.9921.C9
Gene No.	1055	Strand	-
Start	14805	End	23240
Name	OJ990503_11.9921.C9.o4.gs	Method	GENSCAN
Start	14805	End	23240
GI	none	Score	.68
Exons	14805..15475, 15545..15649, 15749..16321, 16810..17052, 17187..18369, 18590..18807, 19630..19759, 22313..22351, 22790..23048, 23146..23240		

Seq. No.	519	Seq. ID	OJ990503_11.9921.C9
Gene No.	1055	Strand	-
Start	14805	End	23240
Name	OJ990503_11.9921.C9.o3.gp	Method	AAT/GAP
Start	22452	End	22972
GI	LIB3431-001-P1-N1-B5	Score	766
Exons	22452..22684, 22790..22972		
GI Descrip.	'4680203/gb|AAD27566.1|AF114171_7 1.0e-39 (AF114171) TNP2-like protein [Sorghum bicolor]'		

Seq. No.	520	Seq. ID	OJ990503_11.9921.C10
Gene No.	1056	Strand	-
Start	203	End	332
Name	OJ990503_11.9921.C10.o1.gs	Method	GENSCAN
Start	203	End	332
GI	none	Score	.8
Exons	203..332		

Seq. No.	521	Seq. ID	OJ990503_11.9921.C11
Gene No.	1057	Strand	-
Start	175	End	324
Name	OJ990503_11.9921.C11.o1.gp	Method	AAT/GAP
Start	175	End	324
GI	5002953	Score	231
Exons	175..324		
GI Descrip.	4680203/gb|AAD27566.1|AF114171_7 1.0e-39 (AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	522	Seq. ID	OJ990503_11.9921.C12
Gene No.	1058	Strand	+
Start	896	End	1134
Name	OJ990503_11.9921.C12.o1.gs	Method	GENSCAN
Start	896	End	1134
GI	none	Score	.64
Exons	896..955, 961..1134		

Seq. No.	523	Seq. ID	OJ990503_11.9921.C13
Gene No.	1059	Strand	+
Start	1	End	2984
Name	OJ990503_11.9921.C13.o1.np	Method	AAT/NAP
Start	1	End	2984
GI	3738337	Score	71
Exons	1..20, 680..899, 2931..2984		
GI Descrip.	(AC005170) putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	523	Seq. ID	OJ990503_11.9921.C13
Gene No.	1059	Strand	+
Start	1	End	2984
Name	OJ990503_11.9921.C13.o2.np	Method	AAT/NAP
Start	171	End	1156
GI	6069646	Score	346
Exons	171..1156		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	523	Seq. ID	OJ990503_11.9921.C13
Gene No.	1059	Strand	+
Start	1	End	2984
Name	OJ990503_11.9921.C13.o1.gs	Method	GENSCAN
Start	239	End	1132
GI	none	Score	.52
Exons	239..499, 524..688, 862..886, 912..1132		

Seq. No.	523	Seq. ID	OJ990503_11.9921.C13
Gene No.	1059	Strand	+
Start	1	End	2984
Name	OJ990503_11.9921.C13.o1.tw	Method	TBLASTX:Wheat
Start	344	End	730
GI	none	Score	76
Exons	344..517, 578..730, 590..727		

Seq. No.	523	Seq. ID	OJ990503_11.9921.C13
Gene No.	1059	Strand	+
Start	1	End	2984
Name	OJ990503_11.9921.C13.o1.tm	Method	TBLASTX:Maize
Start	668	End	951
GI	none	Score	301
Exons	668..853, 674..949, 679..951		

Seq. No.	524	Seq. ID	OJ990503_11.9921.C16
Gene No.	1060	Strand	-
Start	126	End	774
Name	OJ990503_11.9921.C16.o1.gs	Method	GENSCAN
Start	126	End	774
GI	none	Score	1
Exons	126..338, 638..774		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1061	Strand	-
Start	8	End	613
Name	OJ990503_11.9921.C17.o1.gs	Method	GENSCAN
Start	8	End	613
GI	none	Score	.44
Exons	8..343, 511..613		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1062	Strand	-
Start	1237	End	9230
Name	OJ990503_11.9921.C17.o2.gs	Method	GENSCAN

Start	1237	End	9230
GI	none	Score	.56
Exons	1237..1580, 3329..3394, 7284..7587, 7732..7810, 7882..8003, 8116..8202, 8296..8644, 8917..9230		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1062	Strand	-
Start	1237	End	9230
Name	OJ990503_11.9921.C17.o1.gp	Method	AAT/GAP
Start	6263	End	6778
GI	78266_1.R1084	Score	705
Exons	6263..6778		
GI Descrip.	'3036795/emb|CAA18485| 7.0e-37 (AL022373) putative protein [Arabidopsis thaliana] >gi_3805857_emb_CAA21477.1_ (AL031986) putative protein [Arabidopsis thaliana]'		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1062	Strand	-
Start	1237	End	9230
Name	OJ990503_11.9921.C17.o1.np	Method	AAT/NAP
Start	7243	End	9212
GI	3036795	Score	660
Exons	7243..7587, 7732..8003, 8116..8202, 8296..8659, 8917..9212		
GI Descrip.	(AL022373) putative protein [Arabidopsis thaliana] gi|3805857|emb|CAA21477.1| (AL031986) putative protein [Arabidopsis thaliana]		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1062	Strand	-
Start	1237	End	9230
Name	OJ990503_11.9921.C17.o2.gp	Method	AAT/GAP
Start	7956	End	8609
GI	3759028	Score	858
Exons	7956..8003, 8116..8202, 8296..8609		
GI Descrip.	3036795/emb|CAA18485| 7.0e-37 (AL022373) putative protein [Arabidopsis thaliana] >gi_3805857_emb_CAA21477.1_ (AL031986) putative protein [Arabidopsis thaliana]		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1063	Strand	-
Start	10813	End	11035
Name	OJ990503_11.9921.C17.o1.tm	Method	TBLASTX:Maize
Start	7237	End	7816
GI	none	Score	399
Exons	7237..7608, 7241..7588, 7340..7615, 7725..7811, 7729..7812, 7732..7812, 7736..7816		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1063	Strand	-
Start	10813	End	11035
Name	OJ990503_11.9921.C17.o1.tw	Method	TBLASTX:Wheat
Start	7292	End	7942
GI	none	Score	392
Exons	7292..7588, 7292..7588, 7294..7608, 7732..7812, 7732..7812, 7736..7816, 7868..7942, 7884..7928		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17

Gene No.	1063	Strand	-
Start	10813	End	11035
Name	OJ990503_11.9921.C17.o1.ts	Method	TBLASTX:Soybean
Start	8117	End	9030
GI	none	Score	95
Exons	8117..8200, 8122..8211, 8290..8568, 8293..8646, 8294..8644, 8911..9030, 8916..9029		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1063	Strand	-
Start	10813	End	11035
Name	OJ990503_11.9921.C17.o2.tm	Method	TBLASTX:Maize
Start	8911	End	9212
GI	none	Score	152
Exons	8911..9108, 8916..9212, 9184..9207		

Seq. No.	525	Seq. ID	OJ990503_11.9921.C17
Gene No.	1063	Strand	-
Start	10813	End	11035
Name	OJ990503_11.9921.C17.o2.np	Method	AAT/NAP
Start	10813	End	11035
GI	3297812	Score	77
Exons	10813..11035		
GI Descrip.	(AL031032) putative protein [Arabidopsis thaliana]		

Seq. No.	526	Seq. ID	OJ990503_11.9921.C18
Gene No.	1064	Strand	-
Start	1	End	908
Name	OJ990503_11.9921.C18.o1.np	Method	AAT/NAP
Start	1	End	908
GI	3297812	Score	46
Exons	1..20, 76..183, 858..908		
GI Descrip.	(AL031032) putative protein [Arabidopsis thaliana]		

Seq. No.	526	Seq. ID	OJ990503_11.9921.C18
Gene No.	1064	Strand	-
Start	1	End	908
Name	OJ990503_11.9921.C18.o1.gs	Method	GENSCAN
Start	76	End	872
GI	none	Score	.84
Exons	76..162, 396..872		

Seq. No.	527	Seq. ID	OJ990503_11.9921.C20
Gene No.	1065	Strand	-
Start	668	End	2650
Name	OJ990503_11.9921.C20.o1.gp	Method	AAT/GAP
Start	668	End	2582
GI	7498_1.R1084	Score	1358
Exons	668..1002, 1491..1549, 1977..2126, 2232..2324, 2470..2582		
GI Descrip.	'2499932/sp|Q43199|APT1_WHEAT 6.0e-80 ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]'		

Seq. No.	527	Seq. ID	OJ990503_11.9921.C20
Gene No.	1065	Strand	-
Start	668	End	2650
Name	OJ990503_11.9921.C20.o1.np	Method	AAT/NAP

Start	943	End	2650
GI	2499932	Score	539
Exons	943..1002, 1491..1549, 1977..2126, 2232..2324, 2470..2650		
GI Descrip.	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) gi|726305 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]		

Seq. No.	527	Seq. ID	OJ990503_11.9921.C20
Gene No.	1065	Strand	-
Start	668	End	2650
Name	OJ990503_11.9921.C20.o1.gs	Method	GENSCAN
Start	949	End	2580
GI	none	Score	.91
Exons	949..1002, 1491..1549, 1977..2126, 2470..2580		

Seq. No.	527	Seq. ID	OJ990503_11.9921.C20
Gene No.	1065	Strand	-
Start	668	End	2650
Name	OJ990503_11.9921.C20.o1.tm	Method	TBLASTX:Maize
Start	952	End	2582
GI	none	Score	65
Exons	952..1008, 952..1005, 1489..1545, 1491..1556, 1491..1553, 1945..2127, 1970..2128, 2230..2331, 2238..2324, 2239..2325, 2270..2326, 2468..2581, 2469..2582		

Seq. No.	527	Seq. ID	OJ990503_11.9921.C20
Gene No.	1065	Strand	-
Start	668	End	2650
Name	OJ990503_11.9921.C20.o1.tc	Method	TBLASTX:Cress
Start	1491	End	2582
GI	none	Score	168
Exons	1491..1553, 1945..2127, 1982..2128, 2230..2331, 2233..2325, 2270..2326, 2468..2581, 2469..2582		

Seq. No.	527	Seq. ID	OJ990503_11.9921.C20
Gene No.	1065	Strand	-
Start	668	End	2650
Name	OJ990503_11.9921.C20.o1.tw	Method	TBLASTX:Wheat
Start	1491	End	2322
GI	none	Score	137
Exons	1491..1553, 1978..2127, 1991..2128, 2230..2322, 2270..2320		

Seq. No.	527	Seq. ID	OJ990503_11.9921.C20
Gene No.	1065	Strand	-
Start	668	End	2650
Name	OJ990503_11.9921.C20.o1.ts	Method	TBLASTX:Soybean
Start	1491	End	2582
GI	none	Score	185
Exons	1491..1553, 1945..2127, 1982..2128, 2230..2331, 2251..2325, 2270..2326, 2468..2581, 2469..2582		

Seq. No.	528	Seq. ID	OJ990503_11.9921.C21
Gene No.	1066	Strand	+
Start	82	End	508
Name	OJ990503_11.9921.C21.o1.gs	Method	GENSCAN
Start	82	End	508
GI	none	Score	.71
Exons	82..129, 212..508		

Seq. No.	528	Seq. ID	OJ990503_11.9921.C21
Gene No.	1067	Strand	-
Start	140	End	239
Name	OJ990503_11.9921.C21.o1.gp	Method	AAT/GAP
Start	140	End	239
GI	7498_1.R1084	Score	139
Exons	140..239		
GI Descrip.	'2499932/sp|Q43199|APT1_WHEAT 6.0e-80 ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]'		

Seq. No.	529	Seq. ID	OJ990503_11.9921.C22
Gene No.	1068	Strand	+
Start	1267	End	2520
Name	OJ990503_11.9921.C22.o1.gs	Method	GENSCAN
Start	1267	End	2520
GI	none	Score	.7
Exons	1267..1344, 2309..2393, 2494..2520		

Seq. No.	529	Seq. ID	OJ990503_11.9921.C22
Gene No.	1069	Strand	+
Start	3133	End	5293
Name	OJ990503_11.9921.C22.o2.gs	Method	GENSCAN
Start	3133	End	5293
GI	none	Score	.74
Exons	3133..3309, 3358..4511, 5227..5293		

Seq. No.	529	Seq. ID	OJ990503_11.9921.C22
Gene No.	1070	Strand	+
Start	6497	End	6888
Name	OJ990503_11.9921.C22.o3.gs	Method	GENSCAN
Start	6497	End	6888
GI	none	Score	.8
Exons	6497..6888		

Seq. No.	530	Seq. ID	OJ990503_11.9921.C23
Gene No.	1071	Strand	+
Start	57	End	1717
Name	OJ990503_11.9921.C23.o1.gs	Method	GENSCAN
Start	57	End	1717
GI	none	Score	.9
Exons	57..476, 1636..1717		

Seq. No.	531	Seq. ID	OJ990503_11.9921.C24
Gene No.	1072	Strand	+
Start	4621	End	4765
Name	OJ990503_11.9921.C24.o2.gs	Method	GENSCAN
Start	4621	End	4765
GI	none	Score	.56
Exons	4621..4765		

Seq. No.	531	Seq. ID	OJ990503_11.9921.C24
Gene No.	1073	Strand	-
Start	34	End	3051
Name	OJ990503_11.9921.C24.o1.gs	Method	GENSCAN
Start	34	End	3051

GI	none	Score	.65
Exons	34..485, 699..1520, 1640..1714, 2811..3051		

Seq. No.	531	Seq. ID	OJ990503_11.9921.C24
Gene No.	1073	Strand	-
Start	34	End	3051
Name	OJ990503_11.9921.C24.o1.tw	Method	TBLASTX:Wheat
Start	220	End	501
GI	none	Score	54
Exons	220..501, 274..426, 281..487		

Seq. No.	531	Seq. ID	OJ990503_11.9921.C24
Gene No.	1073	Strand	-
Start	34	End	3051
Name	OJ990503_11.9921.C24.o1.np	Method	AAT/NAP
Start	277	End	1320
GI	6539555	Score	1234
Exons	277..588, 667..1320		
GI Descrip.	(AP000836) Similar to mariner transposase (AF078934) [Oryza sativa] gi|6539592|dbj|BAA88208.1| (AP000837) Similar to mariner transposase (AF078934) [Oryza sativa]		

Seq. No.	531	Seq. ID	OJ990503_11.9921.C24
Gene No.	1073	Strand	-
Start	34	End	3051
Name	OJ990503_11.9921.C24.o1.tm	Method	TBLASTX:Maize
Start	1027	End	1329
GI	none	Score	194
Exons	1027..1329		

Seq. No.	532	Seq. ID	OJ990503_11.9921.C25
Gene No.	1074	Strand	-
Start	1	End	148
Name	OJ990503_11.9921.C25.o1.np	Method	AAT/NAP
Start	1	End	148
GI	5091497	Score	86
Exons	1..148		
GI Descrip.	(AB023482) Similar to Arabidopsis thaliana mRNA for DREB1B, complete cds.(AB007788) [Oryza sativa]		

Seq. No.	532	Seq. ID	OJ990503_11.9921.C25
Gene No.	1075	Strand	-
Start	107	End	1136
Name	OJ990503_11.9921.C25.o1.gs	Method	GENSCAN
Start	107	End	898
GI	none	Score	.48
Exons	107..157, 597..632, 734..898		

Seq. No.	532	Seq. ID	OJ990503_11.9921.C25
Gene No.	1075	Strand	-
Start	107	End	1136
Name	OJ990503_11.9921.C25.o2.np	Method	AAT/NAP
Start	346	End	1136
GI	5777617	Score	69
Exons	346..444, 1060..1136		
GI Descrip.	(AJ245900) CAA30375.1 protein [Oryza sativa]		

Seq. No.	533	Seq. ID	OJ990503_11.9921.C26
Gene No.	1076	Strand	+
Start	90	End	2687
Name	OJ990503_11.9921.C26.o1.gs	Method	GENSCAN
Start	90	End	2687
GI	none	Score	.46
Exons	90..170, 825..842, 1421..1632, 2222..2439, 2542..2687		

Seq. No.	533	Seq. ID	OJ990503_11.9921.C26
Gene No.	1076	Strand	+
Start	90	End	2687
Name	OJ990503_11.9921.C26.o1.np	Method	AAT/NAP
Start	2138	End	2431
GI	6539588	Score	190
Exons	2138..2431		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	533	Seq. ID	OJ990503_11.9921.C26
Gene No.	1077	Strand	-
Start	4383	End	4451
Name	OJ990503_11.9921.C26.o2.gs	Method	GENSCAN
Start	4383	End	4451
GI	none	Score	.65
Exons	4383..4451		

Seq. No.	534	Seq. ID	OJ990503_11.9921.C27
Gene No.	1078	Strand	-
Start	234	End	513
Name	OJ990503_11.9921.C27.o1.gs	Method	GENSCAN
Start	234	End	513
GI	none	Score	.88
Exons	234..513		

Seq. No.	535	Seq. ID	OJ990503_11.9921.C30
Gene No.	1079	Strand	-
Start	44	End	117
Name	OJ990503_11.9921.C30.o1.gs	Method	GENSCAN
Start	44	End	117
GI	none	Score	.59
Exons	44..117		

Seq. No.	536	Seq. ID	OJ990503_11.9921.C31
Gene No.	1080	Strand	-
Start	147	End	297
Name	OJ990503_11.9921.C31.o1.gs	Method	GENSCAN
Start	147	End	297
GI	none	Score	.92
Exons	147..297		

Seq. No.	537	Seq. ID	OJ990503_11.9921.C32
Gene No.	1081	Strand	+
Start	31	End	3254
Name	OJ990503_11.9921.C32.o1.gs	Method	GENSCAN
Start	31	End	3254
GI	none	Score	.49
Exons	31..159, 460..567, 3078..3254		

Seq. No.	537	Seq. ID	OJ990503_11.9921.C32
Gene No.	1082	Strand	-
Start	4533	End	6274
Name	OJ990503_11.9921.C32.o2.gs	Method	GENSCAN
Start	4533	End	6274
GI	none	Score	.67
Exons	4533..4644, 6210..6274		

Seq. No.	538	Seq. ID	OJ990503_11.9921.C33
Gene No.	1083	Strand	+
Start	1	End	711
Name	OJ990503_11.9921.C33.o1.np	Method	AAT/NAP
Start	1	End	711
GI	4680203	Score	395
Exons	1..711		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	538	Seq. ID	OJ990503_11.9921.C33
Gene No.	1083	Strand	+
Start	1	End	711
Name	OJ990503_11.9921.C33.o1.ts	Method	TBLASTX:Soybean
Start	449	End	711
GI	none	Score	266
Exons	449..472, 474..710, 476..694, 507..710, 529..711		

Seq. No.	538	Seq. ID	OJ990503_11.9921.C33
Gene No.	1083	Strand	+
Start	1	End	711
Name	OJ990503_11.9921.C33.o1.tw	Method	TBLASTX:Wheat
Start	456	End	707
GI	none	Score	238
Exons	456..692, 456..707		

Seq. No.	539	Seq. ID	OJ990503_11.9921.C36
Gene No.	1084	Strand	-
Start	423	End	1508
Name	OJ990503_11.9921.C36.o1.gs	Method	GENSCAN
Start	423	End	1508
GI	none	Score	.47
Exons	423..546, 1410..1508		

Seq. No.	540	Seq. ID	OJ990503_11.9921.C37
Gene No.	1085	Strand	+
Start	1	End	4446
Name	OJ990503_11.9921.C37.o1.np	Method	AAT/NAP
Start	1	End	1012
GI	5852084	Score	68
Exons	1..28, 913..1012		
GI Descrip.	(AL117264) zwh0007.1 [Oryza sativa]		

Seq. No.	540	Seq. ID	OJ990503_11.9921.C37
Gene No.	1085	Strand	+
Start	1	End	4446
Name	OJ990503_11.9921.C37.o1.gs	Method	GENSCAN
Start	176	End	4446
GI	none	Score	.79
Exons	176..340, 2249..2340, 3210..3302, 4293..4446		

Seq. No.	540	Seq. ID	OJ990503_11.9921.C37
Gene No.	1085	Strand	+
Start	1	End	4446
Name	OJ990503_11.9921.C37.o2.np	Method	AAT/NAP
Start	272	End	1697
GI	5852084	Score	82
Exons	272..310, 1614..1697		
GI Descrip.	(AL117264) zwh0007.1 [Oryza sativa]		

Seq. No.	540	Seq. ID	OJ990503_11.9921.C37
Gene No.	1086	Strand	+
Start	4574	End	8124
Name	OJ990503_11.9921.C37.o4.np	Method	AAT/NAP
Start	4574	End	8124
GI	4539658	Score	63
Exons	4574..4592, 6141..6247, 8097..8124		
GI Descrip.	(AF061282) serine carboxypeptidase-like protein [Sorghum bicolor]		

Seq. No.	540	Seq. ID	OJ990503_11.9921.C37
Gene No.	1086	Strand	+
Start	4574	End	8124
Name	OJ990503_11.9921.C37.o3.np	Method	AAT/NAP
Start	4712	End	6388
GI	131136	Score	409
Exons	4712..5129, 6340..6388		
GI Descrip.	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 gi|72671|pir||A1RZP7 photosystem I P700 apoprotein A1 - rice chloroplast gi|11982|emb|CAA33996| (X15901) PSI P700 apoprotein A1 [Oryza sativa] gi|226605|prf||1603356AB photosystem I P700 apoprotein A1 [Oryza sativa]		

Seq. No.	540	Seq. ID	OJ990503_11.9921.C37
Gene No.	1087	Strand	-
Start	4800	End	8058
Name	OJ990503_11.9921.C37.o2.gs	Method	GENSCAN
Start	4800	End	8058
GI	none	Score	.7
Exons	4800..4864, 5352..5485, 7967..8058		

Seq. No.	541	Seq. ID	OJ990503_11.9921.C38
Gene No.	1088	Strand	+
Start	96	End	1203
Name	OJ990503_11.9921.C38.o1.gs	Method	GENSCAN
Start	96	End	1203
GI	none	Score	.64
Exons	96..236, 455..570, 784..812, 1114..1203		

Seq. No.	542	Seq. ID	OJ990503_11.9921.C39
Gene No.	1089	Strand	+
Start	80	End	316
Name	OJ990503_11.9921.C39.o1.gs	Method	GENSCAN
Start	80	End	316
GI	none	Score	.65
Exons	80..316		

Seq. No.	543	Seq. ID	OJ990503_11.9921.C40
Gene No.	1090	Strand	+
Start	123	End	517
Name	OJ990503_11.9921.C40.o1.gs	Method	GENSCAN
Start	123	End	517
GI	none	Score	.82
Exons	123..302, 384..517		

Seq. No.	544	Seq. ID	OJ990503_11.9921.C41
Gene No.	1091	Strand	+
Start	92	End	424
Name	OJ990503_11.9921.C41.o1.gs	Method	GENSCAN
Start	92	End	424
GI	none	Score	.78
Exons	92..424		

Seq. No.	545	Seq. ID	OJ990503_11.9921.C46
Gene No.	1092	Strand	-
Start	254	End	2450
Name	OJ990503_11.9921.C46.o1.gs	Method	GENSCAN
Start	254	End	2450
GI	none	Score	.44
Exons	254..339, 1030..2450		

Seq. No.	546	Seq. ID	OJ990503_11.9921.C50
Gene No.	1093	Strand	-
Start	475	End	590
Name	OJ990503_11.9921.C50.o1.gs	Method	GENSCAN
Start	475	End	590
GI	none	Score	.55
Exons	475..590		

Seq. No.	547	Seq. ID	OJ990503_11.9921.C51
Gene No.	1094	Strand	+
Start	19	End	204
Name	OJ990503_11.9921.C51.o1.gs	Method	GENSCAN
Start	19	End	204
GI	none	Score	.66
Exons	19..204		

Seq. No.	548	Seq. ID	OJ990503_11.9921.C52
Gene No.	1095	Strand	+
Start	1	End	583
Name	OJ990503_11.9921.C52.o1.np	Method	AAT/NAP
Start	1	End	583
GI	100488	Score	386
Exons	1..122, 183..583		
GI Descrip.	TNP2 protein - garden snapdragon		

Seq. No.	548	Seq. ID	OJ990503_11.9921.C52
Gene No.	1095	Strand	+
Start	1	End	583
Name	OJ990503_11.9921.C52.o1.tw	Method	TBLASTX:Wheat
Start	191	End	560
GI	none	Score	65
Exons	191..307, 201..404, 203..403,	440..529,	441..560

Seq. No.	548	Seq. ID	OJ990503_11.9921.C52
Gene No.	1095	Strand	+
Start	1	End	583
Name	OJ990503_11.9921.C52.o1.tm	Method	TBLASTX:Maize
Start	207	End	395
GI	none	Score	162
Exons	207..326, 209..316, 333..395		

Seq. No.	549	Seq. ID	OJ990323_13.9917.C1
Gene No.	1096	Strand	
Start	739	End	1144
Name	OJ990323_13.9917.C1.o2.tm	Method	TBLASTX:Maize
Start	739	End	1144
GI	none	Score	206
Exons	739..939, 741..947, 741..947, 1008..1046, 1068..1130, 1072..1131, 1112..1144		

Seq. No.	549	Seq. ID	OJ990323_13.9917.C1
Gene No.	1097	Strand	
Start	28005	End	37066
Name	OJ990323_13.9917.C1.o1.tc	Method	TBLASTX:Cress
Start	28005	End	37066
GI	none	Score	114
Exons	28005..28205, 28223..28306, 28239..28328, 28247..28330, 28248..28328, 36734..36871, 36869..37066		

Seq. No.	549	Seq. ID	OJ990323_13.9917.C1
Gene No.	1097	Strand	
Start	28005	End	37066
Name	OJ990323_13.9917.C1.o1.ts	Method	TBLASTX:Soybean
Start	28035	End	37030
GI	none	Score	138
Exons	28035..28196, 28251..28334, 36728..36811, 36866..37030		

Seq. No.	549	Seq. ID	OJ990323_13.9917.C1
Gene No.	1097	Strand	
Start	28005	End	37066
Name	OJ990323_13.9917.C1.o1.tm	Method	TBLASTX:Maize
Start	28074	End	36991
GI	none	Score	95
Exons	28074..28196, 28209..28337, 28250..28330, 28406..28510, 28455..28514, 36548..36823, 36552..36824, 36869..36991		

Seq. No.	550	Seq. ID	OJ990423_11.9924.C2
Gene No.	1098	Strand	+
Start	60	End	1358
Name	OJ990423_11.9924.C2.o1.gp	Method	AAT/GAP
Start	60	End	1358
GI	38389_1.R1084	Score	1089
Exons	60..178, 340..393, 924..1358		
GI Descrip.	'4138722/emb|CAA70777| 8.0e-30 (Y09590) hexose transporter [Vitis vinifera]'		

Seq. No.	550	Seq. ID	OJ990423_11.9924.C2
Gene No.	1099	Strand	-
Start	3369	End	4216
Name	OJ990423_11.9924.C2.o2.gs	Method	GENSCAN

Start	3369	End	4216
GI	none	Score	.47
Exons	3369..3391, 4159..4216		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1100	Strand	+
Start	2223	End	6466
Name	OJ990423_11.9924.C3.o1.gs	Method	GENSCAN
Start	2223	End	6466
GI	none	Score	.73
Exons	2223..2432, 2544..2709, 2778..2899, 3724..3772, 4056..4138, 5105..5202, 5627..5714, 5846..5962, 6125..6466		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1100	Strand	+
Start	2223	End	6466
Name	OJ990423_11.9924.C3.o1.np	Method	AAT/NAP
Start	2235	End	6463
GI	4454484	Score	1324
Exons	2235..2432, 2544..2666, 2771..2899, 3110..3195, 3491..3608, 3712..3772, 4056..4138, 4631..4698, 5125..5202, 5627..5714, 5846..5962, 6125..6463		
GI Descrip.	(AC006234) putative diacylglycerol kinase [Arabidopsis thaliana]		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1101	Strand	+
Start	9106	End	9560
Name	OJ990423_11.9924.C3.o1.gp	Method	AAT/GAP
Start	9106	End	9560
GI	2311773	Score	741
Exons	9106..9560		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1102	Strand	+
Start	13520	End	14366
Name	OJ990423_11.9924.C3.o5.gs	Method	GENSCAN
Start	13520	End	14366
GI	none	Score	.62
Exons	13520..13602, 13787..13808, 13913..14018, 14091..14175, 14315..14366		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1103	Strand	-
Start	10423	End	11664
Name	OJ990423_11.9924.C3.o3.gs	Method	GENSCAN
Start	10423	End	11664
GI	none	Score	.65
Exons	10423..10709, 11532..11664		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1104	Strand	-
Start	12420	End	12935
Name	OJ990423_11.9924.C3.o4.gs	Method	GENSCAN
Start	12420	End	12935
GI	none	Score	.71
Exons	12420..12935		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o1.tw	Method	TBLASTX:Wheat
Start	2397	End	2904
GI	none	Score	48
Exons	2397..2444, 2541..2672, 2541..2672, 2770..2898, 2771..2899, 2772..2900, 2773..2904		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o2.tc	Method	TBLASTX:Cress
Start	2541	End	2941
GI	none	Score	86
Exons	2541..2621, 2761..2907, 2761..2901, 2768..2941, 2768..2929		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o2.ts	Method	TBLASTX:Soybean
Start	2582	End	2904
GI	none	Score	58
Exons	2582..2668, 2586..2672, 2770..2898, 2771..2899, 2771..2899, 2773..2904		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o3.tm	Method	TBLASTX:Maize
Start	2770	End	3178
GI	none	Score	234
Exons	2770..2898, 2771..2899, 2772..2900, 2773..2904, 3109..3174, 3110..3178		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o3.ts	Method	TBLASTX:Soybean
Start	3109	End	3596
GI	none	Score	91
Exons	3109..3195, 3110..3193, 3462..3527, 3470..3592, 3471..3596		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o4.tm	Method	TBLASTX:Maize
Start	3470	End	5669
GI	none	Score	207
Exons	3470..3598, 3471..3596, 3472..3600, 3473..3601, 3474..3605, 3722..3778, 3723..3788, 3724..3774, 4054..4137, 4055..4147, 4058..4150, 4627..4707, 4628..4732, 4630..4701, 5097..5189, 5120..5194, 5122..5214, 5123..5188, 5625..5669		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580

Name	OJ990423_11.9924.C3.o1.tc	Method	TBLASTX:Cress
Start	3721	End	6481
GI	none	Score	94
Exons	3721..3774, 3723..3779, 4054..4137, 4055..4150, 4628..4717, 4633..4701, 5523..5600, 5654..5722, 5655..5723, 5831..5962, 5839..5958, 5850..5972, 5854..5973, 6122..6328, 6122..6271, 6124..6300, 6401..6481, 6403..6462		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o1.tm	Method	TBLASTX:Maize
Start	5843	End	6466
GI	none	Score	201
Exons	5843..5965, 5845..5964, 6104..6298, 6114..6299, 6121..6306, 6122..6316, 6380..6460, 6395..6466, 6403..6462		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o1.ts	Method	TBLASTX:Soybean
Start	5879	End	6438
GI	none	Score	139
Exons	5879..5962, 5884..5973, 6122..6316, 6130..6306, 6398..6436, 6406..6438		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o2.tw	Method	TBLASTX:Wheat
Start	6188	End	6475
GI	none	Score	206
Exons	6188..6331, 6188..6289, 6190..6318, 6335..6466, 6380..6475		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o6.gs	Method	GENSCAN
Start	15085	End	19580
GI	none	Score	.96
Exons	15085..15211, 15513..15594, 16477..16657, 16749..16821, 17073..17176, 18021..18076, 18176..18240, 18325..19198, 19313..19580		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o3.tw	Method	TBLASTX:Wheat
Start	15382	End	16778
GI	none	Score	36
Exons	15382..15438, 15412..15534, 15465..15587, 15506..15595, 15509..15538, 16450..16650, 16475..16669, 16475..16681, 16749..16778		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580

Name	OJ990423_11.9924.C3.o3.tc	Method	TBLASTX:Cress
Start	15509	End	16814
GI	none	Score	69
Exons	15509..15595, 16473..16601, 16475..16612, 16524..16658, 16749..16814		

Seq. No.	551	Seq. ID	OJ990423_11.9924.C3
Gene No.	1105	Strand	-
Start	15085	End	19580
Name	OJ990423_11.9924.C3.o2.tm	Method	TBLASTX:Maize
Start	15551	End	17179
GI	none	Score	203
Exons	15551..15595, 16468..16638, 16475..16669, 16475..16681, 16749..16820, 16749..16823, 16757..16837, 17072..17179, 17076..17177, 17083..17178		

Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1106	Strand	+
Start	1011	End	2346
Name	OJ990423_11.9924.C4.o1.gs	Method	GENSCAN
Start	1011	End	2346
GI	none	Score	.49
Exons	1011..1021, 2145..2346		

Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o1.gp	Method	AAT/GAP
Start	2840	End	3467
GI	5771166	Score	1173
Exons	2840..3467		
GI Descrip.	5734438/emb|CAB52688.1| 1.0e-49 (AJ132223) hexose transporter [Lycopersicon esculentum]		

Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o2.gs	Method	GENSCAN
Start	2974	End	4053
GI	none	Score	.97
Exons	2974..4053		

Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o1.np	Method	AAT/NAP
Start	2981	End	4062
GI	4138724	Score	1200
Exons	2981..4062		
GI Descrip.	(AJ001061) hexose transporter [Vitis vinifera]		

Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o1.ts	Method	TBLASTX:Soybean
Start	3028	End	4062
GI	none	Score	272

Exons	3028..3399, 3041..3400, 3403..4062, 3404..3907, 3977..4060		
Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o1.tm	Method	TBLASTX:Maize
Start	3038	End	3735
GI	none	Score	882
Exons	3038..3733, 3040..3735		
Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o1.tc	Method	TBLASTX:Cress
Start	3040	End	4062
GI	none	Score	304
Exons	3040..3399, 3041..3400, 3403..4062, 3404..3907, 3980..4060		
Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o1.tw	Method	TBLASTX:Wheat
Start	3052	End	3378
GI	none	Score	292
Exons	3052..3378, 3053..3370		
Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o2.tw	Method	TBLASTX:Wheat
Start	3430	End	3768
GI	none	Score	131
Exons	3430..3768, 3446..3730		
Seq. No.	552	Seq. ID	OJ990423_11.9924.C4
Gene No.	1107	Strand	-
Start	2974	End	4062
Name	OJ990423_11.9924.C4.o2.tm	Method	TBLASTX:Maize
Start	3739	End	4026
GI	none	Score	99
Exons	3739..3939, 3791..3907, 3946..4026		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1108	Strand	+
Start	58	End	493
Name	OJ990423_11.9924.C5.o1.gs	Method	GENSCAN
Start	58	End	493
GI	none	Score	.72
Exons	58..291, 353..493		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1109	Strand	+
Start	9532	End	14708
Name	OJ990423_11.9924.C5.o3.gs	Method	GENSCAN
Start	9532	End	13837
GI	none	Score	.59
Exons	9532..9596, 9868..10278, 10414..10840, 11653..11860,		

12061..12242, 12657..12815, 13359..13406, 13524..13586, 13745..13837

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1109	Strand	+
Start	9532	End	14708
Name	OJ990423_11.9924.C5.o3.np	Method	AAT/NAP
Start	12144	End	14708
GI	6692261	Score	410
Exons	12144..12242, 12657..12815, 13545..13837, 13936..14079, 14521..14708		
GI Descrip.	(AC010870) putative RNase H [Arabidopsis thaliana]		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1110	Strand	-
Start	1	End	386
Name	OJ990423_11.9924.C5.o1.gp	Method	AAT/GAP
Start	1	End	386
GI	2427703	Score	718
Exons	1..386		
GI Descrip.	4138722/emb|CAA70777| 8.0e-30 (Y09590) hexose transporter [Vitis vinifera]		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1110	Strand	-
Start	1	End	386
Name	OJ990423_11.9924.C5.o1.np	Method	AAT/NAP
Start	1	End	336
GI	100347	Score	385
Exons	1..336		
GI Descrip.	monosaccharide transport protein MST1 - common tobacco gi|19885|emb|CAA47324| (X66856) monosaccharid transporter [Nicotiana tabacum]		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o1.tc	Method	TBLASTX:Cress
Start	1	End	328
GI	none	Score	260
Exons	1..306, 11..328		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o1.ts	Method	TBLASTX:Soybean
Start	1	End	318
GI	none	Score	293
Exons	1..318, 2..316		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o2.tm	Method	TBLASTX:Maize
Start	1	End	331
GI	none	Score	459
Exons	1..318, 2..331		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o1.tm	Method	TBLASTX:Maize
Start	1338	End	2839
GI	none	Score	103
Exons	1338..1538, 1369..1554, 1370..1552, 1595..1753, 1619..1744, 1853..2005, 1854..2006, 1855..2064, 1860..2054, 2301..2468, 2310..2471, 2671..2814, 2673..2837, 2801..2839		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o2.gs	Method	GENSCAN
Start	1375	End	8293
GI	none	Score	.96
Exons	1375..1551, 1628..1744, 1841..2005, 2313..2468, 2673..2900, 3063..3251, 3544..3649, 4005..4138, 4964..5042, 5501..5661, 6522..6629, 7393..7512, 7597..7737, 8246..8293		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o2.np	Method	AAT/NAP
Start	1429	End	4138
GI	3123206	Score	262
Exons	1429..1684, 1864..1927, 2286..2468, 2673..2900, 3063..3212, 3518..3662, 4030..4138		
GI Descrip.	DEEP ORANGE PROTEIN gi|2832850|emb|CAA16809.1| (AL021726) EG:171E4.1 [Drosophila melanogaster]		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o4.ts	Method	TBLASTX:Soybean
Start	1478	End	2002
GI	none	Score	80
Exons	1478..1552, 1480..1554, 1664..1744, 1679..1747, 1853..1912, 1857..1913, 1913..2002		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o2.gp	Method	AAT/GAP
Start	2660	End	3609
GI	LIB3434-005-P1-K1-D3	Score	847
Exons	2660..2900, 3063..3251, 3544..3609		
GI Descrip.	'5734438/emb|CAB52688.1| 1.0e-49 (AJ132223) hexose transporter [Lycopersicon esculentum]'		

Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o3.ts	Method	TBLASTX:Soybean
Start	2706	End	3254
GI	none	Score	128

Exons	2706..2843, 2707..2814, 3057..3254, 3070..3219, 3072..3254		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o4.tm	Method	TBLASTX:Maize
Start	3035	End	5602
GI	none	Score	195
Exons	3035..3256, 3054..3257, 3544..3651, 3545..3649, 3996..4151, 4000..4137, 4004..4138, 4005..4175, 4304..4369, 4304..4369, 4305..4370, 4306..4371, 4959..5036, 4964..5044, 4966..5043, 5497..5595, 5497..5595, 5501..5602		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1111	Strand	-
Start	1375	End	10118
Name	OJ990423_11.9924.C5.o5.tm	Method	TBLASTX:Maize
Start	7907	End	10118
GI	none	Score	156
Exons	7907..8005, 7908..8006, 7908..8006, 8846..8911, 8849..8947, 8850..8957, 8854..8958, 9349..9417, 9351..9419, 9818..9919, 9819..9917, 9820..9924, 10016..10117, 10020..10118, 10020..10118		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1112	Strand	
Start	10278	End	10724
Name	OJ990423_11.9924.C5.o2.ts	Method	TBLASTX:Soybean
Start	10278	End	10724
GI	none	Score	95
Exons	10278..10469, 10375..10470, 10589..10723, 10590..10724		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1113	Strand	
Start	12155	End	14668
Name	OJ990423_11.9924.C5.o3.tm	Method	TBLASTX:Maize
Start	12155	End	14668
GI	none	Score	149
Exons	12155..12244, 12156..12248, 12645..12815, 12656..12814, 12663..12815, 13353..13406, 13517..13582, 13524..13592, 13713..13829, 13741..13830, 13745..13840, 13747..13836, 13932..14081, 13935..14081, 13936..14082, 14518..14592, 14519..14569, 14575..14628, 14579..14668		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1113	Strand	
Start	12155	End	14668
Name	OJ990423_11.9924.C5.o6.ts	Method	TBLASTX:Soybean
Start	12159	End	12824
GI	none	Score	40
Exons	12159..12194, 12180..12257, 12656..12817, 12657..12815, 12657..12824		
Seq. No.	553	Seq. ID	OJ990423_11.9924.C5
Gene No.	1113	Strand	
Start	12155	End	14668
Name	OJ990423_11.9924.C5.o5.ts	Method	TBLASTX:Soybean
Start	13781	End	14628

GI	none	Score	84
Exons	13781..13843, 13783..13845, 13936..14082, 13944..14075, 13952..14086, 13955..14086, 14518..14628		

Seq. No.	554	Seq. ID	OJ990423_11.9924.C6
Gene No.	1114	Strand	+
Start	170	End	13301
Name	OJ990423_11.9924.C6.o1.gs	Method	GENSCAN
Start	170	End	13157
GI	none	Score	.43
Exons	170..320, 1253..1379, 1818..1917, 3222..3275, 3946..4109, 4151..4452, 8344..8488, 10777..10915, 11434..11591, 11772..11862, 12004..12123, 12208..12276, 12404..12480, 12572..12674, 12758..12865, 13086..13157		

Seq. No.	554	Seq. ID	OJ990423_11.9924.C6
Gene No.	1114	Strand	+
Start	170	End	13301
Name	OJ990423_11.9924.C6.o2.np	Method	AAT/NAP
Start	10772	End	13301
GI	5524769	Score	844
Exons	10772..10915, 11434..11591, 11772..11862, 12004..12123, 12208..12276, 12404..12480, 12572..12674, 12758..12865, 12947..13009, 13086..13162, 13201..13301		
GI Descrip.	(AJ243822) Mre11 protein [Arabidopsis thaliana]		

Seq. No.	554	Seq. ID	OJ990423_11.9924.C6
Gene No.	1115	Strand	-
Start	1580	End	4503
Name	OJ990423_11.9924.C6.o1.gp	Method	AAT/GAP
Start	1580	End	4503
GI	17582_1.R1084	Score	1098
Exons	1580..1890, 2300..2352, 2716..2787, 4096..4177, 4300..4338, 4441..4503		
GI Descrip.	'4582434/gb|AAD24820.1|AC007196_6 1.0e-41 (AC007196) unknown protein [Arabidopsis thaliana]'		

Seq. No.	554	Seq. ID	OJ990423_11.9924.C6
Gene No.	1115	Strand	-
Start	1580	End	4503
Name	OJ990423_11.9924.C6.o1.np	Method	AAT/NAP
Start	1804	End	4180
GI	4582434	Score	326
Exons	1804..1890, 2300..2352, 2716..2787, 4096..4180		
GI Descrip.	(AC007196) putative snRNP splicing factor [Arabidopsis thaliana]		

Seq. No.	554	Seq. ID	OJ990423_11.9924.C6
Gene No.	1116	Strand	
Start	10777	End	11598
Name	OJ990423_11.9924.C6.o1.ts	Method	TBLASTX:Soybean
Start	10777	End	11598
GI	none	Score	164
Exons	10777..10917, 10778..10918, 11431..11589, 11433..11588, 11434..11598, 11463..11594		

Seq. No.	554	Seq. ID	OJ990423_11.9924.C6
Gene No.	1117	Strand	

Start	12205	End	12793
Name	OJ990423_11.9924.C6.o1.tc	Method	TBLASTX:Cress
Start	12205	End	12793
GI	none	Score	97
Exons	12205..12276, 12395..12445, 12446..12481, 12569..12676, 12570..12674, 12755..12793		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1118	Strand	+
Start	1	End	3541
Name	OJ990423_11.9924.C7.o1.np	Method	AAT/NAP
Start	1	End	1208
GI	5524769	Score	219
Exons	1..62, 324..387, 465..527, 635..695, 852..934, 1104..1208		
GI Descrip.	(AJ243822) Mre11 protein [Arabidopsis thaliana]		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1118	Strand	+
Start	1	End	3541
Name	OJ990423_11.9924.C7.o1.gs	Method	GENSCAN
Start	635	End	3541
GI	none	Score	.66
Exons	635..695, 852..934, 1104..1370, 1464..1625, 1744..1896, 2294..2481, 2544..3085, 3525..3541		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1119	Strand	+
Start	9507	End	13179
Name	OJ990423_11.9924.C7.o3.gs	Method	GENSCAN
Start	9507	End	13179
GI	none	Score	.56
Exons	9507..9557, 11829..11856, 12008..12175, 13151..13179		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1120	Strand	+
Start	15874	End	21456
Name	OJ990423_11.9924.C7.o4.gs	Method	GENSCAN
Start	15874	End	21456
GI	none	Score	.84
Exons	15874..15962, 16037..16091, 16180..16277, 16364..17804, 17872..17991, 18129..18389, 18602..18775, 18894..18921, 19496..19612, 19719..20189, 21365..21456		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1120	Strand	+
Start	15874	End	21456
Name	OJ990423_11.9924.C7.o2.gp	Method	AAT/GAP
Start	17876	End	18357
GI	none	Score	646
Exons	17876..17991, 18129..18357		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1120	Strand	+
Start	15874	End	21456
Name	OJ990423_11.9924.C7.o3.gp	Method	AAT/GAP
Start	18614	End	19909
GI	uC-osflcyp172f01b1	Score	904

Exons	18614..18775, 18894..18974, 19552..19612, 19719..19909		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 2.0e-27 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1121	Strand	-
Start	2300	End	2635
Name	OJ990423_11.9924.C7.o1.gp	Method	AAT/GAP
Start	2300	End	2635
GI	uC-osflcyp029d06b1	Score	586
Exons	2300..2635		
GI Descrip.	'5524769/emb|CAB50793.1| 3.0e-11 (AJ243822) Mre11 protein [Arabidopsis thaliana]'		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1122	Strand	
Start	17912	End	18306
Name	OJ990423_11.9924.C7.o1.tm	Method	TBLASTX:Maize
Start	17912	End	18306
GI	none	Score	119
Exons	17912..17992, 17913..17999, 17914..17991, 18120..18305, 18126..18272, 18127..18306, 18128..18304		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1123	Strand	
Start	18617	End	18920
Name	OJ990423_11.9924.C7.o2.tm	Method	TBLASTX:Maize
Start	18617	End	18920
GI	none	Score	191
Exons	18617..18775, 18618..18746, 18631..18774, 18632..18775, 18894..18920		

Seq. No.	555	Seq. ID	OJ990423_11.9924.C7
Gene No.	1124	Strand	
Start	18897	End	20179
Name	OJ990423_11.9924.C7.o1.ts	Method	TBLASTX:Soybean
Start	18897	End	20179
GI	none	Score	66
Exons	18897..19001, 19860..19901, 19895..19954, 19964..20179, 19966..20178		

Seq. No.	556	Seq. ID	OJ990423_11.9924.C8
Gene No.	1125	Strand	+
Start	458	End	1082
Name	OJ990423_11.9924.C8.o1.gs	Method	GENSCAN
Start	458	End	1082
GI	none	Score	.75
Exons	458..688, 844..1082		

Seq. No.	557	Seq. ID	OJ990423_11.9924.C9
Gene No.	1126	Strand	+
Start	478	End	598
Name	OJ990423_11.9924.C9.o1.gs	Method	GENSCAN
Start	478	End	598
GI	none	Score	.7
Exons	478..598		

Seq. No.	557	Seq. ID	OJ990423_11.9924.C9
Gene No.	1127	Strand	-
Start	536	End	2494
Name	OJ990423_11.9924.C9.o1.np	Method	AAT/NAP
Start	536	End	2494
GI	1272345	Score	361
Exons	536..1649, 2468..2494		
GI Descrip.	(U51738) secreted glycoprotein 1 [Ipomoea trifida]		

Seq. No.	557	Seq. ID	OJ990423_11.9924.C9
Gene No.	1127	Strand	-
Start	536	End	2494
Name	OJ990423_11.9924.C9.o1.tm	Method	TBLASTX:Maize
Start	612	End	820
GI	none	Score	48
Exons	612..689, 620..661, 668..820, 678..794, 683..811		

Seq. No.	557	Seq. ID	OJ990423_11.9924.C9
Gene No.	1127	Strand	-
Start	536	End	2494
Name	OJ990423_11.9924.C9.o2.tm	Method	TBLASTX:Maize
Start	1234	End	1612
GI	none	Score	91
Exons	1234..1299, 1319..1465, 1323..1466, 1436..1552, 1544..1612, 1563..1604		

Seq. No.	557	Seq. ID	OJ990423_11.9924.C9
Gene No.	1127	Strand	-
Start	536	End	2494
Name	OJ990423_11.9924.C9.o2.gs	Method	GENSCAN
Start	1262	End	2403
GI	none	Score	.65
Exons	1262..1667, 2176..2403		

Seq. No.	558	Seq. ID	OJ990423_11.9924.C10
Gene No.	1128	Strand	+
Start	73	End	786
Name	OJ990423_11.9924.C10.o1.gs	Method	GENSCAN
Start	73	End	786
GI	none	Score	.57
Exons	73..236, 570..786		

Seq. No.	558	Seq. ID	OJ990423_11.9924.C10
Gene No.	1129	Strand	-
Start	2676	End	2823
Name	OJ990423_11.9924.C10.o2.gs	Method	GENSCAN
Start	2676	End	2823
GI	none	Score	.72
Exons	2676..2823		

Seq. No.	559	Seq. ID	OJ990423_11.9924.C11
Gene No.	1130	Strand	-
Start	39	End	815
Name	OJ990423_11.9924.C11.o1.gs	Method	GENSCAN
Start	39	End	712
GI	none	Score	.44
Exons	39..215, 638..712		

Seq. No.	559	Seq. ID	OJ990423_11.9924.C11
Gene No.	1130	Strand	-
Start	39	End	815
Name	OJ990423_11.9924.C11.o1.np	Method	AAT/NAP
Start	275	End	815
GI	2829861	Score	79
Exons	275..346, 638..815		
GI Descrip.	(AC002396) Unknown protein [Arabidopsis thaliana]		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1131	Strand	+
Start	1	End	13102
Name	OJ990423_11.9924.C12.o1.np	Method	AAT/NAP
Start	1	End	1420
GI	4680207	Score	338
Exons	1..1263, 1333..1420		
GI Descrip.	(AF114171) disease resistance protein RPM1 homolog [Sorghum bicolor]		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1131	Strand	+
Start	1	End	13102
Name	OJ990423_11.9924.C12.o1.gs	Method	GENSCAN
Start	81	End	4237
GI	none	Score	.86
Exons	81..1454, 4124..4237		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1131	Strand	+
Start	1	End	13102
Name	OJ990423_11.9924.C12.o2.np	Method	AAT/NAP
Start	797	End	10822
GI	4680207	Score	777
Exons	797..826, 5029..5751, 6464..8379, 10787..10822		
GI Descrip.	(AF114171) disease resistance protein RPM1 homolog [Sorghum bicolor]		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1131	Strand	+
Start	1	End	13102
Name	OJ990423_11.9924.C12.o1.gp	Method	AAT/GAP
Start	4990	End	5257
GI	uC-osroM202017g02b1	Score	450
Exons	4990..5257		
GI Descrip.	'4680207/gb|AAD27570.1|AF114171_11 3.0e-16 (AF114171) disease resistance protein RPM1 homolog [Sorghum bicolor]'		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1131	Strand	+
Start	1	End	13102
Name	OJ990423_11.9924.C12.o2.gs	Method	GENSCAN
Start	5231	End	13102
GI	none	Score	.76
Exons	5231..5751, 6380..8438, 9260..9354, 9971..10052, 10256..10629, 11054..11118, 11171..11685, 11746..11839, 11934..12246, 12342..12537, 12761..13102		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1131	Strand	+
Start	1	End	13102
Name	OJ990423_11.9924.C12.o3.np	Method	AAT/NAP
Start	10277	End	12970
GI	4063770	Score	1662
Exons	10277..10962, 11054..11118, 11153..12264, 12357..12970		
GI Descrip.	(AB004906) transposase [Ipomoea purpurea]		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1132	Strand	+
Start	14226	End	14566
Name	OJ990423_11.9924.C12.o3.gp	Method	AAT/GAP
Start	14226	End	14566
GI	5058_1.R1084	Score	643
Exons	14226..14566		
GI Descrip.	'3202044 3.0e-10 (AF069492) SONA [Emericella nidulans]'		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1133	Strand	-
Start	8928	End	9205
Name	OJ990423_11.9924.C12.o2.gp	Method	AAT/GAP
Start	8928	End	9205
GI	none	Score	556
Exons	8928..9205		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o2.ts	Method	TBLASTX:Soybean
Start	396	End	7595
GI	none	Score	65
Exons	396..455, 6420..6509, 6618..6713, 6629..6673, 6717..6950, 6788..6928, 7017..7091, 7215..7247, 7434..7595		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o2.tc	Method	TBLASTX:Cress
Start	6378	End	7094
GI	none	Score	50
Exons	6378..6434, 6549..6749, 6638..6748, 6788..6913, 6789..6914, 7020..7094		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o1.tw	Method	TBLASTX:Wheat
Start	6615	End	6913
GI	none	Score	83
Exons	6615..6716, 6725..6913, 6783..6911		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o3.tm	Method	TBLASTX:Maize

Start	6714	End	6956
GI	none	Score	271
Exons	6714..6956, 6719..6955		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o4.tm	Method	TBLASTX:Maize
Start	11497	End	11896
GI	none	Score	214
Exons	11497..11805, 11527..11652, 11813..11896		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o2.tm	Method	TBLASTX:Maize
Start	12845	End	13306
GI	none	Score	170
Exons	12845..13126, 12848..13126, 12878..13195, 12902..13306, 12926..13306, 12950..13180		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o3.tc	Method	TBLASTX:Cress
Start	12845	End	13312
GI	none	Score	64
Exons	12845..13036, 12848..13045, 12848..12952, 12890..13267, 12899..13072, 12918..13070, 12995..13207, 13008..13193, 13010..13312, 13082..13303, 13097..13303		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o3.ts	Method	TBLASTX:Soybean
Start	12848	End	13312
GI	none	Score	68
Exons	12848..13063, 12857..13060, 12878..12973, 12879..12971, 12885..13052, 12917..13189, 12921..13166, 12965..13165, 12989..13273, 13079..13270, 13080..13268, 13124..13309, 13223..13312		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o4.np	Method	AAT/NAP
Start	12849	End	15089
GI	4455360	Score	235
Exons	12849..13306, 15062..15089		
GI Descrip.	(AL035524) putative protein [Arabidopsis thaliana]		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o3.gs	Method	GENSCAN
Start	14231	End	19224
GI	none	Score	.77

Exons	14231..14329, 14840..14920, 15600..15671, 16144..16221, 17164..17292, 17912..18053, 18520..18713, 18876..18926, 18956..19042, 19174..19224		
Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o5.np	Method	AAT/NAP
Start	14706	End	19224
GI	6503279	Score	1214
Exons	14706..14750, 14840..14920, 15600..15671, 16144..16221, 17164..17292, 17710..17790, 17912..18053, 18520..18713, 18810..18875, 18956..19042, 19174..19224		
GI Descrip.	(AC011713) F23A5.2(form2) [Arabidopsis thaliana]		
Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o4.ts	Method	TBLASTX:Soybean
Start	14712	End	17968
GI	none	Score	37
Exons	14712..14783, 14728..14760, 14840..14920, 14865..14921, 14866..14931, 15597..15674, 15598..15660, 16136..16213, 16142..16213, 16143..16214, 16144..16221, 17161..17298, 17162..17299, 17707..17787, 17708..17794, 17909..17968, 17909..17968		
Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o5.tm	Method	TBLASTX:Maize
Start	14837	End	17963
GI	none	Score	97
Exons	14837..14929, 14840..14920, 15597..15674, 15598..15672, 15602..15676, 16139..16222, 16142..16216, 16144..16221, 17147..17293, 17161..17298, 17162..17293, 17166..17294, 17707..17790, 17708..17794, 17708..17797, 17709..17798, 17912..17962, 17913..17963		
Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o4.gp	Method	AAT/GAP
Start	16194	End	17787
GI	1036964	Score	349
Exons	16194..16221, 17164..17293, 17712..17787		
GI Descrip.	3202044 3.0e-10 (AF069492) SONA [Emericella nidulans]		
Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o1.ts	Method	TBLASTX:Soybean
Start	17969	End	19031
GI	none	Score	92
Exons	17969..18055, 17970..18053, 18519..18719, 18525..18698, 18526..18714, 18807..18857, 18858..18878, 18953..19030, 18954..19031		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o1.tm	Method	TBLASTX:Maize
Start	18516	End	19213
GI	none	Score	238
Exons	18516..18587, 18559..18714, 18561..18713, 18644..18715, 18807..18878, 18808..18876, 18951..19040, 18953..19045, 18953..19045, 18955..19053, 19171..19212, 19175..19213		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o1.tc	Method	TBLASTX:Cress
Start	18564	End	19045
GI	none	Score	101
Exons	18564..18671, 18598..18669, 18666..18713, 18667..18714, 18807..18848, 18808..18840, 18858..18878, 18951..19043, 18953..19045		

Seq. No.	560	Seq. ID	OJ990423_11.9924.C12
Gene No.	1134	Strand	-
Start	12849	End	19729
Name	OJ990423_11.9924.C12.o5.gp	Method	AAT/GAP
Start	18583	End	19729
GI	uC-osflm202104d01b1	Score	899
Exons	18583..18713, 18810..18875, 18956..19042, 19174..19240, 19556..19729		
GI Descrip.	'3122671/sp|Q38942|RA1L_ARATH 1.0e-43 HYPOTHETICAL RAE1-LIKE PROTEIN >gi_2129676_pir__S71241 probable export protein - Arabidopsis thaliana >gi_1297188 (U53501) Theoretical protein with similarity to Swiss-Prot Accession Number P41838 poly A+ RNA export protein [Arabidopsis thaliana]'		

Seq. No.	561	Seq. ID	OJ990423_11.9924.C13
Gene No.	1135	Strand	-
Start	1440	End	2123
Name	OJ990423_11.9924.C13.o1.gp	Method	AAT/GAP
Start	1440	End	2123
GI	59410_1.R1084	Score	609
Exons	1440..1806, 2094..2123		
GI Descrip.	'2499945/sp|Q42586|PYR5_ARATH 3.0e-51 URIDINE 5''-MONOPHOSPHATE SYNTHASE (UMP SYNTHASE) [INCLUDES: OROTATE PHOSPHORIBOSYLTRANSFERASE (OPRTASE); OROTIDINE 5''-PHOSPHATE DECARBOXYLASE (OMPDECASE)] >gi_1076363_pir__S46440 orotate phosphoribosyltransferase (EC 2.4.2.10) / orotidine-5''-phosphate decarboxylase (EC 4.1.1.23) - Arabidopsis thaliana >gi_443818_emb_CAA50686_ (X71842) pyrE-F [Ara'		

Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1136	Strand	+
Start	1029	End	1483
Name	OJ990423_11.9924.C14.o1.gp	Method	AAT/GAP
Start	1029	End	1483
GI	uC-osroM202011d02a1	Score	850

Exons	1029..1483		
GI Descrip.	'1076421/pir||S46523 3.0e-15 transcription factor TGA3 - Arabidopsis thaliana >gi_304113 (L10209) transcription factor [Arabidopsis thaliana]'		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1137	Strand	-
Start	1317	End	3391
Name	OJ990423_11.9924.C14.o1.gs	Method	GENSCAN
Start	1317	End	3168
GI	none	Score	.87
Exons	1317..1451, 1560..2137, 2219..2276, 2375..2452, 2552..2611, 2739..2834, 2956..3168		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1137	Strand	-
Start	1317	End	3391
Name	OJ990423_11.9924.C14.o1.np	Method	AAT/NAP
Start	1320	End	2927
GI	1076422	Score	701
Exons	1320..1469, 1560..1634, 1713..2201, 2375..2452, 2552..2613, 2690..2927		
GI Descrip.	transcription factor OBF4 - Arabidopsis thaliana gi|414613|emb|CAA49524| (X69899) ocs-element binding factor 4 [Arabidopsis thaliana]		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1137	Strand	-
Start	1317	End	3391
Name	OJ990423_11.9924.C14.o2.gp	Method	AAT/GAP
Start	2793	End	3391
GI	none	Score	882
Exons	2793..2852, 2956..3391		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1138	Strand	-
Start	7352	End	7866
Name	OJ990423_11.9924.C14.o1.tc	Method	TBLASTX:Cress
Start	1326	End	2605
GI	none	Score	63
Exons	1326..1472, 1327..1470, 1568..1636, 1698..2138, 1747..1971, 2080..2139, 2393..2455, 2576..2605		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1138	Strand	-
Start	7352	End	7866
Name	OJ990423_11.9924.C14.o1.ts	Method	TBLASTX:Soybean
Start	1326	End	2141
GI	none	Score	92
Exons	1326..1472, 1327..1500, 1595..1621, 1728..2141, 2080..2139		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1138	Strand	-
Start	7352	End	7866
Name	OJ990423_11.9924.C14.o1.tm	Method	TBLASTX:Maize
Start	1326	End	2605
GI	none	Score	100

Exons	1326..1472, 1327..1470, 1728..2141, 1747..1971, 2080..2139, 2393..2455, 2576..2605		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1138	Strand	-
Start	7352	End	7866
Name	OJ990423_11.9924.C14.o1.tw	Method	TBLASTX:Wheat
Start	1887	End	2452
GI	none	Score	53
Exons	1887..2141, 1891..1980, 2080..2139, 2393..2452		
Seq. No.	562	Seq. ID	OJ990423_11.9924.C14
Gene No.	1138	Strand	-
Start	7352	End	7866
Name	OJ990423_11.9924.C14.o2.gs	Method	GENSCAN
Start	7352	End	7866
GI	none	Score	.47
Exons	7352..7428, 7821..7866		
Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1139	Strand	+
Start	6709	End	7148
Name	OJ990423_11.9924.C15.o2.gs	Method	GENSCAN
Start	6709	End	7148
GI	none	Score	.59
Exons	6709..6789, 6990..7148		
Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1140	Strand	-
Start	1771	End	2438
Name	OJ990423_11.9924.C15.o1.gs	Method	GENSCAN
Start	1771	End	2438
GI	none	Score	.95
Exons	1771..1785, 2343..2438		
Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1141	Strand	-
Start	7848	End	8036
Name	OJ990423_11.9924.C15.o3.gs	Method	GENSCAN
Start	7848	End	8036
GI	none	Score	.68
Exons	7848..8036		
Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1142	Strand	-
Start	9880	End	10172
Name	OJ990423_11.9924.C15.o1.gp	Method	AAT/GAP
Start	9880	End	10172
GI	LIB3477-003-P1-K1-E9	Score	118
Exons	9880..9923, 10121..10172		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		
Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1143	Strand	-
Start	10410	End	11244

Name	OJ990423_11.9924.C15.o2.gp	Method	AAT/GAP
Start	10410	End	11244
GI	none	Score	760
Exons	10410..10722, 11153..11244		

Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1144	Strand	-
Start	11883	End	12319
Name	OJ990423_11.9924.C15.o3.tm	Method	TBLASTX:Maize
Start	11209	End	11593
GI	none	Score	59
Exons	11209..11259, 11210..11272, 11211..11270, 11314..11346, 11315..11506, 11348..11506, 11358..11507, 11471..11593, 11508..11591		

Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1144	Strand	-
Start	11883	End	12319
Name	OJ990423_11.9924.C15.o1.tm	Method	TBLASTX:Maize
Start	11594	End	12020
GI	none	Score	104
Exons	11594..11683, 11595..11687, 11595..11687, 11669..11983, 11673..11819, 11683..11961, 11750..11983, 11972..12019, 11973..12020		

Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1144	Strand	-
Start	11883	End	12319
Name	OJ990423_11.9924.C15.o3.gp	Method	AAT/GAP
Start	11883	End	12319
GI	2309698	Score	720
Exons	11883..12319		

Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1145	Strand	
Start	13808	End	14041
Name	OJ990423_11.9924.C15.o4.tm	Method	TBLASTX:Maize
Start	13808	End	14041
GI	none	Score	201
Exons	13808..14041, 13808..14017, 13810..14037		

Seq. No.	563	Seq. ID	OJ990423_11.9924.C15
Gene No.	1146	Strand	
Start	14110	End	15312
Name	OJ990423_11.9924.C15.o2.tm	Method	TBLASTX:Maize
Start	14110	End	15312
GI	none	Score	62
Exons	14110..14193, 14147..14215, 14292..14456, 14292..14450, 14312..14455, 14317..14460, 14468..14485, 14613..14687, 14613..14681, 15183..15305, 15185..15304, 15187..15312		

Seq. No.	564	Seq. ID	OJ990423_11.9924.C16
Gene No.	1147	Strand	+
Start	51	End	762
Name	OJ990423_11.9924.C16.o1.gs	Method	GENSCAN
Start	51	End	762
GI	none	Score	.63

Exons	51..187, 709..762		
Seq. No.	565	Seq. ID	OJ990423_11.9924.C21
Gene No.	1148	Strand	+
Start	243	End	310
Name	OJ990423_11.9924.C21.o1.gp	Method	AAT/GAP
Start	243	End	310
GI	LIB3434-005-P1-K1-D3	Score	78
Exons	243..310		
GI Descrip.	'5734438/emb|CAB52688.1| 1.0e-49 (AJ132223) hexose transporter [Lycopersicon esculentum]'		
Seq. No.	566	Seq. ID	OJ990423_11.9924.C25
Gene No.	1149	Strand	-
Start	234	End	375
Name	OJ990423_11.9924.C25.o1.gs	Method	GENSCAN
Start	234	End	375
GI	none	Score	.69
Exons	234..375		
Seq. No.	567	Seq. ID	OJ990423_11.9924.C28
Gene No.	1150	Strand	+
Start	150	End	236
Name	OJ990423_11.9924.C28.o1.gs	Method	GENSCAN
Start	150	End	236
GI	none	Score	.65
Exons	150..236		
Seq. No.	567	Seq. ID	OJ990423_11.9924.C28
Gene No.	1151	Strand	-
Start	1	End	257
Name	OJ990423_11.9924.C28.o1.gp	Method	AAT/GAP
Start	1	End	257
GI	none	Score	507
Exons	1..257		
Seq. No.	568	Seq. ID	OJ990423_11.9924.C29
Gene No.	1152	Strand	+
Start	1013	End	2337
Name	OJ990423_11.9924.C29.o1.gs	Method	GENSCAN
Start	1013	End	2337
GI	none	Score	.55
Exons	1013..1067, 1156..1295, 1627..1699, 2025..2123, 2303..2337		
Seq. No.	568	Seq. ID	OJ990423_11.9924.C29
Gene No.	1153	Strand	+
Start	3391	End	6613
Name	OJ990423_11.9924.C29.o1.np	Method	AAT/NAP
Start	3391	End	6613
GI	6630682	Score	347
Exons	3391..3444, 6405..6613		
GI Descrip.	(AP000969) EST D22716(C1010) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815074|dbj|BAA90361.1| (AP001080) EST D22716(C1010) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	568	Seq. ID	OJ990423_11.9924.C29
Gene No.	1154	Strand	-
Start	4130	End	10014
Name	OJ990423_11.9924.C29.o2.gs	Method	GENSCAN
Start	4130	End	10014
GI	none	Score	.77
Exons	4130..5186, 5885..6218, 6371..6507, 7806..7978, 8266..8315, 10008..10014		

Seq. No.	569	Seq. ID	OJ990423_11.9924.C30
Gene No.	1155	Strand	+
Start	245	End	1035
Name	OJ990423_11.9924.C30.o1.gs	Method	GENSCAN
Start	245	End	1035
GI	none	Score	.77
Exons	245..298, 880..1035		

Seq. No.	570	Seq. ID	OJ990423_11.9924.C33
Gene No.	1156	Strand	+
Start	1	End	732
Name	OJ990423_11.9924.C33.o1.np	Method	AAT/NAP
Start	1	End	631
GI	5919155	Score	82
Exons	1..141, 551..631		
GI Descrip.	(AF182293) U6 snRNA-associated Sm-like protein LSm7 [Homo sapiens]		

Seq. No.	570	Seq. ID	OJ990423_11.9924.C33
Gene No.	1156	Strand	+
Start	1	End	732
Name	OJ990423_11.9924.C33.o1.gp	Method	AAT/GAP
Start	87	End	732
GI	17582_1.R1084	Score	398
Exons	87..141, 551..732		
GI Descrip.	'4582434/gb|AAD24820.1|AC007196_6 1.0e-41 (AC007196) unknown protein [Arabidopsis thaliana]'		

Seq. No.	570	Seq. ID	OJ990423_11.9924.C33
Gene No.	1156	Strand	+
Start	1	End	732
Name	OJ990423_11.9924.C33.o1.gs	Method	GENSCAN
Start	89	End	637
GI	none	Score	.88
Exons	89..141, 551..637		

Seq. No.	571	Seq. ID	OJ990423_11.9924.C34
Gene No.	1157	Strand	+
Start	328	End	1331
Name	OJ990423_11.9924.C34.o1.gs	Method	GENSCAN
Start	328	End	1331
GI	none	Score	.81
Exons	328..627, 806..1073, 1188..1331		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1158	Strand	+
Start	1008	End	2379
Name	OJ990723_11.9924.C1.o1.np	Method	AAT/NAP

Start	1008	End	2376
GI	4115384	Score	1558
Exons	1008..1157, 1200..2376		
GI Descrip.	(AC005967) unknown protein [Arabidopsis thaliana]		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1158	Strand	+
Start	1008	End	2379
Name	OJ990723_11.9924.C1.o1.gs	Method	GENSCAN
Start	1014	End	2379
GI	none	Score	.91
Exons	1014..1705, 1716..2379		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1159	Strand	+
Start	18962	End	20479
Name	OJ990723_11.9924.C1.o4.gs	Method	GENSCAN
Start	18962	End	20479
GI	none	Score	.62
Exons	18962..18980, 19544..19874, 20437..20479		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1160	Strand	-
Start	4232	End	10714
Name	OJ990723_11.9924.C1.o2.gs	Method	GENSCAN
Start	4232	End	10714
GI	none	Score	.45
Exons	4232..4356, 5694..5868, 5943..6094, 6284..6409, 7221..7343, 7689..7854, 10670..10714		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-
Start	16560	End	20272
Name	OJ990723_11.9924.C1.o1.ts	Method	TBLASTX:Soybean
Start	1032	End	1850
GI	none	Score	145
Exons	1032..1142, 1034..1141, 1197..1343, 1203..1751, 1388..1639, 1572..1718, 1734..1850, 1738..1848		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-
Start	16560	End	20272
Name	OJ990723_11.9924.C1.o3.ts	Method	TBLASTX:Soybean
Start	1866	End	2184
GI	none	Score	267
Exons	1866..2093, 1867..2094, 2086..2151, 2106..2150, 2149..2184		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-
Start	16560	End	20272
Name	OJ990723_11.9924.C1.o2.tm	Method	TBLASTX:Maize
Start	2224	End	2358
GI	none	Score	226
Exons	2224..2358, 2224..2352, 2226..2357		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-

Start	16560	End	20272
Name	OJ990723_11.9924.C1.o3.gs	Method	GENSCAN
Start	16560	End	18424
GI	none	Score	.64
Exons	16560..16771, 17307..17667, 17983..18124, 18211..18265, 18376..18424		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-
Start	16560	End	20272
Name	OJ990723_11.9924.C1.o1.tm	Method	TBLASTX:Maize
Start	17275	End	18442
GI	none	Score	49
Exons	17275..17316, 17323..17376, 17343..17378, 17404..17673, 17408..17668, 17439..17681, 17980..18126, 17982..18143, 17984..18127, 18193..18297, 18210..18296, 18374..18442, 18375..18440		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-
Start	16560	End	20272
Name	OJ990723_11.9924.C1.o2.np	Method	AAT/NAP
Start	17359	End	20272
GI	6587803	Score	589
Exons	17359..17667, 17983..18124, 18211..18294, 18376..18433, 19412..19661, 20225..20272		
GI Descrip.	(AC010924) Contains similarity to gi|112785 DNA-3-methyladenine glycosidase I from Escherichia coli. [Arabidopsis thaliana]		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-
Start	16560	End	20272
Name	OJ990723_11.9924.C1.o2.ts	Method	TBLASTX:Soybean
Start	17395	End	18440
GI	none	Score	167
Exons	17395..17673, 17444..17668, 18198..18296, 18374..18424, 18375..18431, 18375..18440		

Seq. No.	572	Seq. ID	OJ990723_11.9924.C1
Gene No.	1161	Strand	-
Start	16560	End	20272
Name	OJ990723_11.9924.C1.o1.tc	Method	TBLASTX:Cress
Start	17425	End	17664
GI	none	Score	127
Exons	17425..17664, 17434..17646, 17444..17662		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1162	Strand	+
Start	4769	End	7904
Name	OJ990723_11.9924.C2.o2.gs	Method	GENSCAN
Start	4769	End	7455
GI	none	Score	.92
Exons	4769..4839, 5106..5304, 6540..6579, 6931..7291, 7371..7455		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1162	Strand	+
Start	4769	End	7904

Name	OJ990723_11.9924.C2.o2.np	Method	AAT/NAP
Start	6918	End	7452
GI	3122703	Score	588
Exons	6918..7291, 7371..7452		
GI Descrip.	60S RIBOSOMAL PROTEIN L23A gi|2641201 (AF031542) ribosomal protein L23a [Fritillaria agrestis]		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1162	Strand	+
Start	4769	End	7904
Name	OJ990723_11.9924.C2.o1.gp	Method	AAT/GAP
Start	6943	End	7904
GI	480_1.R1084	Score	1573
Exons	6943..7291, 7371..7904		
GI Descrip.	'5670155/gb|AF161269.1|AF161269 4.0e-86 Oryza sativa subsp. japonica BAC clone 34K24, complete sequence'		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1163	Strand	+
Start	13384	End	14104
Name	OJ990723_11.9924.C2.o4.gs	Method	GENSCAN
Start	13384	End	14104
GI	none	Score	.68
Exons	13384..13527, 13615..13834, 13944..14104		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1164	Strand	-
Start	172	End	3898
Name	OJ990723_11.9924.C2.o1.gs	Method	GENSCAN
Start	172	End	3898
GI	none	Score	.71
Exons	172..346, 440..636, 1995..2330, 2413..2541, 3187..3298, 3335..3756, 3881..3898		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1164	Strand	-
Start	172	End	3898
Name	OJ990723_11.9924.C2.o1.np	Method	AAT/NAP
Start	409	End	3722
GI	6503302	Score	1155
Exons	409..636, 1831..1878, 1995..2330, 2413..2541, 3187..3722		
GI Descrip.	(AC011713) Is a member of PF|01544 CorA-like Mg2+ transporter protein family. ESTs gb|Z48392 and gb|Z48391 come from this gene. [Arabidopsis thaliana]		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1165	Strand	-
Start	8317	End	12092
Name	OJ990723_11.9924.C2.o3.gs	Method	GENSCAN
Start	8317	End	11987
GI	none	Score	.6
Exons	8317..8474, 9124..9337, 9629..9683, 10259..10311, 10400..10476, 10814..10931, 11016..11133, 11390..11405, 11804..11873, 11976..11987		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1165	Strand	-

Start	8317	End	12092
Name	OJ990723_11.9924.C2.o3.np	Method	AAT/NAP
Start	9100	End	12092
GI	4584525	Score	338
Exons	9100..9282, 9629..9683, 10259..10311, 10400..10476, 10562..10697, 10809..10956, 10998..11133, 11300..11405, 11804..11873, 11976..12092		
GI Descrip.	(AL049607) protein phosphatase 2C-like protein [Arabidopsis thaliana]		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o2.tc	Method	TBLASTX:Cress
Start	406	End	2144
GI	none	Score	190
Exons	406..636, 407..637, 1817..1879, 1831..1878, 1989..2069, 1996..2031, 2019..2078, 2073..2144		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o2.tm	Method	TBLASTX:Maize
Start	406	End	2060
GI	none	Score	178
Exons	406..636, 406..636, 407..637, 407..640, 486..641, 1817..1879, 1831..1878, 1989..2060, 1997..2059		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o4.ts	Method	TBLASTX:Soybean
Start	517	End	648
GI	none	Score	84
Exons	517..645, 518..643, 523..648		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o2.ts	Method	TBLASTX:Soybean
Start	1996	End	2469
GI	none	Score	40
Exons	1996..2031, 1998..2144, 2018..2197, 2019..2183, 2223..2333, 2223..2333, 2402..2467, 2410..2469		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o4.tm	Method	TBLASTX:Maize
Start	2076	End	2490
GI	none	Score	41
Exons	2076..2144, 2099..2122, 2223..2333, 2247..2330, 2402..2488, 2410..2490, 2416..2490		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618

Name	OJ990723_11.9924.C2.o3.tc	Method	TBLASTX:Cress
Start	2262	End	3249
GI	none	Score	61
Exons	2262..2324, 2262..2333, 2402..2500, 2410..2535, 2410..2544, 3196..3249		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o3.tm	Method	TBLASTX:Maize
Start	3277	End	3616
GI	none	Score	54
Exons	3277..3318, 3277..3330, 3313..3450, 3340..3423, 3395..3616, 3511..3615		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o4.tc	Method	TBLASTX:Cress
Start	3340	End	3615
GI	none	Score	64
Exons	3340..3450, 3535..3615, 3551..3607		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o1.tc	Method	TBLASTX:Cress
Start	6928	End	7458
GI	none	Score	67
Exons	6928..6996, 6941..7015, 7004..7297, 7005..7292, 7368..7457, 7369..7458		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o1.tm	Method	TBLASTX:Maize
Start	6928	End	7465
GI	none	Score	125
Exons	6928..6996, 6929..7021, 7007..7297, 7008..7292, 7357..7458, 7368..7460, 7369..7458, 7370..7465		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o1.tw	Method	TBLASTX:Wheat
Start	6928	End	7228
GI	none	Score	333
Exons	6928..7200, 6932..7228, 6993..7199		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o1.ts	Method	TBLASTX:Soybean
Start	6998	End	7460
GI	none	Score	355
Exons	6998..7297, 6999..7292, 7357..7455, 7368..7460, 7369..7455		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o2.tw	Method	TBLASTX:Wheat
Start	7229	End	7625
GI	none	Score	100
Exons	7229..7297, 7230..7292, 7368..7457, 7369..7461, 7370..7456, 7459..7494, 7459..7491, 7492..7524, 7493..7528, 7494..7526, 7549..7596, 7549..7596, 7557..7625		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o3.ts	Method	TBLASTX:Soybean
Start	10246	End	10902
GI	none	Score	51
Exons	10246..10308, 10391..10477, 10575..10721, 10624..10707, 10807..10896, 10809..10889, 10809..10901, 10813..10902		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o5.tm	Method	TBLASTX:Maize
Start	10246	End	12080
GI	none	Score	54
Exons	10246..10308, 10391..10477, 10575..10721, 10627..10707, 10807..10896, 10809..10898, 10809..10901, 10813..10902, 11335..11406, 11796..11855, 11804..11839, 11950..12045, 11964..12080		

Seq. No.	573	Seq. ID	OJ990723_11.9924.C2
Gene No.	1166	Strand	-
Start	15436	End	15618
Name	OJ990723_11.9924.C2.o5.gs	Method	GENSCAN
Start	15436	End	15618
GI	none	Score	.78
Exons	15436..15618		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1167	Strand	+
Start	427	End	1643
Name	OJ990723_11.9924.C3.o1.gp	Method	AAT/GAP
Start	427	End	1643
GI	1118_1.R1084	Score	2415
Exons	427..1643		
GI Descrip.	'2239089/emb|CAB06430| 2.0e-46 (Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]'		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o1.gs	Method	GENSCAN
Start	35	End	1634
GI	none	Score	.89
Exons	35..190, 619..643, 865..1634		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o1.ts	Method	TBLASTX:Soybean
Start	846	End	1778
GI	none	Score	50
Exons	846..1196, 883..954, 891..1103, 986..1123, 1006..1197, 1212..1490, 1225..1368, 1530..1778, 1545..1766, 1624..1770		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o1.tm	Method	TBLASTX:Maize
Start	858	End	1563
GI	none	Score	213
Exons	858..1358, 873..1103, 1003..1362, 1356..1541, 1360..1488, 1531..1563		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o1.tc	Method	TBLASTX:Cress
Start	859	End	1175
GI	none	Score	71
Exons	859..960, 861..1175, 864..1166		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o1.np	Method	AAT/NAP
Start	864	End	1775
GI	6469032	Score	790
Exons	864..1775		
GI Descrip.	(AB035183) N-hydroxycinnamoyl/benzoyltransferase [Ipomoea batatas]		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o3.tc	Method	TBLASTX:Cress
Start	1212	End	1502
GI	none	Score	73
Exons	1212..1283, 1225..1281, 1281..1502, 1306..1407		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o2.tc	Method	TBLASTX:Cress
Start	1545	End	1778
GI	none	Score	143
Exons	1545..1778, 1624..1764		

Seq. No.	574	Seq. ID	OJ990723_11.9924.C3
Gene No.	1168	Strand	-
Start	35	End	1778
Name	OJ990723_11.9924.C3.o2.tm	Method	TBLASTX:Maize

Start	1564	End	1778
GI	none	Score	234
Exons	1564..1764, 1566..1778, 1617..1769		

Seq. No.	575	Seq. ID	OJ990723_11.9924.C4
Gene No.	1169	Strand	+
Start	393	End	443
Name	OJ990723_11.9924.C4.o1.gs	Method	GENSCAN
Start	393	End	443
GI	none	Score	.64
Exons	393..443		

Seq. No.	576	Seq. ID	OJ990723_11.9924.C5
Gene No.	1170	Strand	+
Start	25	End	198
Name	OJ990723_11.9924.C5.o1.gs	Method	GENSCAN
Start	25	End	198
GI	none	Score	.83
Exons	25..198		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1171	Strand	+
Start	9641	End	17109
Name	OJ990723_11.9924.C6.o2.gs	Method	GENSCAN
Start	9641	End	17109
GI	none	Score	.73
Exons	9641..9654, 10412..10626, 10727..10802, 10882..10945, 11606..11740, 11829..11960, 12270..12353, 12438..12536, 12792..12883, 13080..13152, 13276..13428, 13988..14071, 14231..14305, 14385..14528, 14816..14923, 15140..15259, 15709..16099, 16922..17109		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1171	Strand	+
Start	9641	End	17109
Name	OJ990723_11.9924.C6.o3.gp	Method	AAT/GAP
Start	14850	End	15872
GI	none	Score	642
Exons	14850..14923, 14998..15060, 15140..15214, 15709..15872		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1172	Strand	+
Start	18861	End	20740
Name	OJ990723_11.9924.C6.o4.gp	Method	AAT/GAP
Start	18725	End	19017
GI	569219	Score	460
Exons	18725..19017		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1172	Strand	+
Start	18861	End	20740
Name	OJ990723_11.9924.C6.o3.np	Method	AAT/NAP
Start	18859	End	20716
GI	2980767	Score	483
Exons	18859..19008, 19042..19107, 20397..20716		
GI Descrip.	(AL022198) putative protein [Arabidopsis thaliana]		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1172	Strand	+
Start	18861	End	20740
Name	OJ990723_11.9924.C6.o3.gs	Method	GENSCAN
Start	18861	End	20740
GI	none	Score	.62
Exons	18861..18926, 19011..19104, 19142..19204, 20397..20740		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1173	Strand	+
Start	27298	End	38164
Name	OJ990723_11.9924.C6.o7.gs	Method	GENSCAN
Start	27298	End	38164
GI	none	Score	.69
Exons	27298..27633, 28398..28484, 28660..28753, 29684..30228, 30838..31038, 31143..31325, 31775..31884, 32117..32176, 32420..32711, 33696..33796, 34075..34949, 35646..36605, 36825..37034, 37655..37725, 37976..38164		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1173	Strand	+
Start	27298	End	38164
Name	OJ990723_11.9924.C6.o5.gp	Method	AAT/GAP
Start	29680	End	30056
GI	none	Score	526
Exons	29680..30056		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1173	Strand	+
Start	27298	End	38164
Name	OJ990723_11.9924.C6.o6.gp	Method	AAT/GAP
Start	37034	End	37207
GI	6025123	Score	296
Exons	37034..37207		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1174	Strand	+
Start	57867	End	59891
Name	OJ990723_11.9924.C6.o9.np	Method	AAT/NAP
Start	57867	End	59891
GI	6063554	Score	331
Exons	57867..58222, 58327..58532, 59054..59081, 59717..59891		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1175	Strand	-
Start	1311	End	7659
Name	OJ990723_11.9924.C6.o1.gp	Method	AAT/GAP
Start	951	End	1407
GI	3767832	Score	852
Exons	951..1407		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1175	Strand	-
Start	1311	End	7659

Name	OJ990723_11.9924.C6.o1.gs	Method	GENSCAN
Start	1311	End	7659
GI	none	Score	.92
Exons	1311..1815, 2500..2534, 2605..2673, 2793..2844, 3244..3326, 3425..3526, 3950..4684, 4762..4812, 5592..5783, 5866..6016, 6812..6993, 7129..7332, 7633..7659		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1175	Strand	-
Start	1311	End	7659
Name	OJ990723_11.9924.C6.o2.np	Method	AAT/NAP
Start	1326	End	7653
GI	4584527	Score	541
Exons	1326..1898, 2605..2673, 2793..2844, 3244..3311, 3950..4821, 5479..5783, 5888..6016, 6812..6993, 7129..7344, 7564..7653		
GI Descrip.	(AL049607) putative protein [Arabidopsis thaliana]		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1175	Strand	-
Start	1311	End	7659
Name	OJ990723_11.9924.C6.o2.gp	Method	AAT/GAP
Start	2586	End	4429
GI	none	Score	1383
Exons	2586..2673, 2793..2844, 3244..3326, 3425..3526, 3950..4429		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1176	Strand	-
Start	21826	End	23659
Name	OJ990723_11.9924.C6.o4.gs	Method	GENSCAN
Start	21826	End	23659
GI	none	Score	.84
Exons	21826..22400, 22458..22539, 22668..22706, 23211..23306, 23396..23659		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1176	Strand	-
Start	21826	End	23659
Name	OJ990723_11.9924.C6.o4.np	Method	AAT/NAP
Start	21829	End	22526
GI	6728965	Score	62
Exons	21829..21929, 22170..22355, 22458..22526		
GI Descrip.	(AC018363) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1177	Strand	-
Start	24546	End	24839
Name	OJ990723_11.9924.C6.o5.gs	Method	GENSCAN
Start	24546	End	24839
GI	none	Score	.87
Exons	24546..24839		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1178	Strand	-
Start	26331	End	26966
Name	OJ990723_11.9924.C6.o6.gs	Method	GENSCAN
Start	26331	End	26966
GI	none	Score	.61

Exons 26331..26966

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1179	Strand	-
Start	39105	End	51368
Name	OJ990723_11.9924.C6.o8.gs	Method	GENSCAN
Start	39105	End	49394
GI	none	Score	.47

Exons 39105..39198, 39390..39479, 39547..39729, 40542..40582, 40860..41013, 41566..41598, 41764..41932, 41946..42018, 42451..42535, 42720..43017, 43479..43681, 44880..45736, 46220..46267, 46284..46455, 46573..46694, 47177..47294, 47487..48174, 48434..48933, 48949..49394

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1179	Strand	-
Start	39105	End	51368
Name	OJ990723_11.9924.C6.o6.np	Method	AAT/NAP
Start	39108	End	40594
GI	133866	Score	622

Exons 39108..39198, 39390..39479, 39568..39712, 40354..40454, 40542..40594

GI Descrip. 40S RIBOSOMAL PROTEIN S11-ALPHA gi|81659|pir||C35542 ribosomal protein S11 - Arabidopsis thaliana gi|454808 (L28828) ribosomal protein S11 [Arabidopsis thaliana] gi|6522573|emb|CAB62017.1| (AL132967) cytosolic ribosomal protein S11 [Arabidopsis thaliana]

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1179	Strand	-
Start	39105	End	51368
Name	OJ990723_11.9924.C6.o7.gp	Method	AAT/GAP
Start	39402	End	41101
GI	30446_1.R1084	Score	786

Exons 39402..39479, 39568..39712, 40354..40454, 40542..40582, 40977..41101

GI Descrip. '5708091/emb|CAA18213.2| 8.0e-22 (AL022198) ribosomal protein S11-like [Arabidopsis thaliana]'

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1179	Strand	-
Start	39105	End	51368
Name	OJ990723_11.9924.C6.o7.np	Method	AAT/NAP
Start	47486	End	51368
GI	6539553	Score	6436

Exons 47486..51368

GI Descrip. (AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1180	Strand	-
Start	52618	End	55174
Name	OJ990723_11.9924.C6.o8.np	Method	AAT/NAP
Start	52618	End	55174
GI	6815109	Score	166

Exons	52618..52645, 55011..55174		
GI Descrip.	(AP001081) hypothetical protein [Oryza sativa]		
Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1181	Strand	-
Start	57938	End	58673
Name	OJ990723_11.9924.C6.o10.gs	Method	GENSCAN
Start	57938	End	58673
GI	none	Score	1
Exons	57938..58432, 58452..58673		
Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o12.tm	Method	TBLASTX:Maize
Start	1253	End	1960
GI	none	Score	56
Exons	1253..1360, 1254..1361, 1355..1453, 1382..1447, 1407..1619, 1470..1664, 1481..1546, 1559..1600, 1615..1692, 1654..1713, 1712..1795, 1719..1799, 1720..1800, 1895..1951, 1898..1960		
Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o17.tm	Method	TBLASTX:Maize
Start	4088	End	4444
GI	none	Score	119
Exons	4088..4222, 4089..4223, 4175..4360, 4225..4326, 4346..4444, 4350..4442		
Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o15.tm	Method	TBLASTX:Maize
Start	4445	End	6009
GI	none	Score	49
Exons	4445..4543, 4557..4691, 4580..4693, 4758..4814, 4762..4812, 5580..5717, 5589..5783, 5590..5805, 5905..6009, 5924..6004		
Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o5.tc	Method	TBLASTX:Cress
Start	5914	End	7321
GI	none	Score	59
Exons	5914..6024, 6799..6918, 6814..7017, 6893..7009, 7127..7321, 7129..7317		
Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o12.ts	Method	TBLASTX:Soybean
Start	7127	End	7344
GI	none	Score	119
Exons	7127..7327, 7129..7344		
Seq. No.	577	Seq. ID	OJ990723_11.9924.C6

Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o14.tm	Method	TBLASTX:Maize
Start	7150	End	7662
GI	none	Score	193
Exons	7150..7338, 7151..7342, 7555..7662		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o6.tc	Method	TBLASTX:Cress
Start	10569	End	11912
GI	none	Score	88
Exons	10569..10628, 10570..10626, 11600..11740, 11604..11741, 11605..11736, 11823..11912, 11825..11908		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o13.ts	Method	TBLASTX:Soybean
Start	13073	End	13422
GI	none	Score	117
Exons	13073..13153, 13081..13152, 13272..13421, 13276..13422		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o3.tm	Method	TBLASTX:Maize
Start	13265	End	16128
GI	none	Score	37
Exons	13265..13300, 13276..13302, 13305..13430, 13305..13430, 13306..13437, 13514..13639, 13517..13636, 13521..13697, 13725..13778, 13726..13779, 13960..14070, 13985..14071, 13986..14069, 13988..14071, 14225..14341, 14230..14316, 14357..14437, 14384..14437, 14385..14441, 14440..14529, 14441..14530, 14442..14531, 14601..14729, 14601..14729, 14602..14733, 14603..14734, 14603..14734, 14807..14944, 14821..14937, 14986..15066, 14993..15103, 14995..15063, 14997..15122, 15138..15212, 15138..15212, 15139..15252, 15708..15782, 15708..15908, 15709..15903, 15993..16100, 15993..16103, 15994..16125, 15994..16128		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o6.ts	Method	TBLASTX:Soybean
Start	13987	End	15024
GI	none	Score	125
Exons	13987..14067, 13988..14071, 14225..14329, 14227..14307, 14460..14531, 14465..14530, 14597..14728, 14598..14729, 14602..14730, 14603..14719, 14807..14926, 14821..14925, 14995..15024		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o11.ts	Method	TBLASTX:Soybean

Start	18909	End	20710
GI	none	Score	94
Exons	18909..18977, 19065..19106, 20402..20581, 20415..20588, 20530..20706, 20660..20710		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o13.tm	Method	TBLASTX:Maize
Start	20423	End	20832
GI	none	Score	260
Exons	20423..20581, 20425..20709, 20427..20720, 20427..20708, 20530..20715, 20615..20719, 20749..20832, 20761..20814		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o2.tc	Method	TBLASTX:Cress
Start	29737	End	30129
GI	none	Score	71
Exons	29737..29799, 29800..30129, 29892..30128		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o4.tm	Method	TBLASTX:Maize
Start	31277	End	33881
GI	none	Score	91
Exons	31277..31327, 31278..31328, 31773..31883, 31775..31885, 32114..32182, 32115..32177, 32116..32184, 32391..32699, 32411..32713, 32411..32713, 33604..33846, 33606..33851, 33606..33845, 33607..33846, 33847..33879, 33849..33881		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o5.ts	Method	TBLASTX:Soybean
Start	31775	End	32684
GI	none	Score	84
Exons	31775..31861, 32115..32177, 32376..32672, 32391..32684, 32399..32677		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o10.ts	Method	TBLASTX:Soybean
Start	33664	End	33888
GI	none	Score	245
Exons	33664..33888, 33664..33768, 33666..33887		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o16.tm	Method	TBLASTX:Maize
Start	34220	End	34353
GI	none	Score	218
Exons	34220..34351, 34220..34351, 34222..34353, 34222..34353		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o2.ts	Method	TBLASTX:Soybean
Start	34352	End	34666
GI	none	Score	120
Exons	34352..34564, 34354..34665, 34354..34665, 34355..34666		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o1.tm	Method	TBLASTX:Maize
Start	34354	End	34951
GI	none	Score	940
Exons	34354..34950, 34355..34951		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o1.ts	Method	TBLASTX:Soybean
Start	34813	End	36202
GI	none	Score	136
Exons	34813..34869, 34858..34950, 35651..35779, 35683..35778, 35860..35934, 35864..36202, 35977..35997, 36034..36159		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o2.tm	Method	TBLASTX:Maize
Start	35766	End	36478
GI	none	Score	68
Exons	35766..35822, 35768..35821, 35855..36019, 35855..35935, 36023..36412, 36025..36420, 36443..36478, 36443..36478		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o3.tc	Method	TBLASTX:Cress
Start	36200	End	36612
GI	none	Score	228
Exons	36200..36403, 36208..36372, 36209..36373, 36452..36607, 36452..36607, 36472..36612		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o9.ts	Method	TBLASTX:Soybean
Start	36271	End	37045
GI	none	Score	122
Exons	36271..36372, 36272..36376, 36418..36621, 36452..36607, 36823..37041, 36824..37045		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o9.tm	Method	TBLASTX:Maize

Start	36478	End	37118
GI	none	Score	219
Exons	36478..36621, 36479..36607, 36814..37041, 36821..37072, 36824..37060, 36825..37070, 37098..37118		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o5.tw	Method	TBLASTX:Wheat
Start	36868	End	37212
GI	none	Score	291
Exons	36868..37041, 36869..37060, 36869..37060, 37089..37130, 37099..37131, 37136..37174, 37138..37212		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o6.tm	Method	TBLASTX:Maize
Start	39073	End	40586
GI	none	Score	41
Exons	39073..39135, 39105..39140, 39126..39200, 39145..39201, 39388..39480, 39389..39481, 39390..39482, 39390..39482, 39564..39710, 39567..39713, 39568..39726, 39568..39714, 40353..40406, 40353..40439, 40354..40437, 40544..40585, 40545..40586		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o3.ts	Method	TBLASTX:Soybean
Start	39126	End	40586
GI	none	Score	94
Exons	39126..39200, 39127..39201, 39388..39480, 39389..39481, 39390..39482, 39564..39713, 39567..39713, 39568..39726, 40350..40448, 40352..40450, 40544..40585, 40545..40586		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o1.tc	Method	TBLASTX:Cress
Start	39138	End	40585
GI	none	Score	84
Exons	39138..39200, 39148..39201, 39385..39474, 39389..39481, 39390..39479, 39564..39713, 39567..39713, 39574..39729, 39575..39718, 40353..40403, 40355..40411, 40359..40433, 40544..40585		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o1.tw	Method	TBLASTX:Wheat
Start	47609	End	48074
GI	none	Score	323
Exons	47609..47983, 47622..47984, 47631..47984, 47779..47985, 47999..48073, 48003..48074		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6

Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o14.ts	Method	TBLASTX:Soybean
Start	47711	End	48079
GI	none	Score	104
Exons	47711..47935, 47954..48079		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o11.tm	Method	TBLASTX:Maize
Start	47930	End	48270
GI	none	Score	164
Exons	47930..48160, 47931..48149, 48057..48179, 48150..48269, 48157..48270		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o7.ts	Method	TBLASTX:Soybean
Start	48080	End	48426
GI	none	Score	119
Exons	48080..48130, 48147..48425, 48226..48426		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o3.tw	Method	TBLASTX:Wheat
Start	48279	End	48809
GI	none	Score	45
Exons	48279..48485, 48309..48458, 48480..48809, 48535..48669, 48784..48807		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o8.tm	Method	TBLASTX:Maize
Start	48360	End	48818
GI	none	Score	138
Exons	48360..48818, 48463..48810		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o4.ts	Method	TBLASTX:Soybean
Start	48495	End	48959
GI	5509260	Score	52
Exons	48495..48959, 48514..48573, 48640..48864		
GI Descrip.	-		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o4.tc	Method	TBLASTX:Cress
Start	48606	End	48866
GI	none	Score	100
Exons	48606..48866, 48694..48864		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o2.tw	Method	TBLASTX:Wheat
Start	48879	End	49633
GI	none	Score	204
Exons	48879..49127, 48879..49067, 48896..49126, 49132..49356, 49185..49421, 49343..49633, 49354..49497, 49356..49625, 49543..49626		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o10.tm	Method	TBLASTX:Maize
Start	49284	End	49777
GI	none	Score	68
Exons	49284..49358, 49346..49450, 49469..49777, 49493..49648, 49503..49694		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o8.ts	Method	TBLASTX:Soybean
Start	49284	End	49681
GI	none	Score	38
Exons	49284..49358, 49340..49456, 49410..49448, 49457..49681, 49472..49666, 49503..49673		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o6.tw	Method	TBLASTX:Wheat
Start	49634	End	49825
GI	none	Score	175
Exons	49634..49825, 49634..49825		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o5.tm	Method	TBLASTX:Maize
Start	50105	End	50427
GI	none	Score	392
Exons	50105..50272, 50106..50411, 50107..50406, 50173..50427		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o7.tm	Method	TBLASTX:Maize
Start	50926	End	51239
GI	none	Score	296
Exons	50926..51231, 50928..51239		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o4.tw	Method	TBLASTX:Wheat

Start	50988	End	51374
GI	none	Score	242
Exons	50988..51374, 50989..51363		

Seq. No.	577	Seq. ID	OJ990723_11.9924.C6
Gene No.	1182	Strand	-
Start	60259	End	60515
Name	OJ990723_11.9924.C6.o9.gp	Method	AAT/GAP
Start	60259	End	60515
GI	61605_3.R1084	Score	434
Exons	60259..60515		
GI Descrip.	'1402920/emb|CAA66965| 2.0e-20 (X98321) peroxidase [Arabidopsis thaliana]'		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1183	Strand	+
Start	1	End	6006
Name	OJ990723_11.9924.C7.o1.gp	Method	AAT/GAP
Start	1	End	423
GI	700148	Score	754
Exons	1..423		
GI Descrip.	6091732/gb|AAF03444.1|AC010797_20 3.0e-14 (AC010797) unknown protein [Arabidopsis thaliana]		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1183	Strand	+
Start	1	End	6006
Name	OJ990723_11.9924.C7.o1.np	Method	AAT/NAP
Start	1	End	4596
GI	6730730	Score	1359
Exons	1..247, 2829..3739, 4116..4596		
GI Descrip.	(AC018849) nodulin-like protein [Arabidopsis thaliana]		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1183	Strand	+
Start	1	End	6006
Name	OJ990723_11.9924.C7.o2.gs	Method	GENSCAN
Start	2898	End	6006
GI	none	Score	.71
Exons	2898..3711, 4364..4507, 4685..4847, 5453..5498, 5870..6006		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1183	Strand	+
Start	1	End	6006
Name	OJ990723_11.9924.C7.o2.gp	Method	AAT/GAP
Start	4509	End	4983
GI	none	Score	804
Exons	4509..4983		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1184	Strand	-
Start	14	End	3176
Name	OJ990723_11.9924.C7.o2.tc	Method	TBLASTX:Cress
Start	1	End	3008
GI	none	Score	239
Exons	1..90, 2..232, 136..225, 2819..2923, 2829..3008, 2835..3005		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1184	Strand	-
Start	14	End	3176
Name	OJ990723_11.9924.C7.o1.gs	Method	GENSCAN
Start	14	End	687
GI	none	Score	.6
Exons	14..402, 666..687		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1184	Strand	-
Start	14	End	3176
Name	OJ990723_11.9924.C7.o3.ts	Method	TBLASTX:Soybean
Start	20	End	211
GI	none	Score	216
Exons	20..211, 29..211		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1184	Strand	-
Start	14	End	3176
Name	OJ990723_11.9924.C7.o3.tm	Method	TBLASTX:Maize
Start	2856	End	3119
GI	none	Score	287
Exons	2856..3119, 2856..3119		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1184	Strand	-
Start	14	End	3176
Name	OJ990723_11.9924.C7.o4.ts	Method	TBLASTX:Soybean
Start	2922	End	3176
GI	none	Score	154
Exons	2922..3107, 2928..3089, 2975..3091, 3105..3176, 3128..3172		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1185	Strand	
Start	3429	End	4602
Name	OJ990723_11.9924.C7.o2.tm	Method	TBLASTX:Maize
Start	3429	End	4241
GI	none	Score	503
Exons	3429..3743, 3431..3742, 3688..3744, 4103..4240, 4113..4241, 4114..4239		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1185	Strand	
Start	3429	End	4602
Name	OJ990723_11.9924.C7.o3.tc	Method	TBLASTX:Cress
Start	3464	End	3746
GI	none	Score	228
Exons	3464..3745, 3492..3746		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1185	Strand	
Start	3429	End	4602
Name	OJ990723_11.9924.C7.o2.ts	Method	TBLASTX:Soybean
Start	3501	End	4215
GI	none	Score	317
Exons	3501..3743, 3506..3739, 4114..4215		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1185	Strand	
Start	3429	End	4602
Name	OJ990723_11.9924.C7.o1.tc	Method	TBLASTX:Cress
Start	4110	End	4572
GI	none	Score	144
Exons	4110..4256, 4114..4257, 4266..4388, 4267..4392, 4431..4568, 4432..4572		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1185	Strand	
Start	3429	End	4602
Name	OJ990723_11.9924.C7.o1.ts	Method	TBLASTX:Soybean
Start	4230	End	4584
GI	none	Score	221
Exons	4230..4433, 4231..4407, 4435..4584, 4440..4577		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1185	Strand	
Start	3429	End	4602
Name	OJ990723_11.9924.C7.o1.tm	Method	TBLASTX:Maize
Start	4242	End	4594
GI	none	Score	183
Exons	4242..4457, 4242..4589, 4243..4590, 4243..4590, 4286..4594		

Seq. No.	578	Seq. ID	OJ990723_11.9924.C7
Gene No.	1185	Strand	
Start	3429	End	4602
Name	OJ990723_11.9924.C7.o1.tw	Method	TBLASTX:Wheat
Start	4342	End	4602
GI	none	Score	418
Exons	4342..4602, 4344..4601, 4375..4602		

Seq. No.	579	Seq. ID	OJ990723_11.9924.C8
Gene No.	1186	Strand	+
Start	1503	End	1815
Name	OJ990723_11.9924.C8.o1.gs	Method	GENSCAN
Start	1503	End	1815
GI	none	Score	.97
Exons	1503..1815		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o3.tm	Method	TBLASTX:Maize
Start	237	End	481
GI	none	Score	41
Exons	237..299, 269..481, 360..449		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o1.gs	Method	GENSCAN
Start	242	End	1315
GI	none	Score	.82
Exons	242..1315		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o1.np	Method	AAT/NAP
Start	245	End	1423
GI	4680179	Score	1942
Exons	245..1423		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o2.tw	Method	TBLASTX:Wheat
Start	290	End	623
GI	none	Score	68
Exons	290..622, 506..595, 555..623		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o1.tm	Method	TBLASTX:Maize
Start	482	End	1069
GI	none	Score	174
Exons	482..751, 483..743, 812..910, 852..908, 908..1069, 915..1061, 917..1066		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o1.tw	Method	TBLASTX:Wheat
Start	623	End	1249
GI	none	Score	363
Exons	623..1249, 624..1193		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o2.tm	Method	TBLASTX:Maize
Start	1118	End	1410
GI	none	Score	161
Exons	1118..1408, 1122..1307, 1127..1339, 1219..1410		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o1.ts	Method	TBLASTX:Soybean
Start	1208	End	1423
GI	none	Score	268
Exons	1208..1423		

Seq. No.	580	Seq. ID	OJ990713_10.9924.C2
Gene No.	1187	Strand	-
Start	242	End	1423
Name	OJ990713_10.9924.C2.o3.tw	Method	TBLASTX:Wheat
Start	1256	End	1423
GI	none	Score	90
Exons	1256..1423, 1257..1421, 1289..1423		

Seq. No.	581	Seq. ID	OJ990713_10.9924.C3
Gene No.	1188	Strand	-
Start	129	End	347
Name	OJ990713_10.9924.C3.o1.gs	Method	GENSCAN
Start	129	End	347
GI	none	Score	.48
Exons	129..347		

Seq. No.	582	Seq. ID	OJ990713_10.9924.C4
Gene No.	1189	Strand	-
Start	1	End	391
Name	OJ990713_10.9924.C4.o1.np	Method	AAT/NAP
Start	1	End	391
GI	4538896	Score	236
Exons	1..391		
GI Descrip.	(AL049482) putative protein [Arabidopsis thaliana]		

Seq. No.	582	Seq. ID	OJ990713_10.9924.C4
Gene No.	1189	Strand	-
Start	1	End	391
Name	OJ990713_10.9924.C4.o1.gs	Method	GENSCAN
Start	10	End	66
GI	none	Score	.49
Exons	10..66		

Seq. No.	583	Seq. ID	OJ990713_10.9924.C5
Gene No.	1190	Strand	+
Start	1	End	763
Name	OJ990713_10.9924.C5.o1.np	Method	AAT/NAP
Start	1	End	763
GI	1587206	Score	265
Exons	1..364, 697..763		
GI Descrip.	T complex protein [Cucumis sativus]		

Seq. No.	583	Seq. ID	OJ990713_10.9924.C5
Gene No.	1190	Strand	+
Start	1	End	763
Name	OJ990713_10.9924.C5.o1.ts	Method	TBLASTX:Soybean
Start	26	End	329
GI	none	Score	91
Exons	26..55, 66..125, 67..144, 125..325, 126..329		

Seq. No.	583	Seq. ID	OJ990713_10.9924.C5
Gene No.	1190	Strand	+
Start	1	End	763
Name	OJ990713_10.9924.C5.o1.tc	Method	TBLASTX:Cress
Start	58	End	329
GI	none	Score	80
Exons	58..117, 59..133, 67..144, 69..125, 125..325, 126..329		

Seq. No.	583	Seq. ID	OJ990713_10.9924.C5
Gene No.	1190	Strand	+
Start	1	End	763
Name	OJ990713_10.9924.C5.o1.tm	Method	TBLASTX:Maize
Start	65	End	640
GI	none	Score	80

Exons	65..121, 65..121, 66..122, 66..125, 67..144, 67..144, 118..309, 119..169, 124..309, 125..325, 126..329, 517..570, 517..570, 563..640, 565..636		
Seq. No.	583	Seq. ID	OJ990713_10.9924.C5
Gene No.	1190	Strand	+
Start	1	End	763
Name	OJ990713_10.9924.C5.o2.np	Method	AAT/NAP
Start	189	End	763
GI	4206124	Score	93
Exons	189..309, 663..763		
GI Descrip.	(AF097668) T-complex protein 1 epsilon subunit [Mesembryanthemum crystallinum]		
Seq. No.	584	Seq. ID	OJ990713_10.9924.C6
Gene No.	1191	Strand	+
Start	1	End	566
Name	OJ990713_10.9924.C6.o1.np	Method	AAT/NAP
Start	1	End	306
GI	2584803	Score	349
Exons	1..306		
GI Descrip.	(Y14825) RIR1a protein [Oryza sativa]		
Seq. No.	584	Seq. ID	OJ990713_10.9924.C6
Gene No.	1191	Strand	+
Start	1	End	566
Name	OJ990713_10.9924.C6.o1.gp	Method	AAT/GAP
Start	96	End	566
GI	367_1.R1084	Score	834
Exons	96..566		
GI Descrip.	'2584803/emb|CAA75103| 3.0e-31 (Y14825) RIR1a protein [Oryza sativa]'		
Seq. No.	585	Seq. ID	OJ990713_10.9924.C7
Gene No.	1192	Strand	+
Start	130	End	180
Name	OJ990713_10.9924.C7.o1.gs	Method	GENSCAN
Start	130	End	180
GI	none	Score	.97
Exons	130..180		
Seq. No.	585	Seq. ID	OJ990713_10.9924.C7
Gene No.	1193	Strand	-
Start	60	End	137
Name	OJ990713_10.9924.C7.o1.gp	Method	AAT/GAP
Start	60	End	137
GI	90742_1.R1084	Score	110
Exons	60..137		
GI Descrip.	'5734616/dbj|AP000391.1|AP000391 4.0e-29 Oryza sativa genomic DNA, chromosome 6, clone:P0538C01'		
Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1194	Strand	-
Start	587	End	693
Name	OJ990713_10.9924.C8.o1.gp	Method	AAT/GAP
Start	587	End	693
GI	uC-osf1cyp082b07a1	Score	159

Exons	587..693		
GI Descrip.	'218221/dbj|D10675|RICSINE1R6 3.0e-30 Oryza sativa p-SINE1-r6 gene, repeat sequence'		
Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1195	Strand	-
Start	1673	End	1725
Name	OJ990713_10.9924.C8.o2.gp	Method	AAT/GAP
Start	1673	End	1725
GI	2981_1.R1084	Score	55
Exons	1673..1725		
GI Descrip.	'21693/emb|CAA46810| 1.0e-152 (X66012) cathepsin B [Triticum aestivum]'		
Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1196	Strand	-
Start	2073	End	3117
Name	OJ990713_10.9924.C8.o1.tm	Method	TBLASTX:Maize
Start	2066	End	2773
GI	none	Score	64
Exons	2066..2137, 2075..2113, 2108..2215, 2109..2255, 2112..2300, 2254..2364, 2317..2415, 2319..2450, 2418..2480, 2573..2683, 2574..2684, 2702..2773		
Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1196	Strand	-
Start	2073	End	3117
Name	OJ990713_10.9924.C8.o2.tc	Method	TBLASTX:Cress
Start	2070	End	2255
GI	none	Score	65
Exons	2070..2111, 2109..2255, 2111..2254		
Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1196	Strand	-
Start	2073	End	3117
Name	OJ990713_10.9924.C8.o2.tw	Method	TBLASTX:Wheat
Start	2070	End	2297
GI	none	Score	65
Exons	2070..2114, 2075..2113, 2109..2255, 2109..2297, 2254..2295		
Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1196	Strand	-
Start	2073	End	3117
Name	OJ990713_10.9924.C8.o1.np	Method	AAT/NAP
Start	2073	End	3117
GI	6063550	Score	1118
Exons	2073..2483, 2585..3117		
GI Descrip.	(AP000615) hypothetical protein [Oryza sativa]		
Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1196	Strand	-
Start	2073	End	3117
Name	OJ990713_10.9924.C8.o1.ts	Method	TBLASTX:Soybean
Start	2120	End	2779
GI	none	Score	141
Exons	2120..2215, 2121..2255, 2250..2300, 2251..2301, 2317..2415, 2319..2450, 2417..2458, 2418..2480, 2573..2674, 2574..2684,		

2702..2779

Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1196	Strand	-
Start	2073	End	3117
Name	OJ990713_10.9924.C8.o1.tc	Method	TBLASTX:Cress
Start	2260	End	2684
GI	none	Score	48
Exons	2260..2295, 2313..2450, 2317..2415, 2418..2480, 2420..2458, 2573..2674, 2574..2684		

Seq. No.	586	Seq. ID	OJ990713_10.9924.C8
Gene No.	1196	Strand	-
Start	2073	End	3117
Name	OJ990713_10.9924.C8.o1.tw	Method	TBLASTX:Wheat
Start	2317	End	2776
GI	none	Score	151
Exons	2317..2415, 2319..2450, 2418..2480, 2573..2683, 2574..2684, 2702..2776		

Seq. No.	587	Seq. ID	OJ990713_10.9924.C9
Gene No.	1197	Strand	+
Start	467	End	3519
Name	OJ990713_10.9924.C9.o1.gs	Method	GENSCAN
Start	467	End	3519
GI	none	Score	.57
Exons	467..628, 887..1041, 1174..1448, 2274..2314, 2876..2989, 3499..3519		

Seq. No.	587	Seq. ID	OJ990713_10.9924.C9
Gene No.	1198	Strand	-
Start	2886	End	3014
Name	OJ990713_10.9924.C9.o1.np	Method	AAT/NAP
Start	2886	End	3014
GI	2584803	Score	80
Exons	2886..3014		
GI Descrip.	(Y14825) RIR1a protein [Oryza sativa]		

Seq. No.	587	Seq. ID	OJ990713_10.9924.C9
Gene No.	1199	Strand	-
Start	4647	End	10175
Name	OJ990713_10.9924.C9.o2.gs	Method	GENSCAN
Start	4647	End	10157
GI	none	Score	.6
Exons	4647..4835, 5454..5606, 6515..6553, 7326..7444, 7940..8575, 8921..9112, 9428..9808, 10049..10157		

Seq. No.	587	Seq. ID	OJ990713_10.9924.C9
Gene No.	1199	Strand	-
Start	4647	End	10175
Name	OJ990713_10.9924.C9.o1.tm	Method	TBLASTX:Maize
Start	6875	End	7302
GI	none	Score	182
Exons	6875..7093, 6875..7015, 6886..7095, 7081..7302, 7166..7291		

Seq. No.	587	Seq. ID	OJ990713_10.9924.C9
Gene No.	1199	Strand	-

Start	4647	End	10175
Name	OJ990713_10.9924.C9.o2.np	Method	AAT/NAP
Start	6974	End	9113
GI	4538896	Score	1352
Exons	6974..8016, 8077..8592, 8701..9113		
GI Descrip.	(AL049482) putative protein [Arabidopsis thaliana]		

Seq. No.	587	Seq. ID	OJ990713_10.9924.C9
Gene No.	1199	Strand	-
Start	4647	End	10175
Name	OJ990713_10.9924.C9.o2.tm	Method	TBLASTX:Maize
Start	8037	End	8307
GI	none	Score	220
Exons	8037..8306, 8037..8306, 8038..8307		

Seq. No.	587	Seq. ID	OJ990713_10.9924.C9
Gene No.	1199	Strand	-
Start	4647	End	10175
Name	OJ990713_10.9924.C9.o3.np	Method	AAT/NAP
Start	9480	End	10175
GI	2584801	Score	97
Exons	9480..9675, 10041..10175		
GI Descrip.	(Y14824) RIR1b protein [Oryza sativa]		

Seq. No.	588	Seq. ID	OJ990713_10.9924.C10
Gene No.	1200	Strand	+
Start	1280	End	3938
Name	OJ990713_10.9924.C10.o1.gs	Method	GENSCAN
Start	1280	End	3818
GI	none	Score	.45
Exons	1280..1627, 1642..1887, 1986..2038, 2489..2660, 3525..3818		

Seq. No.	588	Seq. ID	OJ990713_10.9924.C10
Gene No.	1200	Strand	+
Start	1280	End	3938
Name	OJ990713_10.9924.C10.o1.gp	Method	AAT/GAP
Start	3124	End	3205
GI	LIB3477-003-P1-K1-E9	Score	94
Exons	3124..3205		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		

Seq. No.	588	Seq. ID	OJ990713_10.9924.C10
Gene No.	1200	Strand	+
Start	1280	End	3938
Name	OJ990713_10.9924.C10.o1.np	Method	AAT/NAP
Start	3437	End	3938
GI	5091507	Score	338
Exons	3437..3657, 3832..3938		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	588	Seq. ID	OJ990713_10.9924.C10
Gene No.	1201	Strand	-
Start	4527	End	5851
Name	OJ990713_10.9924.C10.o2.gs	Method	GENSCAN
Start	4527	End	5088

GI	none	Score	.88
Exons	4527..4696, 5001..5088		

Seq. No.	588	Seq. ID	OJ990713_10.9924.C10
Gene No.	1201	Strand	-
Start	4527	End	5851
Name	OJ990713_10.9924.C10.o2.np	Method	AAT/NAP
Start	4612	End	5851
GI	2584801	Score	193
Exons	4612..4766, 5001..5071, 5796..5851		
GI Descrip.	(Y14824) RIR1b protein [Oryza sativa]		

Seq. No.	588	Seq. ID	OJ990713_10.9924.C10
Gene No.	1202	Strand	-
Start	8170	End	8509
Name	OJ990713_10.9924.C10.o3.gs	Method	GENSCAN
Start	8170	End	8509
GI	none	Score	.82
Exons	8170..8303, 8413..8509		

Seq. No.	589	Seq. ID	OJ990713_10.9924.C11
Gene No.	1203	Strand	+
Start	1	End	1976
Name	OJ990713_10.9924.C11.o2.np	Method	AAT/NAP
Start	1	End	1976
GI	6069646	Score	428
Exons	1..109, 989..1976		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	589	Seq. ID	OJ990713_10.9924.C11
Gene No.	1204	Strand	+
Start	2495	End	2882
Name	OJ990713_10.9924.C11.o3.gp	Method	AAT/GAP
Start	2495	End	2882
GI	none	Score	752
Exons	2495..2882		

Seq. No.	589	Seq. ID	OJ990713_10.9924.C11
Gene No.	1205	Strand	-
Start	1	End	772
Name	OJ990713_10.9924.C11.o1.gp	Method	AAT/GAP
Start	1	End	425
GI	LIB3433-053-P1-K1-G2	Score	795
Exons	1..425		
GI Descrip.	'2584800/emb|Y14824|OSY14824 0.0e+00 Oryza sativa RIR1b gene'		

Seq. No.	589	Seq. ID	OJ990713_10.9924.C11
Gene No.	1205	Strand	-
Start	1	End	772
Name	OJ990713_10.9924.C11.o1.np	Method	AAT/NAP
Start	1	End	748
GI	2584803	Score	172
Exons	1..37, 615..748		

GI Descrip.	(Y14825) RIR1a protein [Oryza sativa]		
Seq. No.	589	Seq. ID	OJ990713_10.9924.C11
Gene No.	1205	Strand	-
Start	1	End	772
Name	OJ990713_10.9924.C11.o2.gp	Method	AAT/GAP
Start	622	End	772
GI	367_1.R1084	Score	279
Exons	622..772		
GI Descrip.	'2584803/emb|CAA75103| 3.0e-31 (Y14825) RIR1a protein [Oryza sativa]'		
Seq. No.	589	Seq. ID	OJ990713_10.9924.C11
Gene No.	1206	Strand	
Start	1401	End	1949
Name	OJ990713_10.9924.C11.o1.tm	Method	TBLASTX:Maize
Start	1401	End	1949
GI	none	Score	75
Exons	1401..1487, 1410..1487, 1522..1593, 1523..1735, 1523..1717, 1809..1949		
Seq. No.	589	Seq. ID	OJ990713_10.9924.C11
Gene No.	1206	Strand	
Start	1401	End	1949
Name	OJ990713_10.9924.C11.o1.tw	Method	TBLASTX:Wheat
Start	1529	End	1696
GI	none	Score	183
Exons	1529..1696		
Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1207	Strand	+
Start	1869	End	2245
Name	OJ990713_10.9924.C12.o1.gp	Method	AAT/GAP
Start	1869	End	2245
GI	44778_1.R1084	Score	711
Exons	1869..2245		
GI Descrip.	'2894612/emb|CAA17146.1| 3.0e-35 (AL021889) putative protein [Arabidopsis thaliana]'		
Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o1.np	Method	AAT/NAP
Start	1	End	2236
GI	4262174	Score	1703
Exons	1..407, 740..1031, 1119..1329, 1598..2236		
GI Descrip.	(AC005508) 9058 [Arabidopsis thaliana]		
Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o2.tw	Method	TBLASTX:Wheat
Start	38	End	355
GI	none	Score	67
Exons	38..97, 43..93, 110..355, 111..347		
Seq. No.	590	Seq. ID	OJ990713_10.9924.C12

Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o1.ts	Method	TBLASTX:Soybean
Start	43	End	2237
GI	none	Score	59
Exons	43..105, 43..108, 110..361, 111..353, 288..368, 365..409, 368..406, 739..771, 790..1056, 818..1033, 1120..1329, 1121..1330, 1154..1336, 1572..1973, 1595..2041, 1596..2024, 2033..2080, 2079..2237, 2090..2233		

Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o1.gs	Method	GENSCAN
Start	128	End	2824
GI	none	Score	.61
Exons	128..407, 740..1031, 1227..1329, 1598..2243, 2695..2824		

Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o1.tc	Method	TBLASTX:Cress
Start	157	End	2254
GI	none	Score	58
Exons	157..294, 158..361, 165..347, 368..406, 369..407, 371..409, 739..792, 743..1033, 778..1032, 1120..1329, 1136..1330, 1157..1336, 1595..1999, 1596..2003, 2033..2077, 2087..2254, 2088..2213, 2090..2215		

Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o1.tm	Method	TBLASTX:Maize
Start	164	End	1708
GI	none	Score	140
Exons	164..358, 165..347, 173..349, 357..407, 368..406, 380..409, 739..774, 784..1032, 820..1032, 830..1066, 1116..1286, 1120..1329, 1129..1329, 1136..1330, 1595..1648, 1596..1646, 1649..1708, 1649..1702		

Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o1.tw	Method	TBLASTX:Wheat
Start	368	End	1032
GI	none	Score	43
Exons	368..406, 739..771, 739..774, 790..1032, 830..1012		

Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o3.tw	Method	TBLASTX:Wheat
Start	1160	End	1807
GI	none	Score	255
Exons	1160..1330, 1161..1328, 1162..1329, 1595..1807, 1596..1802, 1598..1807		

Seq. No.	590	Seq. ID	OJ990713_10.9924.C12
Gene No.	1208	Strand	-
Start	1	End	2824
Name	OJ990713_10.9924.C12.o2.tm	Method	TBLASTX:Maize
Start	1862	End	2243
GI	none	Score	102
Exons	1862..2029, 1863..1988, 2018..2227, 2040..2204, 2058..2243		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o1.gp	Method	AAT/GAP
Start	1201	End	2184
GI	LIB3432-026-P1-K1-A10	Score	880
Exons	1201..1422, 1935..2184		
GI Descrip.	'5911685/emb|CAA72721.1| 2.0e-35 (Y11996) PRT1 protein [Nicotiana tabacum]'		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o3.tm	Method	TBLASTX:Maize
Start	1257	End	2184
GI	none	Score	83
Exons	1257..1346, 1284..1343, 1285..1422, 1289..1417, 1900..2184, 1921..1992, 1977..2177, 2032..2181		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o4.tc	Method	TBLASTX:Cress
Start	1279	End	2180
GI	none	Score	99
Exons	1279..1422, 1328..1417, 1939..2175, 1960..2178, 2013..2180		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o3.tw	Method	TBLASTX:Wheat
Start	1290	End	2129
GI	none	Score	65
Exons	1290..1343, 1297..1422, 1298..1417, 1900..2127, 1921..1992, 1932..2129		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o1.ts	Method	TBLASTX:Soybean
Start	1300	End	5177
GI	none	Score	100
Exons	1300..1422, 1301..1417, 1939..2175, 1972..2178, 2001..2180, 2537..2683, 2538..2693, 2538..2690, 2539..2697, 2802..2912, 2806..2934, 2815..2931, 2816..2941, 2819..2938, 3060..3194, 3062..3178, 3063..3191, 3239..3328, 3246..3344, 3258..3344, 3413..3538, 3415..3546, 3416..3541, 3421..3543, 3619..3837, 3628..3846, 3635..3847, 3636..3848, 3920..4252, 3922..4236, 4255..4458, 4256..4456, 4271..4468, 4719..4793, 4721..4831,		

4722..4832, 4926..5177

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o1.gs	Method	GENSCAN
Start	1301	End	5270
GI	none	Score	.98
Exons	1301..1422, 1935..2175, 2542..2688, 2816..2944, 3060..3188, 3261..3344, 3416..3540, 3637..3835, 3923..4455, 4724..4832, 4929..5270		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o1.np	Method	AAT/NAP
Start	1301	End	5267
GI	6685536	Score	2528
Exons	1301..1422, 1935..2175, 2542..2688, 2816..2944, 3060..3188, 3261..3344, 3416..3540, 3637..3835, 3923..4455, 4724..4832, 4929..5267		
GI Descrip.	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF-3 ETA) (EIF3 P110) gi|5911685|emb|CAA72721.1| (Y11996) PRT1 protein [Nicotiana tabacum]		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o2.tm	Method	TBLASTX:Maize
Start	2541	End	3475
GI	none	Score	151
Exons	2541..2693, 2545..2706, 2546..2689, 2547..2699, 2802..2942, 2815..2943, 2816..2944, 3053..3190, 3057..3182, 3059..3196, 3060..3194, 3259..3354, 3261..3344, 3413..3469, 3415..3474, 3416..3475		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o1.tc	Method	TBLASTX:Cress
Start	3059	End	3729
GI	none	Score	40
Exons	3059..3190, 3060..3194, 3062..3172, 3260..3337, 3260..3298, 3261..3338, 3415..3543, 3416..3541, 3436..3543, 3604..3720, 3621..3707, 3628..3729, 3635..3724		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o2.gp	Method	AAT/GAP
Start	3078	End	3850
GI	91852_1.R1084	Score	981
Exons	3078..3188, 3261..3344, 3416..3540, 3637..3850		
GI Descrip.	'5911685/emb|CAA72721.1| 4.0e-80 (Y11996) PRT1 protein [Nicotiana tabacum]'		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13

Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o1.tw	Method	TBLASTX:Wheat
Start	3443	End	4092
GI	none	Score	149
Exons	3443..3541, 3445..3543, 3448..3543, 3631..3840, 3631..3840, 3635..3847, 3920..4090, 3922..4092		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o1.tm	Method	TBLASTX:Maize
Start	3475	End	5247
GI	none	Score	81
Exons	3475..3543, 3476..3541, 3604..3840, 3631..3840, 3635..3847, 3639..3845, 3906..4451, 3920..4456, 3922..4458, 4717..4830, 4722..4832, 4723..4845, 4724..4846, 4926..5177, 4936..5247, 5104..5181		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o3.tc	Method	TBLASTX:Cress
Start	3730	End	4102
GI	none	Score	74
Exons	3730..3837, 3730..3837, 3731..3847, 3920..3994, 3922..3993, 3987..4049, 3992..4051, 3992..4051, 4049..4102		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o2.tc	Method	TBLASTX:Cress
Start	4165	End	5138
GI	none	Score	372
Exons	4165..4458, 4193..4456, 4713..4787, 4721..4828, 4722..4835, 4926..5138		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o2.tw	Method	TBLASTX:Wheat
Start	4405	End	5183
GI	none	Score	91
Exons	4405..4455, 4406..4456, 4413..4463, 4414..4461, 4713..4787, 4721..4825, 4722..4832, 4925..5134, 4926..5177, 5023..5172, 5098..5181, 5100..5183		

Seq. No.	591	Seq. ID	OJ990713_10.9924.C13
Gene No.	1209	Strand	+
Start	1201	End	5347
Name	OJ990713_10.9924.C13.o3.gp	Method	AAT/GAP
Start	4946	End	5347
GI	24039_1.R1084	Score	782
Exons	4946..5347		
GI Descrip.	'5911685/emb|CAA72721.1| 3.0e-25 (Y11996) PRT1 protein [Nicotiana tabacum]'		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1210	Strand	+
Start	1	End	1808
Name	OJ990713_10.9924.C14.o1.np	Method	AAT/NAP
Start	1	End	595
GI	6685536	Score	391
Exons	1..64, 161..379, 476..595		
GI Descrip.	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 9 (EIF-3 ETA) (EIF3 P110) gi|5911685|emb|CAA72721.1| (Y11996) PRT1 protein [Nicotiana tabacum]		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1210	Strand	+
Start	1	End	1808
Name	OJ990713_10.9924.C14.o1.gs	Method	GENSCAN
Start	161	End	1808
GI	none	Score	.56
Exons	161..337, 1047..1348, 1471..1590, 1646..1808		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1210	Strand	+
Start	1	End	1808
Name	OJ990713_10.9924.C14.o1.gp	Method	AAT/GAP
Start	169	End	821
GI	24039_1.R1084	Score	891
Exons	169..385, 487..821		
GI Descrip.	'5911685/emb|CAA72721.1| 3.0e-25 (Y11996) PRT1 protein [Nicotiana tabacum]'		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1210	Strand	+
Start	1	End	1808
Name	OJ990713_10.9924.C14.o2.np	Method	AAT/NAP
Start	1178	End	1805
GI	3056602	Score	160
Exons	1178..1348, 1471..1635, 1720..1805		
GI Descrip.	(AC004255) T1F9.23 [Arabidopsis thaliana]		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-
Start	2269	End	4014
Name	OJ990713_10.9924.C14.o1.tm	Method	TBLASTX:Maize
Start	1	End	742
GI	none	Score	108
Exons	1..57, 2..64, 6..77, 6..62, 7..78, 158..364, 168..365, 501..575, 671..742		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-
Start	2269	End	4014
Name	OJ990713_10.9924.C14.o1.tw	Method	TBLASTX:Wheat
Start	1	End	393
GI	none	Score	76
Exons	1..63, 1..57, 2..64, 158..364, 255..365, 331..393		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-

Start	2269	End	4014
Name	OJ990713_10.9924.C14.o1.tc	Method	TBLASTX:Cress
Start	2	End	384
GI	none	Score	85
Exons	2..67, 158..352, 160..384		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-
Start	2269	End	4014
Name	OJ990713_10.9924.C14.o1.ts	Method	TBLASTX:Soybean
Start	2	End	364
GI	none	Score	93
Exons	2..64, 158..364		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-
Start	2269	End	4014
Name	OJ990713_10.9924.C14.o2.gp	Method	AAT/GAP
Start	2269	End	3224
GI	1880_1.R1084	Score	927
Exons	2269..2639, 3109..3224		
GI Descrip.	'2344897 2.0e-23 (AC002388) unknown protein [Arabidopsis thaliana]'		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-
Start	2269	End	4014
Name	OJ990713_10.9924.C14.o2.tm	Method	TBLASTX:Maize
Start	2434	End	3274
GI	none	Score	192
Exons	2434..2640, 2444..2641, 2445..2642, 2463..2657, 3102..3212, 3104..3274, 3104..3232, 3109..3270		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-
Start	2269	End	4014
Name	OJ990713_10.9924.C14.o2.gs	Method	GENSCAN
Start	2469	End	3640
GI	none	Score	.51
Exons	2469..2626, 3628..3640		

Seq. No.	592	Seq. ID	OJ990713_10.9924.C14
Gene No.	1211	Strand	-
Start	2269	End	4014
Name	OJ990713_10.9924.C14.o3.np	Method	AAT/NAP
Start	2472	End	4014
GI	2344897	Score	240
Exons	2472..2639, 3109..3234, 3968..4014		
GI Descrip.	(AC002388) unknown protein [Arabidopsis thaliana]		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1212	Strand	+
Start	42	End	476
Name	OJ990713_10.9924.C15.o1.gs	Method	GENSCAN
Start	42	End	476
GI	none	Score	.97
Exons	42..476		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1213	Strand	-
Start	1	End	444
Name	OJ990713_10.9924.C15.o1.gp	Method	AAT/GAP
Start	1	End	444
GI	none	Score	799
Exons	1..444		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1213	Strand	-
Start	1	End	444
Name	OJ990713_10.9924.C15.o1.np	Method	AAT/NAP
Start	1	End	206
GI	2344897	Score	135
Exons	1..206		
GI Descrip.	(AC002388) unknown protein [Arabidopsis thaliana]		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1214	Strand	-
Start	1152	End	3657
Name	OJ990713_10.9924.C15.o2.gp	Method	AAT/GAP
Start	895	End	1732
GI	72571_1.R1084	Score	1126
Exons	895..1340, 1489..1732		
GI Descrip.	'3785998 5.0e-13 (AC005499) unknown protein [Arabidopsis thaliana]'		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1214	Strand	-
Start	1152	End	3657
Name	OJ990713_10.9924.C15.o2.np	Method	AAT/NAP
Start	1143	End	3657
GI	6069666	Score	467
Exons	1143..1340, 1489..1750, 1972..2126, 2238..2351, 3637..3657		
GI Descrip.	(AP000616) ESTs AU070998(R10588),D46106(S10554) correspond to a region of the predicted gene.; similar to Arabidopsis thaliana chromosome II BAC T6A23; unknown protein (AC005499) [Oryza sativa]		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1214	Strand	-
Start	1152	End	3657
Name	OJ990713_10.9924.C15.o2.gs	Method	GENSCAN
Start	1152	End	2677
GI	none	Score	.87
Exons	1152..1340, 1489..1750, 1972..2126, 2238..2352, 2661..2677		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1214	Strand	-
Start	1152	End	3657
Name	OJ990713_10.9924.C15.o3.gp	Method	AAT/GAP
Start	1625	End	2873
GI	23945_1.R1084	Score	1067
Exons	1625..1750, 1972..2126, 2238..2349, 2661..2873		
GI Descrip.	'6069666/dbj|BAA85442.1| 1.0e-22 (AP000616) ESTs AU070998(R10588),D46106(S10554) correspond to a region of the		

predicted gene.; similar to Arabidopsis thaliana chromosome II BAC T6A23; unknown protein (AC005499) [Oryza sativa]'

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1215	Strand	-
Start	8050	End	8149
Name	OJ990713_10.9924.C15.o2.tm	Method	TBLASTX:Maize
Start	2	End	379
GI	none	Score	212
Exons	2..265, 3..266, 325..372, 332..379		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1215	Strand	-
Start	8050	End	8149
Name	OJ990713_10.9924.C15.o1.tm	Method	TBLASTX:Maize
Start	1167	End	2078
GI	none	Score	86
Exons	1167..1349, 1185..1328, 1234..1341, 1487..1750, 1489..1752, 1947..2078, 1970..2074, 1986..2078		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1215	Strand	-
Start	8050	End	8149
Name	OJ990713_10.9924.C15.o1.tw	Method	TBLASTX:Wheat
Start	1185	End	1711
GI	none	Score	97
Exons	1185..1352, 1489..1569, 1526..1711, 1546..1710		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1215	Strand	-
Start	8050	End	8149
Name	OJ990713_10.9924.C15.o1.tc	Method	TBLASTX:Cress
Start	1471	End	2391
GI	none	Score	128
Exons	1471..1707, 1487..1726, 1489..1752, 1932..2024, 2023..2124, 2028..2129, 2229..2354, 2235..2315, 2245..2391		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1215	Strand	-
Start	8050	End	8149
Name	OJ990713_10.9924.C15.o1.ts	Method	TBLASTX:Soybean
Start	1541	End	2361
GI	none	Score	144
Exons	1541..1759, 1543..1752, 1610..1753, 1947..2024, 2031..2129, 2032..2127, 2235..2315, 2245..2361		

Seq. No.	593	Seq. ID	OJ990713_10.9924.C15
Gene No.	1215	Strand	-
Start	8050	End	8149
Name	OJ990713_10.9924.C15.o3.np	Method	AAT/NAP
Start	8050	End	8149
GI	5922634	Score	121
Exons	8050..8149		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016867|dbj|BAA85210.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1216	Strand	+
Start	50	End	510
Name	OJ990713_10.9924.C16.o1.gs	Method	GENSCAN
Start	50	End	510
GI	none	Score	.48
Exons	50..510		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1217	Strand	+
Start	1427	End	7730
Name	OJ990713_10.9924.C16.o2.np	Method	AAT/NAP
Start	1427	End	7730
GI	6721549	Score	582
Exons	1427..1657, 3468..5353, 7675..7730		
GI Descrip.	(AP001073) Similar to Disease resistance gene homolog 9N. (AF105140) [Oryza sativa]		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1217	Strand	+
Start	1427	End	7730
Name	OJ990713_10.9924.C16.o1.np	Method	AAT/NAP
Start	1600	End	6565
GI	6721547	Score	613
Exons	1600..1657, 3630..4262, 4308..5387, 6541..6565		
GI Descrip.	(AP001073) Similar to Oryza sativa gene for Pib. (AB013448)		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1217	Strand	+
Start	1427	End	7730
Name	OJ990713_10.9924.C16.o3.np	Method	AAT/NAP
Start	6918	End	7218
GI	5777617	Score	97
Exons	6918..7218		
GI Descrip.	(AJ245900) CAA30375.1 protein [Oryza sativa]		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1218	Strand	+
Start	16452	End	19570
Name	OJ990713_10.9924.C16.o7.np	Method	AAT/NAP
Start	16452	End	19570
GI	2245094	Score	202
Exons	16452..16653, 16832..16928, 17702..18049, 18144..18181, 19535..19570		
GI Descrip.	(Z97343) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1218	Strand	+
Start	16452	End	19570
Name	OJ990713_10.9924.C16.o5.gs	Method	GENSCAN
Start	17674	End	19046
GI	none	Score	.63
Exons	17674..18067, 18144..18287, 18859..19046		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1219	Strand	+
Start	20401	End	20479

Name	OJ990713_10.9924.C16.o1.gp	Method	AAT/GAP
Start	20401	End	20479
GI	90742_1.R1084	Score	116
Exons	20401..20479		
GI Descrip.	'5734616/dbj|AP000391.1|AP000391 4.0e-29 Oryza sativa genomic DNA, chromosome 6, clone:P0538C01'		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1220	Strand	+
Start	22711	End	23805
Name	OJ990713_10.9924.C16.o7.gs	Method	GENSCAN
Start	22711	End	23805
GI	none	Score	.47
Exons	22711..22722, 23261..23318, 23726..23805		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1220	Strand	+
Start	22711	End	23805
Name	OJ990713_10.9924.C16.o9.np	Method	AAT/NAP
Start	23192	End	23327
GI	2584801	Score	64
Exons	23192..23327		
GI Descrip.	(Y14824) RIR1b protein [Oryza sativa]		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1221	Strand	+
Start	26453	End	27229
Name	OJ990713_10.9924.C16.o10.np	Method	AAT/NAP
Start	26453	End	27229
GI	2584801	Score	116
Exons	26453..26576, 27084..27229		
GI Descrip.	(Y14824) RIR1b protein [Oryza sativa]		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1222	Strand	-
Start	1	End	16523
Name	OJ990713_10.9924.C16.o6.np	Method	AAT/NAP
Start	1	End	10681
GI	1648881	Score	74
Exons	1..23, 9088..9409, 10561..10681		
GI Descrip.	(Z81331) infB [Mycobacterium tuberculosis]		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1222	Strand	-
Start	1	End	16523
Name	OJ990713_10.9924.C16.o2.gs	Method	GENSCAN
Start	547	End	1038
GI	none	Score	.79
Exons	547..807, 925..1038		

Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1222	Strand	-
Start	1	End	16523
Name	OJ990713_10.9924.C16.o5.np	Method	AAT/NAP
Start	5714	End	10221
GI	2230959	Score	98
Exons	5714..5741, 8399..8623, 10173..10221		

GI Descrip.	(Y10149) subtilisin-like protease [Lycopersicon esculentum] gi|4200336|emb|CAA76725| (Y17276) P69B protein [Lycopersicon esculentum]		
Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1222	Strand	-
Start	1	End	16523
Name	OJ990713_10.9924.C16.o4.np	Method	AAT/NAP
Start	6296	End	8636
GI	2924509	Score	75
Exons	6296..6319, 8399..8636		
GI Descrip.	(AL022023) subtilisin proteinase-like [Arabidopsis thaliana]		
Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1222	Strand	-
Start	1	End	16523
Name	OJ990713_10.9924.C16.o4.gs	Method	GENSCAN
Start	7204	End	16523
GI	none	Score	.68
Exons	7204..7271, 7353..7578, 7961..8314, 8415..8774, 8865..8976, 9067..9135, 10473..10574, 10818..11023, 11709..11888, 13730..13827, 14449..14562, 16394..16523		
Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1223	Strand	-
Start	19590	End	24412
Name	OJ990713_10.9924.C16.o1.ts	Method	TBLASTX:Soybean
Start	3664	End	4068
GI	none	Score	121
Exons	3664..3789, 3669..3767, 3814..4068, 3852..4067		
Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1223	Strand	-
Start	19590	End	24412
Name	OJ990713_10.9924.C16.o1.tw	Method	TBLASTX:Wheat
Start	3715	End	4013
GI	none	Score	88
Exons	3715..3792, 3729..3791, 3814..4011, 3879..4013		
Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1223	Strand	-
Start	19590	End	24412
Name	OJ990713_10.9924.C16.o1.tm	Method	TBLASTX:Maize
Start	3814	End	4053
GI	none	Score	220
Exons	3814..4053, 3841..4029, 3948..4034		
Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1223	Strand	-
Start	19590	End	24412
Name	OJ990713_10.9924.C16.o6.gs	Method	GENSCAN
Start	19590	End	20409
GI	none	Score	.87
Exons	19590..19760, 20359..20409		
Seq. No.	594	Seq. ID	OJ990713_10.9924.C16
Gene No.	1223	Strand	-

Start	19590	End	24412
Name	OJ990713_10.9924.C16.o8.np	Method	AAT/NAP
Start	19593	End	24412
GI	1587206	Score	201
Exons	19593..19740, 20103..20215, 20359..20462, 24392..24412		
GI Descrip.	T complex protein [Cucumis sativus]		

Seq. No.	595	Seq. ID	OJ990713_10.9924.C17
Gene No.	1224	Strand	+
Start	240	End	6256
Name	OJ990713_10.9924.C17.o1.gs	Method	GENSCAN
Start	240	End	2097
GI	none	Score	.9
Exons	240..397, 1651..2097		

Seq. No.	595	Seq. ID	OJ990713_10.9924.C17
Gene No.	1224	Strand	+
Start	240	End	6256
Name	OJ990713_10.9924.C17.o1.np	Method	AAT/NAP
Start	1352	End	6256
GI	6907086	Score	1340
Exons	1352..2114, 2172..2412, 2641..2697, 2804..2867, 5973..6256		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	595	Seq. ID	OJ990713_10.9924.C17
Gene No.	1224	Strand	+
Start	240	End	6256
Name	OJ990713_10.9924.C17.o2.gs	Method	GENSCAN
Start	2675	End	4248
GI	none	Score	.87
Exons	2675..2867, 3259..3405, 3650..3808, 3851..4248		

Seq. No.	595	Seq. ID	OJ990713_10.9924.C17
Gene No.	1225	Strand	+
Start	7211	End	7316
Name	OJ990713_10.9924.C17.o2.gp	Method	AAT/GAP
Start	7211	End	7316
GI	5816518	Score	155
Exons	7211..7316		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 3.0e-40 Oryza sativa DNA, similar sequence to Pib gene		

Seq. No.	595	Seq. ID	OJ990713_10.9924.C17
Gene No.	1226	Strand	-
Start	4618	End	6944
Name	OJ990713_10.9924.C17.o3.gs	Method	GENSCAN
Start	4618	End	6944
GI	none	Score	.66
Exons	4618..4706, 5114..5173, 5712..5850, 6886..6944		

Seq. No.	595	Seq. ID	OJ990713_10.9924.C17
Gene No.	1227	Strand	-
Start	6975	End	7202
Name	OJ990713_10.9924.C17.o1.gp	Method	AAT/GAP
Start	6975	End	7202
GI	3761181	Score	354
Exons	6975..7202		

GI Descrip.	4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o1.np	Method	AAT/NAP
Start	869	End	2872
GI	6721517	Score	2538
Exons	869..932, 986..1140, 1220..1972, 2021..2872		
GI Descrip.	(AP001072) Similar to polyprotein. (AF061282) [Oryza sativa]		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o1.gs	Method	GENSCAN
Start	872	End	2832
GI	none	Score	.65
Exons	872..2416, 2534..2832		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o2.tw	Method	TBLASTX:Wheat
Start	1138	End	1501
GI	none	Score	292
Exons	1138..1242, 1142..1501, 1267..1500		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o3.tm	Method	TBLASTX:Maize
Start	1382	End	1678
GI	none	Score	192
Exons	1382..1678, 1399..1569		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o2.tm	Method	TBLASTX:Maize
Start	2024	End	2344
GI	none	Score	205
Exons	2024..2344		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o3.tw	Method	TBLASTX:Wheat
Start	2027	End	2413
GI	none	Score	165
Exons	2027..2254, 2062..2196, 2258..2413, 2281..2406		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o1.tw	Method	TBLASTX:Wheat
Start	2602	End	2872

GI	none	Score	297
Exons	2602..2865, 2606..2872, 2606..2872		
Seq. No.	596	Seq. ID	OJ990713_10.9924.C18
Gene No.	1228	Strand	+
Start	869	End	2872
Name	OJ990713_10.9924.C18.o1.tm	Method	TBLASTX:Maize
Start	2615	End	2872
GI	none	Score	283
Exons	2615..2872, 2617..2688, 2716..2868		
Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o1.np	Method	AAT/NAP
Start	1	End	991
GI	6721517	Score	1695
Exons	1..991		
GI Descrip.	(AP001072) Similar to polyprotein. (AF061282) [Oryza sativa]		
Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o3.tw	Method	TBLASTX:Wheat
Start	1	End	240
GI	none	Score	105
Exons	1..66, 3..62, 66..176, 70..240, 97..213		
Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o2.tm	Method	TBLASTX:Maize
Start	79	End	579
GI	none	Score	158
Exons	79..258, 244..579		
Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o1.gs	Method	GENSCAN
Start	100	End	813
GI	none	Score	.58
Exons	100..813		
Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o1.ts	Method	TBLASTX:Soybean
Start	133	End	528
GI	none	Score	57
Exons	133..165, 133..192, 169..528, 172..246, 176..310, 285..527		
Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o2.tw	Method	TBLASTX:Wheat
Start	241	End	543

GI	none	Score	397
Exons	241..543, 279..542		

Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o1.tw	Method	TBLASTX:Wheat
Start	544	End	985
GI	none	Score	622
Exons	544..969, 576..962, 671..985		

Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o2.ts	Method	TBLASTX:Soybean
Start	553	End	795
GI	none	Score	197
Exons	553..795		

Seq. No.	597	Seq. ID	OJ990713_10.9924.C19
Gene No.	1229	Strand	+
Start	1	End	991
Name	OJ990713_10.9924.C19.o1.tm	Method	TBLASTX:Maize
Start	616	End	969
GI	none	Score	477
Exons	616..969, 618..794, 658..954		

Seq. No.	598	Seq. ID	OJ990713_10.9924.C20
Gene No.	1230	Strand	-
Start	594	End	615
Name	OJ990713_10.9924.C20.o1.gs	Method	GENSCAN
Start	594	End	615
GI	none	Score	.44
Exons	594..615		

Seq. No.	599	Seq. ID	OJ990713_10.9924.C21
Gene No.	1231	Strand	-
Start	306	End	379
Name	OJ990713_10.9924.C21.o1.gs	Method	GENSCAN
Start	306	End	379
GI	none	Score	.99
Exons	306..379		

Seq. No.	600	Seq. ID	OJ990713_10.9924.C22
Gene No.	1232	Strand	+
Start	1	End	131
Name	OJ990713_10.9924.C22.o1.np	Method	AAT/NAP
Start	1	End	131
GI	1800051	Score	170
Exons	1..131		
GI Descrip.	(D90890) UNKNOWN PROTEIN FROM 2D-PAGE (SPOT LM6) (FRAGMENT). [Escherichia coli]		

Seq. No.	600	Seq. ID	OJ990713_10.9924.C22
Gene No.	1232	Strand	+
Start	1	End	131
Name	OJ990713_10.9924.C22.o1.gs	Method	GENSCAN

Start	24	End	110
GI	none	Score	.99
Exons	24..110		

Seq. No.	601	Seq. ID	OJ990713_10.9924.C25
Gene No.	1233	Strand	-
Start	410	End	593
Name	OJ990713_10.9924.C25.o1.gs	Method	GENSCAN
Start	410	End	593
GI	none	Score	.73
Exons	410..593		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1234	Strand	-
Start	1	End	2611
Name	OJ990713_10.9924.C27.o1.np	Method	AAT/NAP
Start	1	End	2541
GI	6651401	Score	687
Exons	1..133, 849..910, 1003..1053, 1321..1422, 2022..2129, 2220..2283, 2395..2541		
GI Descrip.	(AF180733) dynamin-like protein 4 [Arabidopsis thaliana]		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1234	Strand	-
Start	1	End	2611
Name	OJ990713_10.9924.C27.o1.gp	Method	AAT/GAP
Start	1342	End	2611
GI	63201_1.R1084	Score	839
Exons	1342..1422, 2022..2129, 2220..2283, 2395..2611		
GI Descrip.	'2129826/pir||S63668 1.0e-39 dynamin-like protein phragmoplastin 5 - soybean >gi_1218004 (U36430) SDL5A [Glycine max]'		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1235	Strand	-
Start	3690	End	5020
Name	OJ990713_10.9924.C27.o1.tc	Method	TBLASTX:Cress
Start	71	End	2545
GI	none	Score	63
Exons	71..133, 72..137, 807..908, 849..911, 1004..1054, 1005..1055, 1322..1423, 2023..2148, 2024..2131, 2212..2286, 2219..2284, 2395..2469, 2443..2535, 2468..2545		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1235	Strand	-
Start	3690	End	5020
Name	OJ990713_10.9924.C27.o1.ts	Method	TBLASTX:Soybean
Start	71	End	2542
GI	none	Score	84
Exons	71..133, 72..137, 849..911, 853..912, 1004..1054, 1008..1055, 1313..1444, 1322..1423, 1336..1443, 2023..2148, 2024..2131, 2212..2286, 2219..2284, 2395..2466, 2396..2467, 2402..2542, 2458..2535		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1235	Strand	-
Start	3690	End	5020
Name	OJ990713_10.9924.C27.o1.tm	Method	TBLASTX:Maize

Start	2023	End	2569
GI	none	Score	62
Exons	2023..2082, 2024..2083, 2083..2148, 2156..2299, 2212..2298, 2395..2451, 2399..2446, 2467..2565, 2468..2569		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1235	Strand	-
Start	3690	End	5020
Name	OJ990713_10.9924.C27.o2.tm	Method	TBLASTX:Maize
Start	3688	End	3987
GI	none	Score	102
Exons	3688..3846, 3717..3845, 3717..3986, 3721..3987		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1235	Strand	-
Start	3690	End	5020
Name	OJ990713_10.9924.C27.o2.np	Method	AAT/NAP
Start	3690	End	5020
GI	117188	Score	193
Exons	3690..4012, 4969..5020		
GI Descrip.	CYTOCHROME P450 71A1 (CYPLXXIA1) (ARP-2) gi|81423|pir||A35867 cytochrome P450 71A1 - avocado		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1235	Strand	-
Start	3690	End	5020
Name	OJ990713_10.9924.C27.o2.tc	Method	TBLASTX:Cress
Start	3717	End	4102
GI	none	Score	69
Exons	3717..3833, 3849..4004, 3853..4005, 4028..4099, 4034..4102		

Seq. No.	602	Seq. ID	OJ990713_10.9924.C27
Gene No.	1235	Strand	-
Start	3690	End	5020
Name	OJ990713_10.9924.C27.o2.ts	Method	TBLASTX:Soybean
Start	3717	End	4108
GI	none	Score	59
Exons	3717..3836, 3843..4007, 3844..4008, 4013..4096, 4013..4108		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1236	Strand	+
Start	727	End	9367
Name	OJ990713_10.9924.C28.o1.gs	Method	GENSCAN
Start	727	End	5434
GI	none	Score	.48
Exons	727..874, 1119..1309, 1702..3914, 4354..5434		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1236	Strand	+
Start	727	End	9367
Name	OJ990713_10.9924.C28.o1.np	Method	AAT/NAP
Start	1907	End	4071
GI	4538896	Score	1418
Exons	1907..2343, 2452..2966, 3027..4071		
GI Descrip.	(AL049482) putative protein [Arabidopsis thaliana]		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28

Gene No.	1236	Strand	+
Start	727	End	9367
Name	OJ990713_10.9924.C28.o2.np	Method	AAT/NAP
Start	4901	End	9367
GI	4539386	Score	46
Exons	4901..4977, 9071..9230, 9316..9367		
GI Descrip.	(AL035526) extensin-like protein [Arabidopsis thaliana]		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1237	Strand	-
Start	7849	End	9100
Name	OJ990713_10.9924.C28.o1.gp	Method	AAT/GAP
Start	7686	End	8136
GI	none	Score	723
Exons	7686..8136		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1237	Strand	-
Start	7849	End	9100
Name	OJ990713_10.9924.C28.o2.gs	Method	GENSCAN
Start	7849	End	9100
GI	none	Score	.95
Exons	7849..8127, 8195..9100		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1238	Strand	-
Start	10022	End	12690
Name	OJ990713_10.9924.C28.o3.tm	Method	TBLASTX:Maize
Start	2640	End	2867
GI	none	Score	198
Exons	2640..2867, 2641..2850		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1238	Strand	-
Start	10022	End	12690
Name	OJ990713_10.9924.C28.o2.tm	Method	TBLASTX:Maize
Start	2883	End	3264
GI	none	Score	254
Exons	2883..3035, 2887..3168, 3058..3168, 3172..3264, 3193..3264		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1238	Strand	-
Start	10022	End	12690
Name	OJ990713_10.9924.C28.o1.tm	Method	TBLASTX:Maize
Start	3742	End	4167
GI	none	Score	325
Exons	3742..3849, 3745..4167, 3898..4164, 3906..4166		

Seq. No.	603	Seq. ID	OJ990713_10.9924.C28
Gene No.	1238	Strand	-
Start	10022	End	12690
Name	OJ990713_10.9924.C28.o3.gs	Method	GENSCAN
Start	10022	End	12690
GI	none	Score	.65
Exons	10022..10212, 10519..10538, 11261..11523, 11543..11677, 12135..12275, 12529..12690		

Seq. No.	604	Seq. ID	OJ990713_10.9924.C29
Gene No.	1239	Strand	-
Start	110	End	873
Name	OJ990713_10.9924.C29.o1.gs	Method	GENSCAN
Start	110	End	873
GI	none	Score	.58
Exons	110..501, 792..873		

Seq. No.	605	Seq. ID	OJ990503_04.9924.C1
Gene No.	1240	Strand	-
Start	100	End	677
Name	OJ990503_04.9924.C1.o1.tm	Method	TBLASTX:Maize
Start	49	End	317
GI	none	Score	124
Exons	49..144, 57..143, 61..147, 147..263, 148..252, 165..263, 255..317, 257..307		

Seq. No.	605	Seq. ID	OJ990503_04.9924.C1
Gene No.	1240	Strand	-
Start	100	End	677
Name	OJ990503_04.9924.C1.o1.tw	Method	TBLASTX:Wheat
Start	49	End	356
GI	none	Score	50
Exons	49..87, 57..89, 81..143, 83..136, 85..144, 85..147, 147..263, 148..252, 163..270, 164..292, 165..263, 260..355, 261..356		

Seq. No.	605	Seq. ID	OJ990503_04.9924.C1
Gene No.	1240	Strand	-
Start	100	End	677
Name	OJ990503_04.9924.C1.o1.tc	Method	TBLASTX:Cress
Start	97	End	611
GI	none	Score	55
Exons	97..147, 100..144, 148..270, 150..263, 160..273, 188..274, 260..352, 264..353, 268..357, 269..370, 356..604, 356..604, 360..611		

Seq. No.	605	Seq. ID	OJ990503_04.9924.C1
Gene No.	1240	Strand	-
Start	100	End	677
Name	OJ990503_04.9924.C1.o1.np	Method	AAT/NAP
Start	100	End	677
GI	3914863	Score	664
Exons	100..677		
GI Descrip.	CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 gi|2293074|emb|CAA92560| (Z68262) ribosomal protein S4 [Sisyrinchium sp. 'Lejeune 1997'] gi|2293081|emb|CAA92561| (Z68263) ribosomal protein S4 [Sisyrinchium striatum]		

Seq. No.	605	Seq. ID	OJ990503_04.9924.C1
Gene No.	1240	Strand	-
Start	100	End	677
Name	OJ990503_04.9924.C1.o1.ts	Method	TBLASTX:Soybean
Start	313	End	611
GI	none	Score	47
Exons	313..357, 314..355, 356..604, 357..611		

Seq. No.	605	Seq. ID	OJ990503_04.9924.C1

Gene No.	1240	Strand	-
Start	100	End	677
Name	OJ990503_04.9924.C1.o1.gs	Method	GENSCAN
Start	450	End	576
GI	none	Score	.46
Exons	450..576		

Seq. No.	606	Seq. ID	OJ990503_04.9924.C2
Gene No.	1241	Strand	+
Start	128	End	252
Name	OJ990503_04.9924.C2.o1.gs	Method	GENSCAN
Start	128	End	252
GI	none	Score	.58
Exons	128..252		

Seq. No.	607	Seq. ID	OJ990503_04.9924.C4
Gene No.	1242	Strand	+
Start	251	End	824
Name	OJ990503_04.9924.C4.o1.gp	Method	AAT/GAP
Start	251	End	688
GI	uC-osflcyp011b01b1	Score	782
Exons	251..688		
GI Descrip.	'343210 5.0e-78 (M35995) apocytochrome b6 (alt.) [Oryza sativa] >gi_226762_prf__1604469A cytochrome b6 [Oryza sativa]'		

Seq. No.	607	Seq. ID	OJ990503_04.9924.C4
Gene No.	1242	Strand	+
Start	251	End	824
Name	OJ990503_04.9924.C4.o1.ts	Method	TBLASTX:Soybean
Start	316	End	688
GI	none	Score	90
Exons	316..360, 317..379, 317..376, 324..686, 356..688, 368..688		

Seq. No.	607	Seq. ID	OJ990503_04.9924.C4
Gene No.	1242	Strand	+
Start	251	End	824
Name	OJ990503_04.9924.C4.o1.gs	Method	GENSCAN
Start	347	End	660
GI	none	Score	.74
Exons	347..660		

Seq. No.	607	Seq. ID	OJ990503_04.9924.C4
Gene No.	1242	Strand	+
Start	251	End	824
Name	OJ990503_04.9924.C4.o1.np	Method	AAT/NAP
Start	347	End	824
GI	343210	Score	594
Exons	347..824		
GI Descrip.	(M35995) apocytochrome b6 (alt.) [Oryza sativa] gi|226762|prf||1604469A cytochrome b6 [Oryza sativa]		

Seq. No.	607	Seq. ID	OJ990503_04.9924.C4
Gene No.	1242	Strand	+
Start	251	End	824
Name	OJ990503_04.9924.C4.o1.tc	Method	TBLASTX:Cress
Start	395	End	688
GI	none	Score	496

Exons	395..688, 398..688		
Seq. No.	607	Seq. ID	OJ990503_04.9924.C4
Gene No.	1242	Strand	+
Start	251	End	824
Name	OJ990503_04.9924.C4.o1.tm	Method	TBLASTX:Maize
Start	401	End	688
GI	none	Score	446
Exons	401..688, 463..687		
Seq. No.	608	Seq. ID	OJ990503_04.9924.C5
Gene No.	1243	Strand	+
Start	509	End	774
Name	OJ990503_04.9924.C5.o2.gp	Method	AAT/GAP
Start	509	End	774
GI	0_2:R1084	Score	500
Exons	509..774		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		
Seq. No.	608	Seq. ID	OJ990503_04.9924.C5
Gene No.	1244	Strand	-
Start	466	End	852
Name	OJ990503_04.9924.C5.o1.tc	Method	TBLASTX:Cress
Start	1	End	487
GI	none	Score	205
Exons	1..129, 2..130, 3..131, 197..307, 197..367, 198..356, 338..364, 449..487		
Seq. No.	608	Seq. ID	OJ990503_04.9924.C5
Gene No.	1244	Strand	-
Start	466	End	852
Name	OJ990503_04.9924.C5.o1.tw	Method	TBLASTX:Wheat
Start	37	End	526
GI	none	Score	138
Exons	37..129, 44..130, 44..130, 197..526, 198..521		
Seq. No.	608	Seq. ID	OJ990503_04.9924.C5
Gene No.	1244	Strand	-
Start	466	End	852
Name	OJ990503_04.9924.C5.o1.gs	Method	GENSCAN
Start	466	End	825
GI	none	Score	.57
Exons	466..659, 735..825		
Seq. No.	608	Seq. ID	OJ990503_04.9924.C5
Gene No.	1244	Strand	-
Start	466	End	852
Name	OJ990503_04.9924.C5.o1.tm	Method	TBLASTX:Maize
Start	471	End	852
GI	none	Score	101
Exons	471..587, 482..595, 517..591, 520..609, 584..634, 592..612, 611..634, 645..779, 646..783, 659..784, 697..783, 698..793, 722..850, 790..852, 790..852		
Seq. No.	608	Seq. ID	OJ990503_04.9924.C5
Gene No.	1245	Strand	

Start	787	End	971
Name	OJ990503_04.9924.C5.o2.tw	Method	TBLASTX:Wheat
Start	787	End	971
GI	none	Score	188
Exons	787..924, 787..924, 921..965, 925..969, 927..971, 928..969	922..966, 922..966, 923..967,	

Seq. No.	609	Seq. ID	OJ990503_04.9924.C7
Gene No.	1246	Strand	
Start	355	End	639
Name	OJ990503_04.9924.C7.o1.tm	Method	TBLASTX:Maize
Start	355	End	639
GI	none	Score	110
Exons	355..432, 355..435, 413..487, 480..638, 481..639	428..460, 432..482, 433..543,	

Seq. No.	610	Seq. ID	OJ990503_04.9924.C9
Gene No.	1247	Strand	+
Start	54	End	974
Name	OJ990503_04.9924.C9.o1.gs	Method	GENSCAN
Start	54	End	849
GI	none	Score	.46
Exons	54..156, 719..849		

Seq. No.	610	Seq. ID	OJ990503_04.9924.C9
Gene No.	1247	Strand	+
Start	54	End	974
Name	OJ990503_04.9924.C9.o1.np	Method	AAT/NAP
Start	574	End	974
GI	1304247	Score	556
Exons	574..974		
GI Descrip.	(D84426) ABC-type heme transporter subunit [Lycopersicon esculentum]		

Seq. No.	611	Seq. ID	OJ990503_04.9924.C10
Gene No.	1248	Strand	+
Start	82	End	275
Name	OJ990503_04.9924.C10.o1.gs	Method	GENSCAN
Start	82	End	275
GI	none	Score	.85
Exons	82..275		

Seq. No.	612	Seq. ID	OJ990503_04.9924.C11
Gene No.	1249	Strand	
Start	1	End	149
Name	OJ990503_04.9924.C11.o1.tc	Method	TBLASTX:Cress
Start	1	End	149
GI	none	Score	134
Exons	1..120, 7..120, 9..122, 120..149		

Seq. No.	613	Seq. ID	OJ990503_04.9924.C13
Gene No.	1250	Strand	+
Start	41	End	278
Name	OJ990503_04.9924.C13.o1.gs	Method	GENSCAN
Start	41	End	278
GI	none	Score	.79
Exons	41..51, 239..278		

Seq. No.	614	Seq. ID	OJ990503_04.9924.C15
Gene No.	1251	Strand	+
Start	128	End	600
Name	OJ990503_04.9924.C15.o1.np	Method	AAT/NAP
Start	128	End	600
GI	2326759	Score	225
Exons	128..283, 563..600		
GI Descrip.	(Y14433) NADH dehydrogenase subunit 2 [Triticum aestivum]		

Seq. No.	615	Seq. ID	OJ990503_04.9924.C16
Gene No.	1252	Strand	+
Start	455	End	604
Name	OJ990503_04.9924.C16.o1.gs	Method	GENSCAN
Start	455	End	604
GI	none	Score	.57
Exons	455..604		

Seq. No.	616	Seq. ID	OJ990503_04.9924.C17
Gene No.	1253	Strand	+
Start	147	End	303
Name	OJ990503_04.9924.C17.o1.gs	Method	GENSCAN
Start	147	End	303
GI	none	Score	.93
Exons	147..303		

Seq. No.	617	Seq. ID	OJ990503_04.9924.C18
Gene No.	1254	Strand	+
Start	71	End	1169
Name	OJ990503_04.9924.C18.o1.gs	Method	GENSCAN
Start	71	End	1155
GI	none	Score	.71
Exons	71..149, 988..1155		

Seq. No.	617	Seq. ID	OJ990503_04.9924.C18
Gene No.	1254	Strand	+
Start	71	End	1169
Name	OJ990503_04.9924.C18.o2.np	Method	AAT/NAP
Start	666	End	1169
GI	72689	Score	656
Exons	666..1169		
GI Descrip.	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain ndhK - maize chloroplast gi|12427|emb|CAA35482| (X17438) PSII-G protein (AA 1 - 248) [Zea mays] gi|552735 (M12704) PSII-G [Zea mays]		

Seq. No.	617	Seq. ID	OJ990503_04.9924.C18
Gene No.	1255	Strand	-
Start	1	End	1169
Name	OJ990503_04.9924.C18.o1.np	Method	AAT/NAP
Start	1	End	582
GI	629831	Score	911
Exons	1..582		
GI Descrip.	NADH dehydrogenase 30K chain - wheat mitochondrion gi|416536|emb|CAA49376| (X69720) 30 kDa subunit of complex I NADH dehydrogenase [Triticum aestivum]		

Seq. No.	617	Seq. ID	OJ990503_04.9924.C18

Gene No.	1255	Strand	-
Start	1	End	1169
Name	OJ990503_04.9924.C18.o1.tm	Method	TBLASTX:Maize
Start	474	End	1169
GI	none	Score	40
Exons	474..518, 475..516, 504..620, 517..627, 518..568, 522..569, 586..621, 652..672, 718..846, 737..865, 741..845, 844..870, 847..870, 869..919, 871..909, 881..1168, 902..1111, 903..1169, 909..1169		

Seq. No.	617	Seq. ID	OJ990503_04.9924.C18
Gene No.	1255	Strand	-
Start	1	End	1169
Name	OJ990503_04.9924.C18.o1.tc	Method	TBLASTX:Cress
Start	741	End	1169
GI	none	Score	115
Exons	741..845, 741..845, 742..846, 844..900, 847..870, 870..908, 871..909, 881..1135, 903..1133, 1130..1165, 1131..1169		

Seq. No.	617	Seq. ID	OJ990503_04.9924.C18
Gene No.	1255	Strand	-
Start	1	End	1169
Name	OJ990503_04.9924.C18.o1.ts	Method	TBLASTX:Soybean
Start	741	End	1169
GI	none	Score	111
Exons	741..845, 741..845, 742..846, 846..869, 847..870, 870..908, 871..909, 881..1165, 902..1165, 903..1169		

Seq. No.	617	Seq. ID	OJ990503_04.9924.C18
Gene No.	1255	Strand	-
Start	1	End	1169
Name	OJ990503_04.9924.C18.o1.tw	Method	TBLASTX:Wheat
Start	744	End	1169
GI	none	Score	108
Exons	744..845, 744..845, 745..846, 748..852, 749..865, 844..900, 847..870, 870..908, 871..909, 881..1165, 903..1169		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1256	Strand	+
Start	615	End	1198
Name	OJ990503_04.9924.C19.o2.np	Method	AAT/NAP
Start	615	End	1198
GI	6002089	Score	787
Exons	615..1198		
GI Descrip.	(X84147) ribosomal protein S4 [Typha angustifolia]		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1256	Strand	+
Start	615	End	1198
Name	OJ990503_04.9924.C19.o1.gs	Method	GENSCAN
Start	737	End	863
GI	none	Score	.85
Exons	737..863		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1257	Strand	-
Start	1	End	288

Name	OJ990503_04.9924.C19.o1.np	Method	AAT/NAP
Start	1	End	288
GI	6723724	Score	94
Exons	1..288		
GI Descrip.	(AJ271079) hypothetical protein [Oenothera elata subsp. hookeri]		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1258	Strand	-
Start	1314	End	1962
Name	OJ990503_04.9924.C19.o1.tc	Method	TBLASTX:Cress
Start	600	End	1216
GI	none	Score	482
Exons	600..953, 602..745, 607..957, 610..957, 708..959, 943..1044, 956..1045, 960..1049, 961..1053, 1039..1125, 1043..1165, 1050..1163, 1060..1164, 1166..1216, 1169..1213		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1258	Strand	-
Start	1314	End	1962
Name	OJ990503_04.9924.C19.o1.ts	Method	TBLASTX:Soybean
Start	600	End	1000
GI	none	Score	488
Exons	600..956, 602..745, 607..957, 610..957, 708..959, 956..1000, 958..999		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1258	Strand	-
Start	1314	End	1962
Name	OJ990503_04.9924.C19.o1.tw	Method	TBLASTX:Wheat
Start	957	End	1264
GI	none	Score	115
Exons	957..1052, 957..1052, 958..1053, 1021..1149, 1043..1150, 1050..1166, 1050..1148, 1061..1165, 1166..1228, 1169..1228, 1170..1232, 1224..1256, 1226..1264		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1258	Strand	-
Start	1314	End	1962
Name	OJ990503_04.9924.C19.o2.tm	Method	TBLASTX:Maize
Start	996	End	1454
GI	none	Score	54
Exons	996..1058, 1006..1056, 1050..1166, 1050..1148, 1061..1165, 1166..1252, 1168..1260, 1169..1264, 1268..1333, 1335..1412, 1338..1397, 1399..1425, 1406..1426, 1428..1454		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1258	Strand	-
Start	1314	End	1962
Name	OJ990503_04.9924.C19.o1.gp	Method	AAT/GAP
Start	1314	End	1673
GI	99002_1.R1084	Score	696
Exons	1314..1673		
GI Descrip.	'287392/dbj|D13112|RICMT16 0.0e+00 Oryza sativa mitochondrial gene for tRNAs, complete sequences'		

Seq. No.	618	Seq. ID	OJ990503_04.9924.C19
Gene No.	1258	Strand	-

Start	1314	End	1962
Name	OJ990503_04.9924.C19.o1.tm	Method	TBLASTX:Maize
Start	1546	End	1962
GI	none	Score	47
Exons	1546..1587, 1554..1586, 1573..1638, 1587..1634, 1692..1727, 1695..1733, 1699..1731, 1724..1816, 1725..1817, 1726..1818, 1729..1818, 1790..1819, 1813..1875, 1820..1879, 1822..1875, 1876..1962, 1878..1961, 1879..1962		

Seq. No.	619	Seq. ID	OJ990503_04.9924.C20
Gene No.	1259	Strand	-
Start	1	End	546
Name	OJ990503_04.9924.C20.o1.np	Method	AAT/NAP
Start	1	End	531
GI	114419	Score	579
Exons	1..531		
GI Descrip.	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL gi|67820|pir||PWWTAM H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - wheat mitochondrion		

Seq. No.	619	Seq. ID	OJ990503_04.9924.C20
Gene No.	1259	Strand	-
Start	1	End	546
Name	OJ990503_04.9924.C20.o1.ts	Method	TBLASTX:Soybean
Start	18	End	516
GI	none	Score	70
Exons	18..83, 19..84, 124..516, 167..445, 307..468		

Seq. No.	619	Seq. ID	OJ990503_04.9924.C20
Gene No.	1259	Strand	-
Start	1	End	546
Name	OJ990503_04.9924.C20.o1.tc	Method	TBLASTX:Cress
Start	124	End	546
GI	none	Score	142
Exons	124..546, 170..445		

Seq. No.	619	Seq. ID	OJ990503_04.9924.C20
Gene No.	1259	Strand	-
Start	1	End	546
Name	OJ990503_04.9924.C20.o1.gs	Method	GENSCAN
Start	130	End	372
GI	none	Score	.92
Exons	130..372		

Seq. No.	619	Seq. ID	OJ990503_04.9924.C20
Gene No.	1259	Strand	-
Start	1	End	546
Name	OJ990503_04.9924.C20.o1.tm	Method	TBLASTX:Maize
Start	194	End	543
GI	none	Score	200
Exons	194..448, 196..471, 196..543		

Seq. No.	620	Seq. ID	OJ990503_04.9924.C21
Gene No.	1260	Strand	+
Start	310	End	492
Name	OJ990503_04.9924.C21.o1.gs	Method	GENSCAN
Start	310	End	492

GI	none	Score	.45
Exons	310..492		

Seq. No.	621	Seq. ID	OJ990503_04.9924.C22
Gene No.	1261	Strand	+
Start	384	End	732
Name	OJ990503_04.9924.C22.o1.np	Method	AAT/NAP
Start	384	End	732
GI	82484	Score	520
Exons	384..732		
GI Descrip.	hypothetical protein 1 - rice gi|20382|emb|CAA29825| (X06611) put. ORF 2 [Oryza sativa]		

Seq. No.	621	Seq. ID	OJ990503_04.9924.C22
Gene No.	1262	Strand	-
Start	214	End	434
Name	OJ990503_04.9924.C22.o1.gs	Method	GENSCAN
Start	214	End	434
GI	none	Score	.73
Exons	214..434		

Seq. No.	622	Seq. ID	OJ990503_04.9924.C23
Gene No.	1263	Strand	+
Start	14	End	494
Name	OJ990503_04.9924.C23.o1.np	Method	AAT/NAP
Start	14	End	494
GI	128857	Score	732
Exons	14..494		
GI Descrip.	NADH-PLASTOQUINONE OXIDOREDUCTASE SUBUNIT J (ORF 159) gi|82539|pir||S05106 hypothetical protein 159 - rice chloroplast gi|11987|emb|CAA33999| (X15901) ORF159 [Oryza sativa] gi|226608|prf||1603356AE ORF 159 [Oryza sativa]		

Seq. No.	622	Seq. ID	OJ990503_04.9924.C23
Gene No.	1263	Strand	+
Start	14	End	494
Name	OJ990503_04.9924.C23.o1.tc	Method	TBLASTX:Cress
Start	67	End	489
GI	none	Score	436
Exons	67..348, 68..352, 68..349, 348..488, 349..489, 349..489		

Seq. No.	622	Seq. ID	OJ990503_04.9924.C23
Gene No.	1263	Strand	+
Start	14	End	494
Name	OJ990503_04.9924.C23.o1.tm	Method	TBLASTX:Maize
Start	67	End	489
GI	none	Score	504
Exons	67..348, 68..352, 348..488, 349..489, 349..489		

Seq. No.	622	Seq. ID	OJ990503_04.9924.C23
Gene No.	1263	Strand	+
Start	14	End	494
Name	OJ990503_04.9924.C23.o1.ts	Method	TBLASTX:Soybean
Start	67	End	458
GI	none	Score	317
Exons	67..351, 67..348, 68..352, 294..350, 348..458, 349..450, 351..458		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1264	Strand	+
Start	8784	End	10310
Name	OJ990503_04.9924.C26.o1.np	Method	AAT/NAP
Start	8784	End	10310
GI	114409	Score	2543
Exons	8784..10310		
GI Descrip.	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL gi|67822|pir||PWRZAM H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - rice mitochondrion gi|13959|emb|CAA35787| (X51422) F-1-ATPase alpha subunit (AA 1-509) [Oryza sativa]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1265	Strand	+
Start	14112	End	14469
Name	OJ990503_04.9924.C26.o1.gp	Method	AAT/GAP
Start	14112	End	14469
GI	99002_1.R1084	Score	678
Exons	14112..14469		
GI Descrip.	'287392/dbj|D13112|RICMT16 0.0e+00 Oryza sativa mitochondrial gene for tRNAs, complete sequences'		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o7.np	Method	AAT/NAP
Start	16412	End	24948
GI	2326759	Score	1445
Exons	16412..16488, 20231..20391, 22789..23358, 24761..24948		
GI Descrip.	(Y14433) NADH dehydrogenase subunit 2 [Triticum aestivum]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o6.np	Method	AAT/NAP
Start	17907	End	18763
GI	629831	Score	1407
Exons	17907..18763		
GI Descrip.	NADH dehydrogenase 30K chain - wheat mitochondrion gi|416536|emb|CAA49376| (X69720) 30 kDa subunit of complex I NADH dehydrogenase [Triticum aestivum]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o4.gs	Method	GENSCAN
Start	18002	End	21384
GI	none	Score	.52
Exons	18002..18752, 19110..19336, 19573..19844, 20618..20778, 21012..21189, 21252..21384		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o2.gp	Method	AAT/GAP
Start	19613	End	19961

GI	3767032	Score	650
Exons	19613..19961		
GI Descrip.	2326760/emb|Y14434|MTTANAD2X 1.0e-147 Triticum aestivum mitochondrial nad2 gene exons 3, 4 and 5, and trnY gene		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o3.gp	Method	AAT/GAP
Start	20362	End	20792
GI	2310739	Score	788
Exons	20362..20792		
GI Descrip.	2326760/emb|Y14434|MTTANAD2X 0.0e+00 Triticum aestivum mitochondrial nad2 gene exons 3, 4 and 5, and trnY gene		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o4.gp	Method	AAT/GAP
Start	21395	End	21695
GI	3767033	Score	578
Exons	21395..21695		
GI Descrip.	2326760/emb|Y14434|MTTANAD2X 1.0e-53 Triticum aestivum mitochondrial nad2 gene exons 3, 4 and 5, and trnY gene		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o9.np	Method	AAT/NAP
Start	23193	End	29990
GI	6692688	Score	176
Exons	23193..23216, 29754..29990		
GI Descrip.	(AC007592) F12K11.17 [Arabidopsis thaliana]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o6.gs	Method	GENSCAN
Start	25930	End	30941
GI	none	Score	.7
Exons	25930..26176, 26316..26375, 26480..26634, 27282..27322, 28311..28627, 28738..28778, 29488..29658, 29710..29856, 30269..30317, 30817..30941		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1266	Strand	+
Start	16412	End	30941
Name	OJ990503_04.9924.C26.o8.np	Method	AAT/NAP
Start	29048	End	29710
GI	1143422	Score	459
Exons	29048..29710		
GI Descrip.	(Z34298) dpo-r [Beta vulgaris]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1267	Strand	-
Start	7366	End	13687
Name	OJ990503_04.9924.C26.o2.np	Method	AAT/NAP

Start	7366	End	13687
GI	133443	Score	249
Exons	7366..7430, 11345..11787, 13659..13687		
GI Descrip.	DNA-DIRECTED RNA POLYMERASE BETA" CHAIN gi|66987|pir||RNZMB2 DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain - maize chloroplast gi|12482|emb|CAA35197| (X17318) RNA polymerase beta-2 subunit (AA 1-1527) [Zea mays] gi|902214|emb|CAA60278| (X86563) RNA polymerase beta' subunit-2 [Zea mays]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1267	Strand	-
Start	7366	End	13687
Name	OJ990503_04.9924.C26.o2.gs	Method	GENSCAN
Start	11808	End	13318
GI	none	Score	.63
Exons	11808..11999, 13265..13318		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1268	Strand	-
Start	14585	End	15167
Name	OJ990503_04.9924.C26.o3.np	Method	AAT/NAP
Start	14585	End	15167
GI	6002089	Score	750
Exons	14585..15167		
GI Descrip.	(X84147) ribosomal protein S4 [Typha angustifolia]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1269	Strand	-
Start	16514	End	16994
Name	OJ990503_04.9924.C26.o4.np	Method	AAT/NAP
Start	16514	End	16994
GI	128857	Score	851
Exons	16514..16994		
GI Descrip.	NADH-PLASTOQUINONE OXIDOREDUCTASE SUBUNIT J (ORF 159) gi|82539|pir||S05106 hypothetical protein 159 - rice chloroplast gi|11987|emb|CAA33999| (X15901) ORF159 [Oryza sativa] gi|226608|prf||1603356AE ORF 159 [Oryza sativa]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1270	Strand	-
Start	17095	End	17823
Name	OJ990503_04.9924.C26.o5.np	Method	AAT/NAP
Start	17095	End	17823
GI	131326	Score	1006
Exons	17095..17823		
GI Descrip.	NADH-PLASTOQUINONE OXIDOREDUCTASE SUBUNIT K gi|100799|pir||S09666 psbG protein - wheat chloroplast gi|556460 (J04954) thylakoid membrane protein [Triticum aestivum]		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1271	Strand	-
Start	21774	End	24296
Name	OJ990503_04.9924.C26.o5.gs	Method	GENSCAN
Start	21774	End	24296
GI	none	Score	.63
Exons	21774..21965, 22232..22379, 23319..23431, 23437..23552, 23605..24150, 24239..24296		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o2.tm	Method	TBLASTX:Maize
Start	1097	End	1388
GI	none	Score	184
Exons	1097..1198, 1103..1198, 1104..1217, 1213..1386, 1215..1388		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o3.tm	Method	TBLASTX:Maize
Start	8796	End	9121
GI	none	Score	348
Exons	8796..9119, 8844..9119, 8867..9121		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o2.ts	Method	TBLASTX:Soybean
Start	8799	End	9689
GI	none	Score	560
Exons	8799..9359, 8847..9140, 8870..9337, 9162..9350, 9375..9689, 9395..9622		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o5.tc	Method	TBLASTX:Cress
Start	8799	End	9263
GI	none	Score	411
Exons	8799..9263, 8870..9262		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o8.tw	Method	TBLASTX:Wheat
Start	9041	End	9344
GI	none	Score	184
Exons	9041..9262, 9042..9344		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o6.tc	Method	TBLASTX:Cress
Start	9647	End	9939
GI	none	Score	402
Exons	9647..9931, 9648..9932, 9652..9939		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o5.ts	Method	TBLASTX:Soybean
Start	9837	End	10211
GI	none	Score	330
Exons	9837..10211, 9839..10153		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o5.tm	Method	TBLASTX:Maize
Start	9839	End	10016
GI	none	Score	250
Exons	9839..10015, 9840..10016		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o3.tw	Method	TBLASTX:Wheat
Start	9903	End	10247
GI	none	Score	97
Exons	9903..9986, 9904..9987, 9926..10012, 9930..10022, 9933..10046, 9963..10046, 9988..10047, 9988..10047, 9989..10048, 10047..10109, 10048..10110, 10049..10111, 10105..10176, 10110..10190, 10110..10187, 10167..10226, 10167..10247		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o9.tc	Method	TBLASTX:Cress
Start	9941	End	10184
GI	none	Score	204
Exons	9941..10153, 9942..10184		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o8.tc	Method	TBLASTX:Cress
Start	11439	End	11788
GI	none	Score	52
Exons	11439..11510, 11442..11516, 11523..11597, 11526..11612, 11617..11664, 11622..11663, 11657..11788, 11663..11788		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o7.tw	Method	TBLASTX:Wheat
Start	11523	End	11790
GI	none	Score	65
Exons	11523..11600, 11524..11601, 11543..11611, 11546..11620, 11577..11663, 11613..11663, 11636..11788, 11659..11790, 11660..11788, 11661..11789		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o4.tm	Method	TBLASTX:Maize
Start	13823	End	14239
GI	none	Score	141
Exons	13823..13909, 13823..13906, 13824..13907, 13825..13917, 13825..13908, 13906..13965, 13910..13972, 13910..13963, 13921..13965, 13967..14056, 13968..14060, 13969..14061, 14052..14090, 14054..14086, 14058..14093, 14147..14212,		

14151..14198, 14198..14239, 14199..14231

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o6.tm	Method	TBLASTX:Maize
Start	14357	End	14787
GI	none	Score	35
Exons	14357..14377, 14358..14384, 14371..14448, 14386..14445, 14450..14515, 14519..14614, 14523..14615, 14531..14617, 14617..14733, 14618..14722, 14635..14733, 14725..14787, 14727..14777		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o5.tw	Method	TBLASTX:Wheat
Start	14527	End	14826
GI	none	Score	71
Exons	14527..14559, 14551..14613, 14553..14606, 14555..14614, 14555..14617, 14617..14733, 14618..14722, 14633..14740, 14634..14762, 14635..14733, 14730..14825, 14731..14826, 14731..14826		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o3.tc	Method	TBLASTX:Cress
Start	14567	End	15182
GI	none	Score	55
Exons	14567..14617, 14570..14614, 14618..14740, 14619..14723, 14620..14733, 14630..14743, 14658..14744, 14730..14822, 14734..14823, 14738..14827, 14739..14840, 14826..15077, 14826..15050, 14830..15051, 14834..15052, 15001..15174, 15048..15182, 15049..15180		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o4.ts	Method	TBLASTX:Soybean
Start	14783	End	15182
GI	none	Score	47
Exons	14783..14827, 14784..14825, 14826..15050, 14826..15050, 14827..15051, 15001..15174, 15048..15182, 15050..15172, 15055..15180		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o11.tc	Method	TBLASTX:Cress
Start	15430	End	15578
GI	none	Score	139
Exons	15430..15549, 15436..15549, 15438..15551, 15549..15578		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737

Name	OJ990503_04.9924.C26.o1.tm	Method	TBLASTX:Maize
Start	16280	End	18661
GI	none	Score	110
Exons	16280..16357, 16280..16360, 16282..16359, 16338..16412, 16353..16385, 16358..16468, 16406..16657, 16411..16659, 16413..16658, 16421..16660, 16656..17075, 16660..17055, 16660..17076, 16661..17068, 17051..17089, 17052..17090, 17055..17285, 17069..17209, 17080..17247, 17166..17279, 17251..17586, 17255..17608, 17378..17587, 17570..17620, 17580..17618, 17619..17645, 17619..17642, 17624..17752, 17643..17771, 17644..17748, 17817..17837, 17862..17972, 17868..17903, 17869..17985, 17921..17971, 17971..18015, 17973..18014, 18482..18661		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o2.tc	Method	TBLASTX:Cress
Start	16498	End	18661
GI	none	Score	193
Exons	16498..16659, 16499..16660, 16656..16979, 16659..16970, 16660..16977, 18482..18661		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o2.tw	Method	TBLASTX:Wheat
Start	16550	End	18828
GI	none	Score	63
Exons	16550..16573, 16601..16657, 18425..18463, 18425..18463, 18426..18464, 18427..18465, 18463..18525, 18463..18525, 18465..18557, 18467..18541, 18525..18584, 18526..18627, 18526..18585, 18586..18642, 18587..18643, 18587..18643, 18588..18644, 18626..18721, 18627..18713, 18646..18732, 18705..18764, 18706..18765, 18707..18763, 18707..18766, 18786..18824, 18787..18828		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o3.ts	Method	TBLASTX:Soybean
Start	16550	End	18634
GI	none	Score	112
Exons	16550..16657, 16550..16660, 16558..16659, 16656..16988, 16659..16988, 16660..17004, 18482..18634		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o1.tc	Method	TBLASTX:Cress
Start	17065	End	17748
GI	none	Score	86
Exons	17065..17358, 17066..17206, 17092..17250, 17166..17255, 17303..17359, 17352..17576, 17353..17580, 17353..17586, 17354..17608, 17580..17618, 17581..17619, 17589..17645, 17619..17642, 17623..17643, 17643..17747, 17644..17748, 17644..17748		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o1.ts	Method	TBLASTX:Soybean
Start	17135	End	17748
GI	none	Score	50
Exons	17135..17209, 17136..17573, 17137..17586, 17146..17580, 17156..17587, 17246..17608, 17570..17611, 17580..17618, 17581..17619, 17619..17642, 17620..17643, 17643..17747, 17644..17748, 17644..17748		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o1.tw	Method	TBLASTX:Wheat
Start	17221	End	17745
GI	none	Score	353
Exons	17221..17586, 17230..17580, 17246..17608, 17580..17618, 17581..17619, 17589..17645, 17619..17642, 17623..17643, 17624..17740, 17637..17741, 17643..17744, 17644..17745, 17644..17745		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o4.tc	Method	TBLASTX:Cress
Start	20422	End	20843
GI	none	Score	59
Exons	20422..20478, 20423..20464, 20427..20483, 20428..20484, 20445..20546, 20446..20544, 20481..20567, 20571..20774, 20571..20774, 20572..20778, 20612..20632, 20760..20843, 20779..20841		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o6.tw	Method	TBLASTX:Wheat
Start	29738	End	29939
GI	none	Score	79
Exons	29738..29815, 29754..29816, 29779..29817, 29803..29934, 29817..29927, 29865..29939		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o6.ts	Method	TBLASTX:Soybean
Start	29750	End	29934
GI	none	Score	76
Exons	29750..29815, 29751..29816, 29803..29934, 29817..29927, 29818..29934		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o7.tm	Method	TBLASTX:Maize
Start	29753	End	29934

GI	none	Score	70
Exons	29753..29815, 29754..29816, 29803..29934, 29826..29930		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o10.tc	Method	TBLASTX:Cress
Start	29754	End	29939
GI	none	Score	57
Exons	29754..29816, 29803..29934, 29817..29939		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o5.gp	Method	AAT/GAP
Start	36515	End	36737
GI	57581_1.R1084	Score	410
Exons	36515..36737		
GI Descrip.	'1785675/emb|CAA69780| 1.0e-23 (Y08501) orf107a [Arabidopsis thaliana]'		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o4.tw	Method	TBLASTX:Wheat
Start	36522	End	36737
GI	none	Score	133
Exons	36522..36593, 36525..36593, 36526..36594, 36590..36673, 36591..36656, 36594..36674, 36604..36678, 36627..36719, 36656..36736, 36657..36737, 36659..36736		

Seq. No.	623	Seq. ID	OJ990503_04.9924.C26
Gene No.	1272	Strand	-
Start	36515	End	36737
Name	OJ990503_04.9924.C26.o7.tc	Method	TBLASTX:Cress
Start	36538	End	36737
GI	none	Score	104
Exons	36538..36594, 36539..36595, 36540..36596, 36540..36596, 36590..36736, 36591..36737		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1273	Strand	+
Start	86	End	307
Name	OJ990503_04.9924.C27.o2.gp	Method	AAT/GAP
Start	86	End	307
GI	427402	Score	139
Exons	86..112, 197..307		
GI Descrip.	14277/emb|X57968|TSNADA 1.0e-105 Triticum aestivum mitochondrial nad1 gene, exon 1 (and joined CDS)		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1274	Strand	+
Start	635	End	3724
Name	OJ990503_04.9924.C27.o1.gs	Method	GENSCAN
Start	635	End	3724
GI	none	Score	.49
Exons	635..788, 874..910, 1788..1910, 2909..3078, 3424..3521,		

3667..3724

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1275	Strand	+
Start	7787	End	14683
Name	OJ990503_04.9924.C27.o4.np	Method	AAT/NAP
Start	7787	End	14683
GI	6466937	Score	1148
Exons	7787..7841, 10783..12104, 14635..14683		
GI Descrip.	(AC011621) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1275	Strand	+
Start	7787	End	14683
Name	OJ990503_04.9924.C27.o2.np	Method	AAT/NAP
Start	8310	End	8927
GI	1304247	Score	943
Exons	8310..8927		
GI Descrip.	(D84426) ABC-type heme transporter subunit [Lycopersicon esculentum]		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1275	Strand	+
Start	7787	End	14683
Name	OJ990503_04.9924.C27.o3.np	Method	AAT/NAP
Start	8612	End	12138
GI	4539660	Score	745
Exons	8612..8677, 10804..12138		
GI Descrip.	(AF061282) polyprotein [Sorghum bicolor]		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1275	Strand	+
Start	7787	End	14683
Name	OJ990503_04.9924.C27.o3.gp	Method	AAT/GAP
Start	12196	End	12709
GI	uC-osf1cyp011b01b1	Score	952
Exons	12196..12709		
GI Descrip.	'343210 5.0e-78 (M35995) apocytochrome b6 (alt.) [Oryza sativa] >gi_226762_prf__1604469A cytochrome b6 [Oryza sativa]'		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1275	Strand	+
Start	7787	End	14683
Name	OJ990503_04.9924.C27.o5.np	Method	AAT/NAP
Start	12292	End	12986
GI	343210	Score	1120
Exons	12292..12986		
GI Descrip.	(M35995) apocytochrome b6 (alt.) [Oryza sativa] gi|226762|prf||1604469A cytochrome b6 [Oryza sativa]		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1276	Strand	+
Start	21154	End	23687
Name	OJ990503_04.9924.C27.o9.np	Method	AAT/NAP
Start	21154	End	23656
GI	114521	Score	1121

Exons	21154..21189, 22788..23656		
GI Descrip.	ATP SYNTHASE ALPHA CHAIN gi|67827|pir||PWRZA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - rice chloroplast gi|11979|emb|CAA33993| (X15901) ATPase alpha subunit [Oryza sativa] gi|226696|prf||1603356X ATPase alpha [Oryza sativa]		
Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1276	Strand	+
Start	21154	End	23687
Name	OJ990503_04.9924.C27.o5.gp	Method	AAT/GAP
Start	23271	End	23687
GI	LIB3431-040-P1-K2-C1	Score	692
Exons	23271..23687		
GI Descrip.	'114521/sp|P12084|ATPA_ORYSA 6.0e-53 ATP SYNTHASE ALPHA CHAIN >gi_67827_pir__PWRZA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - rice chloroplast >gi_11979_emb_CAA33993_ (X15901) ATPase alpha subunit [Oryza sativa] >gi_226696_prf__1603356X ATPase alpha [Oryza sativa]'		
Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1277	Strand	-
Start	1	End	138
Name	OJ990503_04.9924.C27.o1.gp	Method	AAT/GAP
Start	1	End	138
GI	5004991	Score	221
Exons	1..138		
GI Descrip.	19560/emb|Z11889|MITTARRNG 0.0e+00 T.aestivum mitochondrion rrn26 gene for rRNA large subunit (26S)		
Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1278	Strand	-
Start	45	End	1635
Name	OJ990503_04.9924.C27.o1.np	Method	AAT/NAP
Start	45	End	1635
GI	1093120	Score	103
Exons	45..178, 1524..1635		
GI Descrip.	allergen Dac g II [Dactylis glomerata]		
Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1279	Strand	-
Start	4661	End	7041
Name	OJ990503_04.9924.C27.o2.gs	Method	GENSCAN
Start	4661	End	7041
GI	none	Score	.53
Exons	4661..4703, 4858..4969, 5810..5963, 6688..7041		
Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1280	Strand	-
Start	8599	End	9429
Name	OJ990503_04.9924.C27.o3.gs	Method	GENSCAN
Start	8599	End	9429
GI	none	Score	.52
Exons	8599..8741, 9381..9429		
Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1281	Strand	-
Start	14514	End	14869

Name	OJ990503_04.9924.C27.o4.gp	Method	AAT/GAP
Start	14514	End	14869
GI	3767421	Score	692
Exons	14514..14869		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1282	Strand	-
Start	16406	End	22095
Name	OJ990503_04.9924.C27.o7.np	Method	AAT/NAP
Start	16406	End	22095
GI	2326759	Score	848
Exons	16406..16463, 20333..20732, 21943..22095		
GI Descrip.	(Y14433) NADH dehydrogenase subunit 2 [Triticum aestivum]		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1282	Strand	-
Start	16406	End	22095
Name	OJ990503_04.9924.C27.o6.np	Method	AAT/NAP
Start	17944	End	19322
GI	629764	Score	103
Exons	17944..17966, 19195..19322		
GI Descrip.	NADH dehydrogenase subunit 4 - Garden lettuce gi|976350 (L12246) NADH dehydrogenase subunit 4 [Lactuca sativa]		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o4.tc	Method	TBLASTX:Cress
Start	1	End	154
GI	none	Score	241
Exons	1..153, 2..154, 2..154		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o3.tm	Method	TBLASTX:Maize
Start	6428	End	11227
GI	none	Score	74
Exons	6428..6526, 10794..10880, 10882..11133, 10958..11047, 11022..11132, 11174..11227, 11176..11205		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o2.tw	Method	TBLASTX:Wheat
Start	10885	End	11327
GI	none	Score	164
Exons	10885..11133, 11022..11129, 11170..11241, 11171..11242, 11244..11327		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o3.ts	Method	TBLASTX:Soybean
Start	11268	End	11645
GI	none	Score	47
Exons	11268..11306, 11301..11369, 11430..11645		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o1.tw	Method	TBLASTX:Wheat
Start	11421	End	11768
GI	none	Score	206
Exons	11421..11642, 11430..11645, 11634..11768, 11634..11723		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o2.tm	Method	TBLASTX:Maize
Start	11430	End	11876
GI	none	Score	251
Exons	11430..11648, 11459..11647, 11652..11876, 11678..11872		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o1.ts	Method	TBLASTX:Soybean
Start	12261	End	12954
GI	none	Score	90
Exons	12261..12305, 12262..12324, 12262..12321, 12301..12954, 12313..12798, 12351..12953		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o1.tc	Method	TBLASTX:Cress
Start	12340	End	12973
GI	none	Score	1024
Exons	12340..12801, 12343..12954, 12351..12953, 12434..12973		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o1.tm	Method	TBLASTX:Maize
Start	12346	End	12954
GI	none	Score	883
Exons	12346..12954, 12349..12801, 12408..12953		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o3.tc	Method	TBLASTX:Cress
Start	21282	End	21632
GI	none	Score	283
Exons	21282..21497, 21282..21518, 21319..21504, 21504..21587, 21505..21588, 21512..21595, 21572..21631, 21580..21630, 21582..21632		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1283	Strand	-
Start	22144	End	22221
Name	OJ990503_04.9924.C27.o8.np	Method	AAT/NAP
Start	22144	End	22221

GI	541993	Score	122
Exons	22144..22221		
GI Descrip.	NADH dehydrogenase (EC 1.6.99.3) 42K chain - fava bean mitochondrion (fragment)		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1284	Strand	
Start	22787	End	23011
Name	OJ990503_04.9924.C27.o4.ts	Method	TBLASTX:Soybean
Start	22787	End	23011
GI	none	Score	131
Exons	22787..22882, 22795..22881, 22873..22899, 22874..22900, 22897..22944, 22898..23011, 22942..23010		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1285	Strand	
Start	22970	End	23110
Name	OJ990503_04.9924.C27.o5.tc	Method	TBLASTX:Cress
Start	22970	End	23110
GI	none	Score	209
Exons	22970..23110, 22972..23109		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1286	Strand	
Start	23230	End	23653
Name	OJ990503_04.9924.C27.o2.tc	Method	TBLASTX:Cress
Start	23230	End	23653
GI	none	Score	437
Exons	23230..23616, 23231..23653, 23240..23647, 23427..23648		

Seq. No.	624	Seq. ID	OJ990503_04.9924.C27
Gene No.	1286	Strand	
Start	23230	End	23653
Name	OJ990503_04.9924.C27.o2.ts	Method	TBLASTX:Soybean
Start	23230	End	23653
GI	none	Score	464
Exons	23230..23616, 23231..23653, 23231..23653		

Seq. No.	625	Seq. ID	OJ990503_04.9924.C28
Gene No.	1287	Strand	+
Start	416	End	1401
Name	OJ990503_04.9924.C28.o1.gs	Method	GENSCAN
Start	416	End	1401
GI	none	Score	.88
Exons	416..449, 530..823, 1304..1401		

Seq. No.	625	Seq. ID	OJ990503_04.9924.C28
Gene No.	1288	Strand	+
Start	2393	End	2647
Name	OJ990503_04.9924.C28.o2.np	Method	AAT/NAP
Start	2393	End	2647
GI	82486	Score	437
Exons	2393..2647		
GI Descrip.	hypothetical protein 3 - rice gi|20381|emb|CAA29824| (X06611) put. ORF 1 [Oryza sativa]		

Seq. No.	625	Seq. ID	OJ990503_04.9924.C28

Gene No.	1289	Strand	+
Start	3299	End	4474
Name	OJ990503_04.9924.C28.o3.np	Method	AAT/NAP
Start	3125	End	4474
GI	5852179	Score	369
Exons	3125..3373, 4122..4143, 4395..4474		
GI Descrip.	(AL117265) zhb0009.1 [Oryza sativa]		

Seq. No.	625	Seq. ID	OJ990503_04.9924.C28
Gene No.	1289	Strand	+
Start	3299	End	4474
Name	OJ990503_04.9924.C28.o2.gs	Method	GENSCAN
Start	3299	End	4143
GI	none	Score	.66
Exons	3299..3373, 4122..4143		

Seq. No.	625	Seq. ID	OJ990503_04.9924.C28
Gene No.	1290	Strand	-
Start	1630	End	2087
Name	OJ990503_04.9924.C28.o1.np	Method	AAT/NAP
Start	1630	End	2087
GI	82484	Score	717
Exons	1630..2087		
GI Descrip.	hypothetical protein 1 - rice gi|20382|emb|CAA29825| (X06611) put. ORF 2 [Oryza sativa]		

Seq. No.	626	Seq. ID	OJ990503_04.9924.C29
Gene No.	1291	Strand	-
Start	1	End	550
Name	OJ990503_04.9924.C29.o1.np	Method	AAT/NAP
Start	1	End	550
GI	2326759	Score	619
Exons	1..550		
GI Descrip.	(Y14433) NADH dehydrogenase subunit 2 [Triticum aestivum]		

Seq. No.	627	Seq. ID	OJ990503_04.9924.C30
Gene No.	1292	Strand	+
Start	725	End	822
Name	OJ990503_04.9924.C30.o1.gs	Method	GENSCAN
Start	725	End	822
GI	none	Score	.7
Exons	725..822		

Seq. No.	628	Seq. ID	OJ990503_04.9924.C31
Gene No.	1293	Strand	+
Start	399	End	407
Name	OJ990503_04.9924.C31.o1.gs	Method	GENSCAN
Start	399	End	407
GI	none	Score	.95
Exons	399..407		

Seq. No.	628	Seq. ID	OJ990503_04.9924.C31
Gene No.	1294	Strand	-
Start	255	End	496
Name	OJ990503_04.9924.C31.o1.tc	Method	TBLASTX:Cress
Start	2	End	492
GI	none	Score	144

Exons	2..91, 3..92, 3..92, 258..455, 262..429, 437..490, 441..491, 442..492, 442..489		
Seq. No.	628	Seq. ID	OJ990503_04.9924.C31
Gene No.	1294	Strand	-
Start	255	End	496
Name	OJ990503_04.9924.C31.o1.tw	Method	TBLASTX:Wheat
Start	4	End	396
GI	none	Score	163
Exons	4..108, 5..109, 21..107, 254..385, 255..386, 256..396		
Seq. No.	628	Seq. ID	OJ990503_04.9924.C31
Gene No.	1294	Strand	-
Start	255	End	496
Name	OJ990503_04.9924.C31.o1.gp	Method	AAT/GAP
Start	255	End	496
GI	57581_2.R1084	Score	426
Exons	255..496		
GI Descrip.	'343690/gb|M37274|WHTMT26SRR 0.0e+00 Wheat mitochondrial 26S rRNA gene, complete cds'		
Seq. No.	629	Seq. ID	OJ990503_04.9924.C32
Gene No.	1295	Strand	+
Start	1	End	417
Name	OJ990503_04.9924.C32.o1.np	Method	AAT/NAP
Start	1	End	417
GI	602034	Score	302
Exons	1..417		
GI Descrip.	(X16828) unidentified reading frame (AA 1-510) (1980 is 1st base in codon) [Beta vulgaris]		
Seq. No.	630	Seq. ID	OJ990503_07.9924.C3
Gene No.	1296	Strand	
Start	11	End	182
Name	OJ990503_07.9924.C3.o1.tw	Method	TBLASTX:Wheat
Start	11	End	182
GI	none	Score	274
Exons	11..181, 12..182, 19..180		
Seq. No.	631	Seq. ID	OJ990503_07.9924.C6
Gene No.	1297	Strand	
Start	429	End	549
Name	OJ990503_07.9924.C6.o1.tw	Method	TBLASTX:Wheat
Start	429	End	549
GI	none	Score	197
Exons	429..548, 430..549, 431..547		
Seq. No.	632	Seq. ID	OJ990503_07.9924.C8
Gene No.	1298	Strand	
Start	128	End	439
Name	OJ990503_07.9924.C8.o1.tc	Method	TBLASTX:Cress
Start	128	End	439
GI	none	Score	206
Exons	128..307, 134..313, 135..317, 135..317, 136..318, 300..347, 316..381, 317..373, 330..422, 331..432, 356..430, 425..439		
Seq. No.	632	Seq. ID	OJ990503_07.9924.C8

Gene No.	1299	Strand	
Start	440	End	717
Name	OJ990503_07.9924.C8.o2.tc	Method	TBLASTX:Cress
Start	440	End	717
GI	none	Score	151
Exons	440..601, 448..600, 450..602, 486..602, 598..660, 602..682, 604..681, 605..688, 606..686, 682..717		

Seq. No.	633	Seq. ID	OJ990503_07.9924.C9
Gene No.	1300	Strand	
Start	20	End	475
Name	OJ990503_07.9924.C9.o1.ts	Method	TBLASTX:Soybean
Start	20	End	475
GI	none	Score	57
Exons	20..91, 45..143, 50..142, 54..143, 55..144, 313..474, 323..475, 341..472, 342..473		

Seq. No.	634	Seq. ID	OJ990503_07.9924.C14
Gene No.	1301	Strand	+
Start	13737	End	13970
Name	OJ990503_07.9924.C14.o1.tm	Method	TBLASTX:Maize
Start	2972	End	3264
GI	none	Score	285
Exons	2972..3145, 2974..3147, 2974..3147, 3132..3257, 3141..3161, 3163..3264, 3163..3258		

Seq. No.	634	Seq. ID	OJ990503_07.9924.C14
Gene No.	1301	Strand	+
Start	13737	End	13970
Name	OJ990503_07.9924.C14.o1.tc	Method	TBLASTX:Cress
Start	5066	End	5340
GI	none	Score	88
Exons	5066..5131, 5068..5133, 5069..5134, 5152..5337, 5159..5338, 5163..5339, 5164..5340		

Seq. No.	634	Seq. ID	OJ990503_07.9924.C14
Gene No.	1301	Strand	+
Start	13737	End	13970
Name	OJ990503_07.9924.C14.o1.tw	Method	TBLASTX:Wheat
Start	9015	End	9347
GI	none	Score	549
Exons	9015..9347, 9017..9346		

Seq. No.	634	Seq. ID	OJ990503_07.9924.C14
Gene No.	1301	Strand	+
Start	13737	End	13970
Name	OJ990503_07.9924.C14.o1.gp	Method	AAT/GAP
Start	13737	End	13970
GI	61430_1.R1084	Score	444
Exons	13737..13970		
GI Descrip.	'14394/emb|Z14060|MISCREPU4 0.0e+00 T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA'		

Seq. No.	634	Seq. ID	OJ990503_07.9924.C14
Gene No.	1301	Strand	+
Start	13737	End	13970
Name	OJ990503_07.9924.C14.o2.tc	Method	TBLASTX:Cress

Start	13737	End	13970
GI	none	Score	60
Exons	13737..13778, 13737..13778, 13856..13969, 13857..13970		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1302	Strand	+
Start	1161	End	1563
Name	OJ990503_07.9924.C15.o1.gp	Method	AAT/GAP
Start	1161	End	1563
GI	2311596	Score	780
Exons	1161..1563		
GI Descrip.	5852170/emb|AL117265.1|OST17804 0.0e+00 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1303	Strand	+
Start	15202	End	15450
Name	OJ990503_07.9924.C15.o2.tc	Method	TBLASTX:Cress
Start	77	End	240
GI	none	Score	139
Exons	77..175, 82..207, 83..175, 84..179, 165..239, 168..239, 178..240		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1303	Strand	+
Start	15202	End	15450
Name	OJ990503_07.9924.C15.o2.tw	Method	TBLASTX:Wheat
Start	9166	End	9596
GI	none	Score	104
Exons	9166..9216, 9167..9226, 9168..9218, 9211..9276, 9220..9276, 9221..9280, 9278..9337, 9279..9338, 9279..9338, 9280..9339, 9280..9339, 9334..9396, 9339..9398, 9340..9411, 9341..9397, 9379..9459, 9387..9467, 9400..9489, 9459..9518, 9459..9518, 9460..9525, 9460..9525, 9516..9575, 9519..9596, 9520..9576, 9521..9595		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1303	Strand	+
Start	15202	End	15450
Name	OJ990503_07.9924.C15.o2.gp	Method	AAT/GAP
Start	15202	End	15450
GI	uC-osflcyp099d06b1	Score	482
Exons	15202..15450		
GI Descrip.	'4521193/dbj|AB013450.1|AB013450 3.0e-40 Oryza sativa DNA, similar sequence to Pib gene'		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1304	Strand	
Start	16216	End	19582
Name	OJ990503_07.9924.C15.o1.tw	Method	TBLASTX:Wheat
Start	16216	End	19582
GI	none	Score	67
Exons	16216..16245, 19153..19218, 19155..19421, 19179..19220, 19181..19582, 19181..19579		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1304	Strand	
Start	16216	End	19582

Name	OJ990503_07.9924.C15.o2.ts	Method	TBLASTX:Soybean
Start	17275	End	17705
GI	none	Score	176
Exons	17275..17427, 17276..17437, 17277..17408, 17278..17409, 17607..17696, 17607..17705, 17608..17700		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1305	Strand	
Start	23055	End	23540
Name	OJ990503_07.9924.C15.o1.tc	Method	TBLASTX:Cress
Start	23055	End	23393
GI	none	Score	47
Exons	23055..23393, 23062..23121, 23206..23379		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1305	Strand	
Start	23055	End	23540
Name	OJ990503_07.9924.C15.o1.ts	Method	TBLASTX:Soybean
Start	23106	End	23540
GI	none	Score	88
Exons	23106..23393, 23242..23379, 23478..23540		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1306	Strand	
Start	24143	End	24399
Name	OJ990503_07.9924.C15.o3.ts	Method	TBLASTX:Soybean
Start	24143	End	24399
GI	none	Score	88
Exons	24143..24250, 24144..24239, 24154..24252, 24236..24397, 24247..24399, 24248..24397		

Seq. No.	635	Seq. ID	OJ990503_07.9924.C15
Gene No.	1307	Strand	
Start	25677	End	25894
Name	OJ990503_07.9924.C15.o3.tw	Method	TBLASTX:Wheat
Start	25677	End	25894
GI	none	Score	163
Exons	25677..25778, 25678..25779, 25679..25777, 25771..25878, 25772..25894		

Seq. No.	636	Seq. ID	OJ990503_07.9924.C16
Gene No.	1308	Strand	
Start	4939	End	5520
Name	OJ990503_07.9924.C16.o1.tc	Method	TBLASTX:Cress
Start	4939	End	5520
GI	none	Score	60
Exons	4939..5016, 4995..5108, 4996..5169, 5265..5486, 5293..5520		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1309	Strand	+
Start	26738	End	27887
Name	OJ990503_07.9924.C17.o3.gp	Method	AAT/GAP
Start	26738	End	27887
GI	4107135	Score	2072
Exons	26738..27887		
GI Descrip.	342676/gb|M12582|MZEMTTURF 3.0e-66 Maize (cms-T) mitochondrial TURF 2H3 sequence containing 2 ORFs		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1310	Strand	-
Start	1024	End	1446
Name	OJ990503_07.9924.C17.o1.gp	Method	AAT/GAP
Start	1024	End	1446
GI	uC-osflcyp099h10a1	Score	746
Exons	1024..1446		
GI Descrip.	'769724/dbj|BAA06828.1| 3.0e-27 (D32052) ORF92B [Oryza sativa]'		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1311	Strand	
Start	6155	End	6540
Name	OJ990503_07.9924.C17.o2.tw	Method	TBLASTX:Wheat
Start	6155	End	6430
GI	none	Score	225
Exons	6155..6430, 6172..6429, 6174..6350		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1311	Strand	
Start	6155	End	6540
Name	OJ990503_07.9924.C17.o1.tm	Method	TBLASTX:Maize
Start	6161	End	6540
GI	none	Score	240
Exons	6161..6463, 6172..6540		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1311	Strand	
Start	6155	End	6540
Name	OJ990503_07.9924.C17.o2.tc	Method	TBLASTX:Cress
Start	6166	End	6528
GI	none	Score	257
Exons	6166..6528, 6167..6463		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1312	Strand	
Start	6483	End	6878
Name	OJ990503_07.9924.C17.o1.ts	Method	TBLASTX:Soybean
Start	6483	End	6878
GI	4397510	Score	115
Exons	6483..6878, 6487..6567, 6557..6877, 6594..6878		
GI Descrip.	2147784/pir__S71081 4.0e-53 NADH dehydrogenase chain 3 - onion mitochondrion >gi_1518344_emb_CAA89850_ (Z49772) NADH dehydrogenase subunit 3 [Allium cepa]		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1313	Strand	
Start	7532	End	7677
Name	OJ990503_07.9924.C17.o2.tm	Method	TBLASTX:Maize
Start	7532	End	7677
GI	none	Score	158
Exons	7532..7621, 7532..7618, 7533..7619, 7594..7677, 7616..7675, 7617..7676		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1314	Strand	
Start	7759	End	8432

Name	OJ990503_07.9924.C17.o3.tm	Method	TBLASTX:Maize
Start	7759	End	8112
GI	none	Score	92
Exons	7759..8004, 7787..8002, 8023..8112		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1314	Strand	
Start	7759	End	8432
Name	OJ990503_07.9924.C17.o2.ts	Method	TBLASTX:Soybean
Start	7762	End	8432
GI	none	Score	96
Exons	7762..8004, 7832..8005, 8023..8130, 8202..8432, 8210..8410		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1314	Strand	
Start	7759	End	8432
Name	OJ990503_07.9924.C17.o1.tw	Method	TBLASTX:Wheat
Start	7961	End	8384
GI	none	Score	43
Exons	7961..7987, 7962..7988, 7963..7989, 7988..8017, 8013..8117, 8017..8127, 8018..8128, 8123..8194, 8125..8181, 8182..8241, 8185..8241, 8227..8301, 8243..8302, 8243..8311, 8274..8384, 8300..8383, 8301..8384		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1315	Strand	
Start	9188	End	9341
Name	OJ990503_07.9924.C17.o4.tc	Method	TBLASTX:Cress
Start	9188	End	9341
GI	none	Score	240
Exons	9188..9340, 9189..9341, 9189..9341		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1316	Strand	
Start	9345	End	9774
Name	OJ990503_07.9924.C17.o1.tc	Method	TBLASTX:Cress
Start	9345	End	9774
GI	none	Score	142
Exons	9345..9476, 9371..9484, 9372..9485, 9373..9486, 9491..9736, 9502..9699, 9540..9746, 9541..9747, 9551..9754, 9734..9766, 9735..9773, 9750..9773, 9751..9774		

Seq. No.	637	Seq. ID	OJ990503_07.9924.C17
Gene No.	1317	Strand	
Start	9806	End	10330
Name	OJ990503_07.9924.C17.o3.tc	Method	TBLASTX:Cress
Start	9806	End	10330
GI	none	Score	120
Exons	9806..9871, 9806..9862, 9807..9866, 9863..9910, 9864..9920, 9865..9924, 9865..9924, 9984..10013, 10015..10107, 10015..10077, 10017..10082, 10032..10109, 10148..10177, 10154..10177, 10202..10261, 10216..10251, 10280..10303, 10300..10329, 10301..10330		

Seq. No.	638	Seq. ID	OJ990503_07.9924.C18
Gene No.	1318	Strand	
Start	3235	End	3397

Name	OJ990503_07.9924.C18.o1.ts	Method	TBLASTX:Soybean
Start	3235	End	3397
GI	none	Score	199
Exons	3235..3396, 3245..3397, 3263..3394		

Seq. No.	639	Seq. ID	OJ990513_01.9924.C1
Gene No.	1319	Strand	-
Start	393	End	653
Name	OJ990513_01.9924.C1.o1.gs	Method	GENSCAN
Start	393	End	653
GI	none	Score	.57
Exons	393..653		

Seq. No.	640	Seq. ID	OJ990513_01.9924.C2
Gene No.	1320	Strand	-
Start	841	End	1170
Name	OJ990513_01.9924.C2.o1.tm	Method	TBLASTX:Maize
Start	154	End	678
GI	none	Score	59
Exons	154..249, 166..249, 251..355, 274..678, 310..354, 352..675		

Seq. No.	640	Seq. ID	OJ990513_01.9924.C2
Gene No.	1320	Strand	-
Start	841	End	1170
Name	OJ990513_01.9924.C2.o1.np	Method	AAT/NAP
Start	841	End	1170
GI	4185148	Score	147
Exons	841..1170		
GI Descrip.	(AC005724) putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1321	Strand	+
Start	1112	End	1553
Name	OJ990513_01.9924.C3.o1.gs	Method	GENSCAN
Start	1112	End	1553
GI	none	Score	.71
Exons	1112..1138, 1326..1553		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o4.tm	Method	TBLASTX:Maize
Start	1320	End	1545
GI	none	Score	185
Exons	1320..1511, 1323..1514, 1336..1545		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o2.tm	Method	TBLASTX:Maize
Start	2568	End	2984
GI	none	Score	46
Exons	2568..2669, 2569..2667, 2665..2730, 2670..2747, 2739..2978, 2739..2777, 2826..2984		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3

Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o2.tw	Method	TBLASTX:Wheat
Start	2619	End	2933
GI	none	Score	106
Exons	2619..2933, 2638..2859, 2676..2879		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o3.tm	Method	TBLASTX:Maize
Start	3224	End	3749
GI	none	Score	49
Exons	3224..3319, 3225..3320, 3237..3320, 3322..3426, 3345..3749, 3381..3425, 3388..3426, 3423..3746		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o1.tm	Method	TBLASTX:Maize
Start	3993	End	6070
GI	none	Score	126
Exons	3993..4298, 5431..5811, 5441..5683, 5825..6064, 5851..5874, 5963..6070		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o1.tw	Method	TBLASTX:Wheat
Start	4011	End	5787
GI	none	Score	84
Exons	4011..4211, 5344..5394, 5494..5787, 5498..5785		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o1.np	Method	AAT/NAP
Start	4396	End	6072
GI	6069646	Score	545
Exons	4396..5364, 5653..6072		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	641	Seq. ID	OJ990513_01.9924.C3
Gene No.	1322	Strand	-
Start	4396	End	6072
Name	OJ990513_01.9924.C3.o5.tm	Method	TBLASTX:Maize
Start	4684	End	4899
GI	none	Score	62
Exons	4684..4899, 4688..4855		

Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239

Name	OJ990513_01.9924.C4.o1.np	Method	AAT/NAP
Start	1	End	3866
GI	6069646	Score	574
Exons	1..990, 2063..2133, 3775..3866		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239
Name	OJ990513_01.9924.C4.o3.tm	Method	TBLASTX:Maize
Start	70	End	502
GI	none	Score	37
Exons	70..273, 287..502, 313..336, 425..502		

Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239
Name	OJ990513_01.9924.C4.o1.gs	Method	GENSCAN
Start	266	End	6239
GI	none	Score	.61
Exons	266..520, 647..1447, 1466..2281, 2345..2512, 2622..2715, 2838..3130, 3210..3437, 3640..4474, 5776..5821, 6038..6239		

Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239
Name	OJ990513_01.9924.C4.o1.tm	Method	TBLASTX:Maize
Start	506	End	4089
GI	none	Score	80
Exons	506..919, 507..662, 702..905, 3673..4089		

Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239
Name	OJ990513_01.9924.C4.o2.tm	Method	TBLASTX:Maize
Start	1130	End	1519
GI	none	Score	78
Exons	1130..1519, 1179..1379		

Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239
Name	OJ990513_01.9924.C4.o1.tw	Method	TBLASTX:Wheat
Start	1514	End	5026
GI	none	Score	53
Exons	1514..1672, 1703..1861, 4711..4950, 4741..4797, 4847..5026		

Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239
Name	OJ990513_01.9924.C4.o4.tm	Method	TBLASTX:Maize
Start	1718	End	5079
GI	none	Score	41

Exons	1718..1837, 1841..1978, 4849..4938, 5014..5079		
Seq. No.	642	Seq. ID	OJ990513_01.9924.C4
Gene No.	1323	Strand	-
Start	1	End	6239
Name	OJ990513_01.9924.C4.o4.np	Method	AAT/NAP
Start	3616	End	4020
GI	2462640	Score	438
Exons	3616..4020		
GI Descrip.	(Y13370) reverse transcriptase [Oryza sativa]		
Seq. No.	643	Seq. ID	OJ990513_01.9924.C6
Gene No.	1324	Strand	+
Start	597	End	4578
Name	OJ990513_01.9924.C6.o1.gs	Method	GENSCAN
Start	597	End	4578
GI	none	Score	.69
Exons	597..647, 871..1827, 1980..2243, 2301..2565, 3391..3728, 3739..3911, 4170..4335, 4462..4578		
Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1325	Strand	+
Start	570	End	1993
Name	OJ990513_01.9924.C7.o1.gs	Method	GENSCAN
Start	570	End	1993
GI	none	Score	.63
Exons	570..704, 1851..1993		
Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1325	Strand	+
Start	570	End	1993
Name	OJ990513_01.9924.C7.o1.np	Method	AAT/NAP
Start	1427	End	1831
GI	2462640	Score	466
Exons	1427..1831		
GI Descrip.	(Y13370) reverse transcriptase [Oryza sativa]		
Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1326	Strand	+
Start	2007	End	4063
Name	OJ990513_01.9924.C7.o3.np	Method	AAT/NAP
Start	2007	End	3960
GI	4680186	Score	207
Exons	2007..2042, 3756..3960		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		
Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1326	Strand	+
Start	2007	End	4063
Name	OJ990513_01.9924.C7.o2.np	Method	AAT/NAP
Start	2113	End	4063
GI	5080767	Score	123
Exons	2113..2474, 3964..4063		
GI Descrip.	(AC007203) Hypothetical protein [Arabidopsis thaliana]		
Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1327	Strand	-

Start	2996	End	3502
Name	OJ990513_01.9924.C7.o2.gs	Method	GENSCAN
Start	2996	End	3502
GI	none	Score	.54
Exons	2996..3062, 3426..3502		

Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1328	Strand	-
Start	3504	End	3889
Name	OJ990513_01.9924.C7.o1.tw	Method	TBLASTX:Wheat
Start	350	End	768
GI	none	Score	345
Exons	350..739, 359..652, 361..768		

Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1328	Strand	-
Start	3504	End	3889
Name	OJ990513_01.9924.C7.o1.tm	Method	TBLASTX:Maize
Start	1463	End	2397
GI	none	Score	231
Exons	1463..1885, 1801..1884, 1943..2236, 2005..2235, 2225..2374, 2227..2397		

Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1328	Strand	-
Start	3504	End	3889
Name	OJ990513_01.9924.C7.o1.ts	Method	TBLASTX:Soybean
Start	2015	End	2581
GI	none	Score	114
Exons	2015..2242, 2252..2362, 2438..2581		

Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1328	Strand	-
Start	3504	End	3889
Name	OJ990513_01.9924.C7.o2.tw	Method	TBLASTX:Wheat
Start	2387	End	2728
GI	none	Score	264
Exons	2387..2695, 2489..2635, 2696..2728		

Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1328	Strand	-
Start	3504	End	3889
Name	OJ990513_01.9924.C7.o2.tm	Method	TBLASTX:Maize
Start	2402	End	2728
GI	none	Score	180
Exons	2402..2584, 2417..2602, 2573..2632, 2611..2631, 2639..2728, 2652..2720		

Seq. No.	644	Seq. ID	OJ990513_01.9924.C7
Gene No.	1328	Strand	-
Start	3504	End	3889
Name	OJ990513_01.9924.C7.o1.gp	Method	AAT/GAP
Start	3504	End	3889
GI	uC-osf1cyp033a04b1	Score	637
Exons	3504..3889		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	645	Seq. ID	OJ990513_01.9924.C8
Gene No.	1329	Strand	+
Start	125	End	2419
Name	OJ990513_01.9924.C8.o1.np	Method	AAT/NAP
Start	125	End	2121
GI	5852180	Score	38
Exons	125..146, 2050..2121		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	645	Seq. ID	OJ990513_01.9924.C8
Gene No.	1329	Strand	+
Start	125	End	2419
Name	OJ990513_01.9924.C8.o2.np	Method	AAT/NAP
Start	466	End	2419
GI	4680186	Score	222
Exons	466..516, 2215..2419		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	645	Seq. ID	OJ990513_01.9924.C8
Gene No.	1330	Strand	-
Start	1494	End	2348
Name	OJ990513_01.9924.C8.o2.gs	Method	GENSCAN
Start	1494	End	2168
GI	none	Score	.76
Exons	1494..1522, 2093..2168		

Seq. No.	645	Seq. ID	OJ990513_01.9924.C8
Gene No.	1330	Strand	-
Start	1494	End	2348
Name	OJ990513_01.9924.C8.o1.gp	Method	AAT/GAP
Start	1965	End	2348
GI	uC-osflcyp033a04b1	Score	713
Exons	1965..2348		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	646	Seq. ID	OJ990513_01.9924.C9
Gene No.	1331	Strand	-
Start	1189	End	1729
Name	OJ990513_01.9924.C9.o1.gs	Method	GENSCAN
Start	1189	End	1729
GI	none	Score	.42
Exons	1189..1262, 1516..1729		

Seq. No.	647	Seq. ID	OJ990513_01.9924.C10
Gene No.	1332	Strand	+
Start	808	End	1801
Name	OJ990513_01.9924.C10.o1.tm	Method	TBLASTX:Maize
Start	177	End	558
GI	none	Score	67
Exons	177..257, 246..302, 286..558		

Seq. No.	647	Seq. ID	OJ990513_01.9924.C10
Gene No.	1332	Strand	+
Start	808	End	1801
Name	OJ990513_01.9924.C10.o1.gs	Method	GENSCAN

Start	808	End	1801
GI	none	Score	.82
Exons	808..899, 1199..1484, 1718..1801		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o2.ts	Method	TBLASTX:Soybean
Start	156	End	406
GI	none	Score	52
Exons	156..197, 161..406, 234..404		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o1.np	Method	AAT/NAP
Start	167	End	4018
GI	4544372	Score	1085
Exons	167..1724, 1824..2220, 2287..3255, 3916..4018		
GI Descrip.	(AC006920) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o3.tw	Method	TBLASTX:Wheat
Start	182	End	589
GI	none	Score	116
Exons	182..589, 216..581		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o4.tw	Method	TBLASTX:Wheat
Start	626	End	991
GI	none	Score	185
Exons	626..991		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o5.ts	Method	TBLASTX:Soybean
Start	686	End	970
GI	none	Score	183
Exons	686..970		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o3.ts	Method	TBLASTX:Soybean
Start	1585	End	1986
GI	none	Score	62
Exons	1585..1737, 1587..1781, 1749..1832, 1750..1833, 1854..1895, 1854..1919, 1900..1986, 1904..1984		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-

Start	167	End	4018
Name	OJ990513_01.9924.C11.o1.ts	Method	TBLASTX:Soybean
Start	2137	End	2607
GI	none	Score	85
Exons	2137..2325, 2150..2281, 2320..2607, 2432..2569		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o2.tw	Method	TBLASTX:Wheat
Start	2224	End	2629
GI	none	Score	45
Exons	2224..2307, 2228..2296, 2302..2604, 2342..2629		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o1.tm	Method	TBLASTX:Maize
Start	2296	End	2754
GI	none	Score	212
Exons	2296..2754, 2297..2605, 2365..2754		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o1.tw	Method	TBLASTX:Wheat
Start	2638	End	3027
GI	none	Score	227
Exons	2638..2967, 2644..2976, 2666..2968, 2971..3027		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o2.tm	Method	TBLASTX:Maize
Start	2756	End	2973
GI	none	Score	200
Exons	2756..2968, 2758..2973, 2773..2973		

Seq. No.	648	Seq. ID	OJ990513_01.9924.C11
Gene No.	1333	Strand	-
Start	167	End	4018
Name	OJ990513_01.9924.C11.o4.ts	Method	TBLASTX:Soybean
Start	2824	End	3189
GI	none	Score	124
Exons	2824..2958, 2965..3189		

Seq. No.	649	Seq. ID	OJ990513_01.9924.C12
Gene No.	1334	Strand	+
Start	1	End	559
Name	OJ990513_01.9924.C12.o1.np	Method	AAT/NAP
Start	1	End	559
GI	4680186	Score	218
Exons	1..129, 355..559		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	649	Seq. ID	OJ990513_01.9924.C12
Gene No.	1335	Strand	-

Start	103	End	488
Name	OJ990513_01.9924.C12.o1.gp	Method	AAT/GAP
Start	103	End	488
GI	uC-osflcyp033a04b1	Score	637
Exons	103..488		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	649	Seq. ID	OJ990513_01.9924.C12
Gene No.	1336	Strand	-
Start	956	End	1113
Name	OJ990513_01.9924.C12.o2.np	Method	AAT/NAP
Start	956	End	1113
GI	6907087	Score	136
Exons	956..1113		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1337	Strand	+
Start	1	End	4847
Name	OJ990513_01.9924.C15.o1.np	Method	AAT/NAP
Start	1	End	4798
GI	5902445	Score	911
Exons	1..76, 724..1116, 4276..4798		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1337	Strand	+
Start	1	End	4847
Name	OJ990513_01.9924.C15.o2.gp	Method	AAT/GAP
Start	447	End	721
GI	61605_1.R1084	Score	454
Exons	447..721		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1337	Strand	+
Start	1	End	4847
Name	OJ990513_01.9924.C15.o1.gs	Method	GENSCAN
Start	816	End	2550
GI	none	Score	.49
Exons	816..1128, 1537..1705, 1879..2018, 2024..2550		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1337	Strand	+
Start	1	End	4847
Name	OJ990513_01.9924.C15.o2.gs	Method	GENSCAN
Start	3280	End	4847
GI	none	Score	.6
Exons	3280..3343, 3993..4029, 4295..4847		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1338	Strand	+
Start	5384	End	5544

Name	OJ990513_01.9924.C15.o2.np	Method	AAT/NAP
Start	5384	End	5544
GI	5852180	Score	72
Exons	5384..5544		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1339	Strand	-
Start	56	End	721
Name	OJ990513_01.9924.C15.o1.gp	Method	AAT/GAP
Start	56	End	721
GI	4107138	Score	895
Exons	56..721		
GI Descrip.	5852170/emb|AL117265.1|OST17804 1.0e-149 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1340	Strand	
Start	753	End	4757
Name	OJ990513_01.9924.C15.o1.tw	Method	TBLASTX:Wheat
Start	753	End	4331
GI	none	Score	378
Exons	753..1115, 786..995, 962..1099, 4260..4331		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1340	Strand	
Start	753	End	4757
Name	OJ990513_01.9924.C15.o2.tm	Method	TBLASTX:Maize
Start	867	End	1115
GI	none	Score	198
Exons	867..1115, 875..1114		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1340	Strand	
Start	753	End	4757
Name	OJ990513_01.9924.C15.o1.ts	Method	TBLASTX:Soybean
Start	1023	End	4607
GI	none	Score	97
Exons	1023..1115, 4269..4607		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1340	Strand	
Start	753	End	4757
Name	OJ990513_01.9924.C15.o1.tm	Method	TBLASTX:Maize
Start	4278	End	4622
GI	none	Score	232
Exons	4278..4529, 4298..4507, 4548..4622		

Seq. No.	650	Seq. ID	OJ990513_01.9924.C15
Gene No.	1340	Strand	
Start	753	End	4757
Name	OJ990513_01.9924.C15.o2.tw	Method	TBLASTX:Wheat
Start	4380	End	4757
GI	none	Score	187
Exons	4380..4619, 4615..4752, 4617..4751, 4629..4757		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16

Gene No.	1341	Strand	+
Start	1	End	6301
Name	OJ990513_01.9924.C16.o1.gp	Method	AAT/GAP
Start	1	End	301
GI	uC-osflM202048c12b1	Score	440
Exons	1..301		
GI Descrip.	'5257255/dbj|AP000364.1|AP000364 2.0e-16 Oryza sativa genomic DNA, chromosome 8, clone:P0026F07'.		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1341	Strand	+
Start	1	End	6301
Name	OJ990513_01.9924.C16.o1.np	Method	AAT/NAP
Start	1	End	6301
GI	6498441	Score	998
Exons	1..57, 1987..2736, 5550..6139, 6233..6301		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1 (AF098806) [Oryza sativa]		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1341	Strand	+
Start	1	End	6301
Name	OJ990513_01.9924.C16.o1.gs	Method	GENSCAN
Start	882	End	1163
GI	none	Score	.74
Exons	882..1163		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1341	Strand	+
Start	1	End	6301
Name	OJ990513_01.9924.C16.o2.gs	Method	GENSCAN
Start	1990	End	2759
GI	none	Score	.96
Exons	1990..2028, 2094..2759		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1341	Strand	+
Start	1	End	6301
Name	OJ990513_01.9924.C16.o3.gp	Method	AAT/GAP
Start	4034	End	4376
GI	uC-osroM202024h08a1	Score	83
Exons	4034..4104, 4354..4376		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 5.0e-84 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1341	Strand	+
Start	1	End	6301
Name	OJ990513_01.9924.C16.o4.gs	Method	GENSCAN
Start	4872	End	6283
GI	none	Score	.72
Exons	4872..4875, 5606..5871, 5951..6283		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1342	Strand	-
Start	166	End	508

Name	OJ990513_01.9924.C16.o2.gp	Method	AAT/GAP
Start	166	End	508
GI	uC-osroM202024h08a1	Score	87
Exons	166..188, 438..508		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 5.0e-84 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1343	Strand	-
Start	3379	End	3824
Name	OJ990513_01.9924.C16.o3.gs	Method	GENSCAN
Start	3379	End	3824
GI	none	Score	.78
Exons	3379..3793, 3817..3824		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1344	Strand	-
Start	4241	End	4763
Name	OJ990513_01.9924.C16.o3.tw	Method	TBLASTX:Wheat
Start	1801	End	2117
GI	none	Score	118
Exons	1801..1938, 1806..1940, 1963..2115, 2016..2117		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1344	Strand	-
Start	4241	End	4763
Name	OJ990513_01.9924.C16.o4.gp	Method	AAT/GAP
Start	4241	End	4763
GI	uC-osf1M202048c12b1	Score	843
Exons	4241..4763		
GI Descrip.	'5257255/dbj|AP000364.1|AP000364 2.0e-16 Oryza sativa genomic DNA, chromosome 8, clone:P0026F07'		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1345	Strand	
Start	5544	End	5875
Name	OJ990513_01.9924.C16.o2.tw	Method	TBLASTX:Wheat
Start	5544	End	5875
GI	none	Score	84
Exons	5544..5651, 5626..5754, 5627..5875		

Seq. No.	651	Seq. ID	OJ990513_01.9924.C16
Gene No.	1346	Strand	
Start	5897	End	6298
Name	OJ990513_01.9924.C16.o1.tw	Method	TBLASTX:Wheat
Start	5897	End	6298
GI	none	Score	330
Exons	5897..6298, 5912..6085, 6046..6153		

Seq. No.	652	Seq. ID	OJ990513_01.9924.C17
Gene No.	1347	Strand	+
Start	64	End	3595
Name	OJ990513_01.9924.C17.o1.gs	Method	GENSCAN
Start	64	End	3326
GI	none	Score	.6
Exons	64..237, 2580..2797, 2915..3326		

Seq. No.	652	Seq. ID	OJ990513_01.9924.C17
Gene No.	1347	Strand	+
Start	64	End	3595
Name	OJ990513_01.9924.C17.o1.gp	Method	AAT/GAP
Start	1012	End	1396
GI	uC-osf1cyp033a04b1	Score	654
Exons	1012..1396		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	652	Seq. ID	OJ990513_01.9924.C17
Gene No.	1347	Strand	+
Start	64	End	3595
Name	OJ990513_01.9924.C17.o2.np	Method	AAT/NAP
Start	2532	End	3595
GI	4680183	Score	1070
Exons	2532..3595		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	652	Seq. ID	OJ990513_01.9924.C17
Gene No.	1348	Strand	-
Start	945	End	3595
Name	OJ990513_01.9924.C17.o1.np	Method	AAT/NAP
Start	945	End	3595
GI	4680186	Score	342
Exons	945..1146, 1979..2030, 2545..2633, 3392..3595		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	652	Seq. ID	OJ990513_01.9924.C17
Gene No.	1348	Strand	-
Start	945	End	3595
Name	OJ990513_01.9924.C17.o3.gp	Method	AAT/GAP
Start	2067	End	2832
GI	5816562	Score	648
Exons	2067..2485, 2807..2832		
GI Descrip.	6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1349	Strand	+
Start	1	End	5514
Name	OJ990513_01.9924.C18.o1.np	Method	AAT/NAP
Start	1	End	5511
GI	5922631	Score	6219
Exons	1..68, 336..505, 551..1122, 1165..1317, 1444..2370, 2985..5511		
GI Descrip.	(AP000492) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] gi|6016864|dbj|BAA85207.1| (AP000570) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativ		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1349	Strand	+
Start	1	End	5514
Name	OJ990513_01.9924.C18.o1.gs	Method	GENSCAN

Start	8	End	4314
GI	none	Score	.96
Exons	8..134, 288..862, 989..1277, 1282..2362, 2459..2732, 2948..3458, 3647..4314		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1349	Strand	+
Start	1	End	5514
Name	OJ990513_01.9924.C18.o2.gs	Method	GENSCAN
Start	4714	End	5514
GI	none	Score	.64
Exons	4714..5514		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1350	Strand	+
Start	7501	End	10473
Name	OJ990513_01.9924.C18.o3.np	Method	AAT/NAP
Start	7501	End	10473
GI	5042454	Score	164
Exons	7501..7543, 10246..10473		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1351	Strand	+
Start	15498	End	21575
Name	OJ990513_01.9924.C18.o7.np	Method	AAT/NAP
Start	15340	End	21575
GI	4417267	Score	392
Exons	15340..15359, 15678..15706, 16667..16901, 16970..17234, 18965..19097, 19221..19398, 20072..20639, 21521..21575		
GI Descrip.	(AC007019) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1351	Strand	+
Start	15498	End	21575
Name	OJ990513_01.9924.C18.o5.gs	Method	GENSCAN
Start	15498	End	20660
GI	none	Score	.56
Exons	15498..15706, 16667..16868, 17064..17233, 18955..19097, 19221..19398, 20072..20660		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1351	Strand	+
Start	15498	End	21575
Name	OJ990513_01.9924.C18.o2.gp	Method	AAT/GAP
Start	20271	End	20643
GI	8464_1.R1084	Score	652
Exons	20271..20643		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-50 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1352	Strand	-
Start	6114	End	8808
Name	OJ990513_01.9924.C18.o2.np	Method	AAT/NAP
Start	5880	End	8808
GI	6691716	Score	2418

Exons	5880..6328, 6402..6516, 6666..6767, 6842..7029, 7107..7286, 7363..7465, 7548..7722, 7914..8808		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		
Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1352	Strand	-
Start	6114	End	8808
Name	OJ990513_01.9924.C18.o3.gs	Method	GENSCAN
Start	6114	End	8808
GI	none	Score	.7
Exons	6114..6328, 6402..6506, 6578..6767, 6842..6984, 7107..7465, 7548..7777, 7924..8125, 8417..8808		
Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1353	Strand	-
Start	9845	End	10265
Name	OJ990513_01.9924.C18.o1.gp	Method	AAT/GAP
Start	9845	End	10265
GI	5816562	Score	647
Exons	9845..10265		
GI Descrip.	6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10		
Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o7.tw	Method	TBLASTX:Wheat
Start	727	End	1129
GI	none	Score	288
Exons	727..996, 728..1129		
Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o6.tw	Method	TBLASTX:Wheat
Start	1710	End	2387
GI	none	Score	136
Exons	1710..1886, 1931..2167, 1935..2165, 2214..2387		
Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o1.tw	Method	TBLASTX:Wheat
Start	2387	End	2843
GI	none	Score	485
Exons	2387..2842, 2388..2843		
Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o4.ts	Method	TBLASTX:Soybean
Start	2427	End	2792
GI	none	Score	138
Exons	2427..2651, 2658..2792		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o3.tm	Method	TBLASTX:Maize
Start	2517	End	2858
GI	none	Score	348
Exons	2517..2858, 2558..2851		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o2.tw	Method	TBLASTX:Wheat
Start	2966	End	3390
GI	none	Score	427
Exons	2966..3385, 3010..3390		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o2.ts	Method	TBLASTX:Soybean
Start	3044	End	3418
GI	none	Score	307
Exons	3044..3418, 3061..3204, 3241..3411		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o2.tm	Method	TBLASTX:Maize
Start	3112	End	3556
GI	none	Score	273
Exons	3112..3366, 3113..3367, 3113..3370, 3389..3532, 3530..3556		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o8.tw	Method	TBLASTX:Wheat
Start	3395	End	3678
GI	none	Score	183
Exons	3395..3577, 3404..3502, 3583..3675, 3583..3678		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o3.ts	Method	TBLASTX:Soybean
Start	3670	End	4058
GI	none	Score	87
Exons	3670..3774, 3678..3764, 3810..4058, 3814..4056		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o5.tw	Method	TBLASTX:Wheat
Start	3679	End	4110
GI	none	Score	402
Exons	3679..4110, 3684..4025		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18

Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o6.tm	Method	TBLASTX:Maize
Start	3733	End	4005
GI	none	Score	120
Exons	3733..3903, 3907..4005		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o10.tw	Method	TBLASTX:Wheat
Start	4117	End	4416
GI	none	Score	130
Exons	4117..4251, 4120..4260, 4290..4391, 4318..4416		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o1.tm	Method	TBLASTX:Maize
Start	4413	End	4776
GI	none	Score	440
Exons	4413..4736, 4414..4737, 4729..4776		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o4.tw	Method	TBLASTX:Wheat
Start	4419	End	4806
GI	none	Score	416
Exons	4419..4730, 4420..4806, 4615..4806		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o5.tm	Method	TBLASTX:Maize
Start	4878	End	5151
GI	none	Score	99
Exons	4878..4976, 4879..4977, 4968..5042, 4972..5055, 5065..5151		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o3.tw	Method	TBLASTX:Wheat
Start	4921	End	10462
GI	none	Score	362
Exons	4921..5412, 5082..5285, 5404..5535, 10331..10462, 10336..10461		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o4.tm	Method	TBLASTX:Maize
Start	5233	End	10426
GI	none	Score	154
Exons	5233..5415, 5262..5312, 5355..5414, 5394..5495, 5394..5495, 5395..5496, 10238..10342, 10343..10426		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18

Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o9.tw	Method	TBLASTX:Wheat
Start	8398	End	8688
GI	none	Score	193
Exons	8398..8688		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o4.gs	Method	GENSCAN
Start	11084	End	13863
GI	none	Score	.67
Exons	11084..11601, 11700..11851, 11976..12496, 12548..12645, 12697..12868, 12937..13061, 13764..13863		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o5.np	Method	AAT/NAP
Start	11313	End	13863
GI	6721558	Score	240
Exons	11313..11357, 12076..12141, 12840..13061, 13764..13863		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa] gi|6815083|dbj|BAA90369.1| (AP001081) hypothetical protein [Oryza sativa]		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o4.np	Method	AAT/NAP
Start	11918	End	13436
GI	6721561	Score	695
Exons	11918..12865, 13367..13436		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1354	Strand	-
Start	11084	End	14831
Name	OJ990513_01.9924.C18.o6.np	Method	AAT/NAP
Start	13068	End	14831
GI	6721512	Score	110
Exons	13068..13534, 14488..14512, 14555..14693, 14722..14831		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1355	Strand	
Start	17169	End	19258
Name	OJ990513_01.9924.C18.o5.ts	Method	TBLASTX:Soybean
Start	17169	End	19258
GI	none	Score	102
Exons	17169..17240, 17171..17233, 18952..19110, 18953..19096, 19223..19258		

Seq. No.	653	Seq. ID	OJ990513_01.9924.C18
Gene No.	1356	Strand	
Start	19346	End	20641
Name	OJ990513_01.9924.C18.o1.ts	Method	TBLASTX:Soybean
Start	19346	End	20641
GI	none	Score	73
Exons	19346..19399, 20073..20378, 20075..20350, 20453..20641, 20454..20639		

Seq. No.	654	Seq. ID	OJ990513_01.9924.C19
Gene No.	1357	Strand	+
Start	2016	End	2293
Name	OJ990513_01.9924.C19.o1.tw	Method	TBLASTX:Wheat
Start	389	End	2173
GI	none	Score	54
Exons	389..442, 405..437, 435..530, 438..518, 1905..2120, 1922..2173, 1922..2158, 1924..2169		

Seq. No.	654	Seq. ID	OJ990513_01.9924.C19
Gene No.	1357	Strand	+
Start	2016	End	2293
Name	OJ990513_01.9924.C19.o1.gs	Method	GENSCAN
Start	2016	End	2293
GI	none	Score	.46
Exons	2016..2168, 2249..2293		

Seq. No.	654	Seq. ID	OJ990513_01.9924.C19
Gene No.	1357	Strand	+
Start	2016	End	2293
Name	OJ990513_01.9924.C19.o1.tm	Method	TBLASTX:Maize
Start	2039	End	2174
GI	none	Score	187
Exons	2039..2173, 2040..2174		

Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o1.np	Method	AAT/NAP
Start	1	End	2322
GI	6705984	Score	2082
Exons	1..2322		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o2.tm	Method	TBLASTX:Maize
Start	68	End	514
GI	none	Score	175
Exons	68..514, 69..425		

Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o3.ts	Method	TBLASTX:Soybean
Start	68	End	229

GI	none	Score	95
Exons	68..229, 69..227		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o1.gs	Method	GENSCAN
Start	79	End	2278
GI	none	Score	.77
Exons	79..1138, 1247..2278		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o3.tw	Method	TBLASTX:Wheat
Start	137	End	538
GI	none	Score	161
Exons	137..538, 138..500		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o1.ts	Method	TBLASTX:Soybean
Start	251	End	610
GI	none	Score	307
Exons	251..610		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o1.tm	Method	TBLASTX:Maize
Start	533	End	1001
GI	none	Score	120
Exons	533..1000, 552..788, 894..1001		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o1.tw	Method	TBLASTX:Wheat
Start	587	End	1069
GI	none	Score	153
Exons	587..1069, 591..1016		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o1.tc	Method	TBLASTX:Cress
Start	620	End	922
GI	none	Score	193
Exons	620..922		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o2.ts	Method	TBLASTX:Soybean
Start	1400	End	1645
GI	none	Score	82

Exons	1400..1645, 1443..1628		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o3.tm	Method	TBLASTX:Maize
Start	1400	End	1645
GI	none	Score	89
Exons	1400..1645, 1431..1628		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o2.tw	Method	TBLASTX:Wheat
Start	1404	End	1873
GI	none	Score	90
Exons	1404..1586, 1427..1594, 1430..1600, 1599..1856, 1607..1873		
Seq. No.	655	Seq. ID	OJ990513_01.9924.C24
Gene No.	1358	Strand	-
Start	1	End	2322
Name	OJ990513_01.9924.C24.o2.np	Method	AAT/NAP
Start	1832	End	2322
GI	3377854	Score	105
Exons	1832..2130, 2209..2322		
GI Descrip.	(AF076274) No definition line found [Arabidopsis thaliana]		
Seq. No.	656	Seq. ID	OJ990513_01.9924.C25
Gene No.	1359	Strand	-
Start	1	End	1868
Name	OJ990513_01.9924.C25.o1.np	Method	AAT/NAP
Start	1	End	1868
GI	6705984	Score	266
Exons	1..626, 1811..1868		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		
Seq. No.	656	Seq. ID	OJ990513_01.9924.C25
Gene No.	1359	Strand	-
Start	1	End	1868
Name	OJ990513_01.9924.C25.o1.ts	Method	TBLASTX:Soybean
Start	3	End	391
GI	none	Score	94
Exons	3..92, 95..391, 231..389		
Seq. No.	656	Seq. ID	OJ990513_01.9924.C25
Gene No.	1359	Strand	-
Start	1	End	1868
Name	OJ990513_01.9924.C25.o1.tw	Method	TBLASTX:Wheat
Start	12	End	395
GI	none	Score	35
Exons	12..95, 95..181, 201..263, 224..394, 318..395		
Seq. No.	656	Seq. ID	OJ990513_01.9924.C25
Gene No.	1359	Strand	-
Start	1	End	1868
Name	OJ990513_01.9924.C25.o1.gs	Method	GENSCAN
Start	41	End	808

GI	none	Score	.69
Exons	41..808		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o1.gp	Method	AAT/GAP
Start	678	End	2206
GI	61605_1.R1084	Score	567
Exons	678..782, 1938..2206		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-137 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o1.np	Method	AAT/NAP
Start	678	End	4944
GI	5852175	Score	140
Exons	678..733, 1305..1400, 2039..2072, 3106..3165, 4919..4944		
GI Descrip.	(AL117265) zhb0005.1 [Oryza sativa]		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o1.gs	Method	GENSCAN
Start	702	End	4909
GI	none	Score	.69
Exons	702..725, 2040..2072, 2269..3131, 3278..3419, 3494..3551, 3621..4160, 4289..4529, 4626..4909		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o2.np	Method	AAT/NAP
Start	2207	End	4862
GI	4680183	Score	2665
Exons	2207..3708, 4205..4246, 4332..4862		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o4.tw	Method	TBLASTX:Wheat
Start	2543	End	2945
GI	none	Score	254
Exons	2543..2647, 2544..2945		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o2.tw	Method	TBLASTX:Wheat
Start	3508	End	3965
GI	none	Score	130
Exons	3508..3684, 3727..3963, 3729..3965		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26

Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o2.tm	Method	TBLASTX:Maize
Start	3816	End	3994
GI	none	Score	180
Exons	3816..3941, 3817..3963, 3860..3994		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o1.tw	Method	TBLASTX:Wheat
Start	4196	End	4640
GI	none	Score	97
Exons	4196..4315, 4207..4284, 4317..4640, 4331..4639		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o1.tm	Method	TBLASTX:Maize
Start	4313	End	4670
GI	none	Score	364
Exons	4313..4660, 4317..4670		

Seq. No.	657	Seq. ID	OJ990513_01.9924.C26
Gene No.	1360	Strand	+
Start	678	End	4944
Name	OJ990513_01.9924.C26.o3.tw	Method	TBLASTX:Wheat
Start	4640	End	4906
GI	none	Score	269
Exons	4640..4906, 4641..4901		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1361	Strand	+
Start	1	End	3926
Name	OJ990513_01.9924.C27.o1.np	Method	AAT/NAP
Start	1	End	3926
GI	5902445	Score	2575
Exons	1..1745, 3898..3926		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1362	Strand	-
Start	2184	End	3858
Name	OJ990513_01.9924.C27.o1.gp	Method	AAT/GAP
Start	2184	End	3858
GI	2443099	Score	592
Exons	2184..2400, 3070..3136, 3825..3858		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1363	Strand	-
Start	4433	End	5101
Name	OJ990513_01.9924.C27.o2.tm	Method	TBLASTX:Maize
Start	69	End	278
GI	none	Score	240
Exons	69..278, 80..268		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27

Gene No.	1363	Strand	-
Start	4433	End	5101
Name	OJ990513_01.9924.C27.o1.tw	Method	TBLASTX:Wheat
Start	147	End	565
GI	none	Score	452
Exons	147..557, 149..565		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1363	Strand	-
Start	4433	End	5101
Name	OJ990513_01.9924.C27.o1.tm	Method	TBLASTX:Maize
Start	510	End	944
GI	none	Score	49
Exons	510..557, 555..755, 584..754, 776..907, 777..923, 918..944		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1363	Strand	-
Start	4433	End	5101
Name	OJ990513_01.9924.C27.o2.tw	Method	TBLASTX:Wheat
Start	599	End	1031
GI	none	Score	413
Exons	599..1030, 603..1031		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1363	Strand	-
Start	4433	End	5101
Name	OJ990513_01.9924.C27.o1.ts	Method	TBLASTX:Soybean
Start	1059	End	1447
GI	none	Score	247
Exons	1059..1445, 1067..1162, 1199..1447		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1363	Strand	-
Start	4433	End	5101
Name	OJ990513_01.9924.C27.o3.tw	Method	TBLASTX:Wheat
Start	1068	End	1499
GI	none	Score	383
Exons	1068..1499, 1073..1378		

Seq. No.	658	Seq. ID	OJ990513_01.9924.C27
Gene No.	1363	Strand	-
Start	4433	End	5101
Name	OJ990513_01.9924.C27.o2.gs	Method	GENSCAN
Start	4433	End	5101
GI	none	Score	.76
Exons	4433..4620, 4920..5101		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1364	Strand	+
Start	48	End	3732
Name	OJ990513_01.9924.C28.o1.gs	Method	GENSCAN
Start	48	End	3534
GI	none	Score	.59
Exons	48..110, 1106..1204, 2540..2648, 2955..3197, 3341..3534		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1364	Strand	+

Start	48	End	3732
Name	OJ990513_01.9924.C28.o1.np	Method	AAT/NAP
Start	2522	End	3732
GI	5902445	Score	1873
Exons	2522..3732		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1365	Strand	+
Start	9739	End	13519
Name	OJ990513_01.9924.C28.o5.np	Method	AAT/NAP
Start	9739	End	13519
GI	5042454	Score	192
Exons	9739..9812, 11218..11421, 11581..11871, 13333..13519		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1365	Strand	+
Start	9739	End	13519
Name	OJ990513_01.9924.C28.o3.gs	Method	GENSCAN
Start	10124	End	13037
GI	none	Score	.66
Exons	10124..10783, 10916..11304, 11357..11679, 11709..11940, 12674..12727, 12824..13037		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1365	Strand	+
Start	9739	End	13519
Name	OJ990513_01.9924.C28.o6.np	Method	AAT/NAP
Start	11928	End	13025
GI	4680186	Score	361
Exons	11928..11984, 12824..13025		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1366	Strand	-
Start	4169	End	11783
Name	OJ990513_01.9924.C28.o2.np	Method	AAT/NAP
Start	4064	End	6859
GI	6691716	Score	2185
Exons	4064..4489, 4564..4679, 4830..5090, 5169..5350, 5427..5527, 5610..5775, 5971..6859		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1366	Strand	-
Start	4169	End	11783
Name	OJ990513_01.9924.C28.o2.gs	Method	GENSCAN
Start	4169	End	9354
GI	none	Score	.72
Exons	4169..4668, 4741..4983, 5004..5090, 5169..5354, 5427..5510, 5716..5890, 5975..6178, 6692..6898, 9331..9354		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1366	Strand	-

Start	4169	End	11783
Name	OJ990513_01.9924.C28.o4.np	Method	AAT/NAP
Start	8461	End	11783
GI	6721512	Score	76
Exons	8461..8493, 9851..9882, 9925..10049, 10077..10189, 11756..11783		
GI Descrip.	(AP001072) hypothetical protein [Oryza sativa]		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1366	Strand	-
Start	4169	End	11783
Name	OJ990513_01.9924.C28.o3.np	Method	AAT/NAP
Start	9036	End	9405
GI	4417267	Score	87
Exons	9036..9209, 9327..9405		
GI Descrip.	(AC007019) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1367	Strand	-
Start	12576	End	12958
Name	OJ990513_01.9924.C28.o1.tm	Method	TBLASTX:Maize
Start	2602	End	2965
GI	none	Score	420
Exons	2602..2928, 2603..2926, 2918..2965		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1367	Strand	-
Start	12576	End	12958
Name	OJ990513_01.9924.C28.o1.tw	Method	TBLASTX:Wheat
Start	2608	End	2997
GI	none	Score	396
Exons	2608..2919, 2609..2995, 2810..2986, 2950..2997		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1367	Strand	-
Start	12576	End	12958
Name	OJ990513_01.9924.C28.o2.tw	Method	TBLASTX:Wheat
Start	3116	End	3720
GI	none	Score	182
Exons	3116..3319, 3130..3198, 3260..3304, 3318..3401, 3319..3600, 3586..3720		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1367	Strand	-
Start	12576	End	12958
Name	OJ990513_01.9924.C28.o2.tm	Method	TBLASTX:Maize
Start	3430	End	3684
GI	none	Score	154
Exons	3430..3603, 3477..3602, 3586..3684, 3588..3683		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1367	Strand	-
Start	12576	End	12958
Name	OJ990513_01.9924.C28.o3.tw	Method	TBLASTX:Wheat
Start	6449	End	6740
GI	none	Score	93
Exons	6449..6739, 6450..6740		

Seq. No.	659	Seq. ID	OJ990513_01.9924.C28
Gene No.	1367	Strand	-
Start	12576	End	12958
Name	OJ990513_01.9924.C28.o1.gp	Method	AAT/GAP
Start	12576	End	12958
GI	uC-osflcyp033a04b1	Score	664
Exons	12576..12958		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	660	Seq. ID	OJ990513_01.9924.C29
Gene No.	1368	Strand	+
Start	1	End	1715
Name	OJ990513_01.9924.C29.o1.np	Method	AAT/NAP
Start	1	End	1715
GI	5852180	Score	333
Exons	1..117, 217..287, 1267..1384, 1436..1715		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	660	Seq. ID	OJ990513_01.9924.C29
Gene No.	1369	Strand	-
Start	136	End	517
Name	OJ990513_01.9924.C29.o1.gp	Method	AAT/GAP
Start	136	End	517
GI	uC-osflcyp033a04b1	Score	667
Exons	136..517		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	660	Seq. ID	OJ990513_01.9924.C29
Gene No.	1370	Strand	-
Start	946	End	1521
Name	OJ990513_01.9924.C29.o2.gs	Method	GENSCAN
Start	946	End	1521
GI	none	Score	.87
Exons	946..1031, 1359..1521		

Seq. No.	661	Seq. ID	OJ990513_01.9924.C30
Gene No.	1371	Strand	+
Start	1	End	3612
Name	OJ990513_01.9924.C30.o1.np	Method	AAT/NAP
Start	1	End	3612
GI	4680183	Score	717
Exons	1..465, 1926..2534, 3002..3043, 3131..3316, 3545..3612		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	661	Seq. ID	OJ990513_01.9924.C30
Gene No.	1371	Strand	+
Start	1	End	3612
Name	OJ990513_01.9924.C30.o1.gs	Method	GENSCAN
Start	88	End	3345
GI	none	Score	.69
Exons	88..468, 561..586, 1094..1185, 1936..2128, 2396..2690, 2723..2859, 3028..3228, 3337..3345		

Seq. No.	661	Seq. ID	OJ990513_01.9924.C30
Gene No.	1371	Strand	+

Start	1	End	3612
Name	OJ990513_01.9924.C30.o3.tw	Method	TBLASTX:Wheat
Start	90	End	398
GI	none	Score	184
Exons	90..398		

Seq. No.	661	Seq. ID	OJ990513_01.9924.C30
Gene No.	1371	Strand	+
Start	1	End	3612
Name	OJ990513_01.9924.C30.o2.tw	Method	TBLASTX:Wheat
Start	2333	End	2790
GI	none	Score	138
Exons	2333..2515, 2341..2514, 2552..2644, 2554..2640, 2656..2790, 2715..2780		

Seq. No.	661	Seq. ID	OJ990513_01.9924.C30
Gene No.	1371	Strand	+
Start	1	End	3612
Name	OJ990513_01.9924.C30.o1.tw	Method	TBLASTX:Wheat
Start	2947	End	3311
GI	none	Score	384
Exons	2947..3306, 2961..3311		

Seq. No.	661	Seq. ID	OJ990513_01.9924.C30
Gene No.	1371	Strand	+
Start	1	End	3612
Name	OJ990513_01.9924.C30.o1.tm	Method	TBLASTX:Maize
Start	3112	End	3312
GI	none	Score	231
Exons	3112..3312, 3166..3306, 3174..3308		

Seq. No.	662	Seq. ID	OJ990513_01.9924.C31
Gene No.	1372	Strand	+
Start	830	End	5388
Name	OJ990513_01.9924.C31.o1.np	Method	AAT/NAP
Start	830	End	5388
GI	4680179	Score	764
Exons	830..1870, 5281..5388		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	662	Seq. ID	OJ990513_01.9924.C31
Gene No.	1372	Strand	+
Start	830	End	5388
Name	OJ990513_01.9924.C31.o1.gs	Method	GENSCAN
Start	880	End	1995
GI	none	Score	.77
Exons	880..1995		

Seq. No.	662	Seq. ID	OJ990513_01.9924.C31
Gene No.	1372	Strand	+
Start	830	End	5388
Name	OJ990513_01.9924.C31.o1.tw	Method	TBLASTX:Wheat
Start	1051	End	1398
GI	none	Score	276
Exons	1051..1398, 1051..1215, 1249..1389, 1257..1397		

Seq. No.	662	Seq. ID	OJ990513_01.9924.C31

Gene No.	1372	Strand	+
Start	830	End	5388
Name	OJ990513_01.9924.C31.o1.tm	Method	TBLASTX:Maize
Start	1279	End	1593
GI	none	Score	217
Exons	1279..1542, 1302..1466, 1507..1593		

Seq. No.	662	Seq. ID	OJ990513_01.9924.C31
Gene No.	1372	Strand	+
Start	830	End	5388
Name	OJ990513_01.9924.C31.o2.np	Method	AAT/NAP
Start	2871	End	4719
GI	6063554	Score	426
Exons	2871..3068, 3186..3406, 3878..3905, 4545..4719		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	662	Seq. ID	OJ990513_01.9924.C31
Gene No.	1372	Strand	+
Start	830	End	5388
Name	OJ990513_01.9924.C31.o1.gp	Method	AAT/GAP
Start	3372	End	4101
GI	101153_1.R1084	Score	426
Exons	3372..3407, 3878..4101		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-115 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1373	Strand	+
Start	1	End	3598
Name	OJ990513_01.9924.C32.o1.np	Method	AAT/NAP
Start	1	End	3598
GI	5852180	Score	568
Exons	1..64, 392..509, 561..972, 3526..3598		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1373	Strand	+
Start	1	End	3598
Name	OJ990513_01.9924.C32.o1.gs	Method	GENSCAN
Start	392	End	1006
GI	none	Score	.77
Exons	392..495, 561..1006		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1374	Strand	+
Start	5712	End	6803
Name	OJ990513_01.9924.C32.o4.np	Method	AAT/NAP
Start	5712	End	6803
GI	4680186	Score	324
Exons	5712..5765, 6603..6803		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1375	Strand	-
Start	1667	End	4409

Name	OJ990513_01.9924.C32.o2.np	Method	AAT/NAP
Start	1667	End	4409
GI	4680179	Score	2084
Exons	1667..1704, 2138..3290, 3324..4409		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o2.tw	Method	TBLASTX:Wheat
Start	1762	End	2151
GI	none	Score	182
Exons	1762..2151, 1826..2149		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o2.tm	Method	TBLASTX:Maize
Start	1858	End	2119
GI	none	Score	182
Exons	1858..2118, 1859..2119		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o1.tm	Method	TBLASTX:Maize
Start	2190	End	2621
GI	none	Score	65
Exons	2190..2621, 2197..2391, 2403..2582		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o1.tw	Method	TBLASTX:Wheat
Start	2244	End	2726
GI	none	Score	215
Exons	2244..2621, 2287..2622, 2676..2726		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o4.tw	Method	TBLASTX:Wheat
Start	2826	End	3263
GI	none	Score	69
Exons	2826..2867, 2895..3008, 2896..3009, 3054..3263, 3055..3207		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o4.tm	Method	TBLASTX:Maize
Start	2946	End	3299
GI	none	Score	184
Exons	2946..3299		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737

Name	OJ990513_01.9924.C32.o3.tm	Method	TBLASTX:Maize
Start	3627	End	3932
GI	none	Score	90
Exons	3627..3932, 3802..3918		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o3.tw	Method	TBLASTX:Wheat
Start	3813	End	4175
GI	none	Score	153
Exons	3813..4175, 3814..4173		

Seq. No.	663	Seq. ID	OJ990513_01.9924.C32
Gene No.	1376	Strand	-
Start	6354	End	6737
Name	OJ990513_01.9924.C32.o2.gp	Method	AAT/GAP
Start	6354	End	6737
GI	uC-osf1cyp033a04b1	Score	697
Exons	6354..6737		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	664	Seq. ID	OJ990513_01.9924.C33
Gene No.	1377	Strand	+
Start	495	End	632
Name	OJ990513_01.9924.C33.o1.gs	Method	GENSCAN
Start	495	End	632
GI	none	Score	.84
Exons	495..632		

Seq. No.	664	Seq. ID	OJ990513_01.9924.C33
Gene No.	1378	Strand	-
Start	421	End	779
Name	OJ990513_01.9924.C33.o1.np	Method	AAT/NAP
Start	421	End	779
GI	5852180	Score	228
Exons	421..779		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		

Seq. No.	665	Seq. ID	OJ990513_01.9924.C36
Gene No.	1379	Strand	+
Start	418	End	502
Name	OJ990513_01.9924.C36.o1.np	Method	AAT/NAP
Start	418	End	502
GI	6498441	Score	73
Exons	418..502		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	666	Seq. ID	OJ990513_01.9924.C38
Gene No.	1380	Strand	+
Start	374	End	704
Name	OJ990513_01.9924.C38.o1.gs	Method	GENSCAN
Start	374	End	704
GI	none	Score	.5

Exons	374..704		
Seq. No.	667	Seq. ID	OJ990513_01.9924.C39
Gene No.	1381	Strand	-
Start	1	End	774
Name	OJ990513_01.9924.C39.o1.np	Method	AAT/NAP
Start	1	End	774
GI	4206306	Score	179
Exons	1..64, 612..774		
GI Descrip.	(AF049110) prpol [Zea mays]		
Seq. No.	667	Seq. ID	OJ990513_01.9924.C39
Gene No.	1381	Strand	-
Start	1	End	774
Name	OJ990513_01.9924.C39.o1.gs	Method	GENSCAN
Start	126	End	698
GI	none	Score	.42
Exons	126..146, 696..698		
Seq. No.	667	Seq. ID	OJ990513_01.9924.C39
Gene No.	1381	Strand	-
Start	1	End	774
Name	OJ990513_01.9924.C39.o1.tm	Method	TBLASTX:Maize
Start	612	End	774
GI	none	Score	145
Exons	612..764, 616..762, 616..774		
Seq. No.	667	Seq. ID	OJ990513_01.9924.C39
Gene No.	1381	Strand	-
Start	1	End	774
Name	OJ990513_01.9924.C39.o1.tw	Method	TBLASTX:Wheat
Start	612	End	764
GI	none	Score	129
Exons	612..764, 613..750		
Seq. No.	668	Seq. ID	OJ990513_01.9924.C40
Gene No.	1382	Strand	+
Start	356	End	414
Name	OJ990513_01.9924.C40.o1.gs	Method	GENSCAN
Start	356	End	414
GI	none	Score	.63
Exons	356..414		
Seq. No.	669	Seq. ID	OJ990513_01.9924.C41
Gene No.	1383	Strand	+
Start	1	End	608
Name	OJ990513_01.9924.C41.o1.np	Method	AAT/NAP
Start	1	End	605
GI	5902444	Score	792
Exons	1..605		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		
Seq. No.	669	Seq. ID	OJ990513_01.9924.C41
Gene No.	1383	Strand	+
Start	1	End	608
Name	OJ990513_01.9924.C41.o1.tw	Method	TBLASTX:Wheat
Start	78	End	374

GI	none	Score	256
Exons	78..374, 116..358, 177..359		
Seq. No.	669	Seq. ID	OJ990513_01.9924.C41
Gene No.	1383	Strand	+
Start	1	End	608
Name	OJ990513_01.9924.C41.o1.gs	Method	GENSCAN
Start	90	End	608
GI	none	Score	.98
Exons	90..608		
Seq. No.	669	Seq. ID	OJ990513_01.9924.C41
Gene No.	1383	Strand	+
Start	1	End	608
Name	OJ990513_01.9924.C41.o1.tm	Method	TBLASTX:Maize
Start	248	End	426
GI	none	Score	180
Exons	248..373, 249..395, 249..425, 292..426		
Seq. No.	670	Seq. ID	OJ990513_01.9924.C42
Gene No.	1384	Strand	+
Start	1	End	485
Name	OJ990513_01.9924.C42.o1.np	Method	AAT/NAP
Start	1	End	384
GI	5852180	Score	297
Exons	1..384		
GI Descrip.	(AL117265) zhb00010.1 [Oryza sativa]		
Seq. No.	670	Seq. ID	OJ990513_01.9924.C42
Gene No.	1384	Strand	+
Start	1	End	485
Name	OJ990513_01.9924.C42.o1.gs	Method	GENSCAN
Start	71	End	485
GI	none	Score	1
Exons	71..485		
Seq. No.	671	Seq. ID	OJ990513_01.9924.C44
Gene No.	1385	Strand	
Start	232	End	634
Name	OJ990513_01.9924.C44.o1.tw	Method	TBLASTX:Wheat
Start	232	End	634
GI	none	Score	235
Exons	232..411, 308..634, 461..517		
Seq. No.	672	Seq. ID	OJ990513_01.9924.C45
Gene No.	1386	Strand	+
Start	453	End	666
Name	OJ990513_01.9924.C45.o1.gs	Method	GENSCAN
Start	453	End	666
GI	none	Score	.46
Exons	453..666		
Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1387	Strand	+
Start	1	End	4023
Name	OJ990513_01.9924.C46.o1.np	Method	AAT/NAP
Start	1	End	942

GI	6705984	Score	1259
Exons	1..942		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1387	Strand	+
Start	1	End	4023
Name	OJ990513_01.9924.C46.o1.gs	Method	GENSCAN
Start	214	End	4023
GI	none	Score	.43
Exons	214..448, 563..688, 748..1062, 1123..1386, 2106..2415, 2473..2634, 3657..3832, 3920..4023		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1388	Strand	-
Start	2379	End	4094
Name	OJ990513_01.9924.C46.o2.tw	Method	TBLASTX:Wheat
Start	1	End	325
GI	none	Score	145
Exons	1..267, 1..324, 2..325		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1388	Strand	-
Start	2379	End	4094
Name	OJ990513_01.9924.C46.o1.tc	Method	TBLASTX:Cress
Start	2	End	154
GI	none	Score	221
Exons	2..154, 13..153		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1388	Strand	-
Start	2379	End	4094
Name	OJ990513_01.9924.C46.o1.tm	Method	TBLASTX:Maize
Start	19	End	517
GI	none	Score	90
Exons	19..93, 20..100, 109..315, 113..517, 427..516		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1388	Strand	-
Start	2379	End	4094
Name	OJ990513_01.9924.C46.o1.ts	Method	TBLASTX:Soybean
Start	20	End	289
GI	none	Score	81
Exons	20..94, 38..79, 106..168, 107..289		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1388	Strand	-
Start	2379	End	4094
Name	OJ990513_01.9924.C46.o1.tw	Method	TBLASTX:Wheat
Start	356	End	739
GI	none	Score	358
Exons	356..739, 358..639		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1388	Strand	-
Start	2379	End	4094
Name	OJ990513_01.9924.C46.o2.tm	Method	TBLASTX:Maize

Start	674	End	918
GI	none	Score	104
Exons	674..739, 688..738, 738..917, 739..918		

Seq. No.	673	Seq. ID	OJ990513_01.9924.C46
Gene No.	1388	Strand	-
Start	2379	End	4094
Name	OJ990513_01.9924.C46.o2.np	Method	AAT/NAP
Start	2379	End	4094
GI	5902444	Score	497
Exons	2379..2550, 3583..4094		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	674	Seq. ID	OJ990513_01.9924.C47
Gene No.	1389	Strand	+
Start	356	End	2314
Name	OJ990513_01.9924.C47.o2.np	Method	AAT/NAP
Start	356	End	2314
GI	6063554	Score	81
Exons	356..395, 1878..2050, 2161..2314		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	674	Seq. ID	OJ990513_01.9924.C47
Gene No.	1390	Strand	-
Start	1	End	640
Name	OJ990513_01.9924.C47.o1.np	Method	AAT/NAP
Start	1	End	640
GI	5902444	Score	754
Exons	1..640		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	675	Seq. ID	OJ990513_01.9924.C48
Gene No.	1391	Strand	-
Start	878	End	2172
Name	OJ990513_01.9924.C48.o1.np	Method	AAT/NAP
Start	878	End	2172
GI	6056376	Score	81
Exons	878..931, 2027..2172		
GI Descrip.	(AC009894) Similar to serine/threonine kinases [Arabidopsis thaliana]		

Seq. No.	676	Seq. ID	OJ990513_01.9924.C50
Gene No.	1392	Strand	-
Start	223	End	461
Name	OJ990513_01.9924.C50.o1.gs	Method	GENSCAN
Start	223	End	456
GI	none	Score	.65
Exons	223..456		

Seq. No.	676	Seq. ID	OJ990513_01.9924.C50
Gene No.	1392	Strand	-
Start	223	End	461
Name	OJ990513_01.9924.C50.o1.np	Method	AAT/NAP
Start	226	End	461
GI	6691716	Score	252

Exons	226..461		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		
Seq. No.	677	Seq. ID	OJ990513_01.9924.C51
Gene No.	1393	Strand	-
Start	120	End	314
Name	OJ990513_01.9924.C51.o1.gs	Method	GENSCAN
Start	120	End	314
GI	none	Score	.59
Exons	120..314		
Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1394	Strand	+
Start	1	End	4810
Name	OJ990423_08.9924.C1.o1.np	Method	AAT/NAP
Start	1	End	4810
GI	4206306	Score	1766
Exons	1..2122, 4731..4810		
GI Descrip.	(AF049110) prpol [Zea mays]		
Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1394	Strand	+
Start	1	End	4810
Name	OJ990423_08.9924.C1.o1.gs	Method	GENSCAN
Start	106	End	2144
GI	none	Score	.43
Exons	106..953, 1157..1343, 1585..2144		
Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1395	Strand	-
Start	2385	End	7683
Name	OJ990423_08.9924.C1.o2.gs	Method	GENSCAN
Start	2385	End	7683
GI	none	Score	.43
Exons	2385..3106, 3219..3398, 5845..5961, 6055..7071, 7536..7683		
Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o5.tw	Method	TBLASTX:Wheat
Start	201	End	539
GI	none	Score	65
Exons	201..311, 318..539		
Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o1.tw	Method	TBLASTX:Wheat
Start	762	End	1201
GI	none	Score	175
Exons	762..998, 995..1201, 1000..1200		
Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242

Name	OJ990423_08.9924.C1.o2.tm	Method	TBLASTX:Maize
Start	941	End	1231
GI	none	Score	69
Exons	941..997, 942..998, 991..1230, 992..1231, 995..1231		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o4.tm	Method	TBLASTX:Maize
Start	1259	End	1619
GI	none	Score	241
Exons	1259..1498, 1300..1491, 1502..1609, 1502..1606, 1503..1619		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o2.tw	Method	TBLASTX:Wheat
Start	1316	End	1715
GI	none	Score	200
Exons	1316..1498, 1321..1491, 1503..1715, 1508..1606		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o3.ts	Method	TBLASTX:Soybean
Start	1394	End	1727
GI	none	Score	126
Exons	1394..1489, 1399..1491, 1476..1727		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o6.tw	Method	TBLASTX:Wheat
Start	1790	End	2030
GI	none	Score	216
Exons	1790..1933, 1797..2030		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o3.gs	Method	GENSCAN
Start	7915	End	11970
GI	none	Score	.67
Exons	7915..8033, 8476..8515, 8908..9420, 9930..10369, 10458..10686, 10802..10967, 11087..11155, 11631..11777, 11891..11970		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o1.tm	Method	TBLASTX:Maize
Start	8977	End	9437
GI	none	Score	262
Exons	8977..9393, 8978..9394, 9245..9397, 9258..9437, 9259..9399		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242

Name	OJ990423_08.9924.C1.o3.tm	Method	TBLASTX:Maize
Start	9835	End	16907
GI	none	Score	211
Exons	9835..10035, 9838..9987, 9840..10034, 10075..10107, 10108..10173, 10174..10233, 10176..10235, 10236..10265, 12708..12905, 12709..12846, 12711..12905, 12943..12981, 12981..13106, 12982..13110, 16515..16727, 16525..16680, 16533..16715, 16782..16907, 16782..16874		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o2.np	Method	AAT/NAP
Start	9837	End	18236
GI	3426064	Score	867
Exons	9837..10048, 16706..17043, 17144..17367, 17452..17653, 17891..18063, 18157..18236		
GI Descrip.	(AJ007588) monooxygenase [Arabidopsis thaliana] gi|4467141|emb|CAB37510| (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o1.tc	Method	TBLASTX:Cress
Start	9843	End	18066
GI	none	Score	80
Exons	9843..10052, 9898..10017, 10096..10173, 10477..10704, 10487..10687, 10799..10969, 10800..10958, 10823..10960, 11645..11779, 11670..11780, 12708..12917, 12805..12831, 12945..13175, 12949..13101, 13195..13269, 13366..13578, 13367..13588, 13649..13810, 14627..14803, 14694..14804, 16524..16721, 16528..16677, 16776..16874, 17116..17370, 17159..17368, 17449..17607, 17910..18065, 17956..18066		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o2.ts	Method	TBLASTX:Soybean
Start	9843	End	16874
GI	none	Score	131
Exons	9843..9953, 10096..10173, 10176..10274, 12705..12818, 12912..13145, 12931..13146, 16524..16631, 16776..16874		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o1.ts	Method	TBLASTX:Soybean
Start	10465	End	17493
GI	none	Score	170
Exons	10465..10704, 10469..10687, 10799..10843, 13354..13578, 13367..13459, 13478..13582, 13649..13693, 17146..17370, 17150..17251, 17270..17368, 17449..17493		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242

Name	OJ990423_08.9924.C1.o6.tm	Method	TBLASTX:Maize
Start	10486	End	17379
GI	none	Score	152
Exons	10486..10689, 10487..10687, 10516..10689, 10569..10727, 13368..13493, 13370..13576, 13372..13578, 13394..13579, 17125..17379, 17162..17368		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o1.gp	Method	AAT/GAP
Start	10504	End	12040
GI	4715556	Score	1291
Exons	10504..10686, 10802..10967, 11087..11155, 11631..11777, 11891..12040		
GI Descrip.	3426064/emb|CAA07575.1| 7.0e-18 (AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o3.tw	Method	TBLASTX:Wheat
Start	10622	End	17620
GI	none	Score	91
Exons	10622..10687, 10624..10689, 10624..10686, 10794..10970, 10799..10969, 13513..13575, 13514..13576, 13649..13822, 13650..13820, 17305..17367, 17306..17401, 17449..17616, 17450..17620		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o4.tw	Method	TBLASTX:Wheat
Start	11076	End	18200
GI	none	Score	55
Exons	11076..11156, 11087..11158, 11089..11148, 11096..11158, 11629..11700, 11630..11779, 11667..11780, 11752..11784, 14621..14803, 14679..14804, 14688..14804, 14884..14943, 17768..17845, 17772..17837, 17892..18065, 17941..18066, 18156..18200		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o5.tm	Method	TBLASTX:Maize
Start	11614	End	18066
GI	none	Score	87
Exons	11614..11700, 11615..11692, 11618..11779, 11619..11780, 11752..11799, 14636..14803, 14654..14803, 14682..14837, 14688..14804, 14884..14943, 17928..18065, 17944..18066		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o4.gs	Method	GENSCAN
Start	12687	End	14970

GI	none	Score	.79
Exons	12687..13240, 13347..13600, 13900..13968, 14655..14801, 14885..14970		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o2.gp	Method	AAT/GAP
Start	12779	End	13135
GI	71705_1.R1084	Score	669
Exons	12779..13135		
GI Descrip.	'3426064/emb|CAA07575.1| 1.0e-18 (AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]'		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o3.gp	Method	AAT/GAP
Start	13678	End	15026
GI	25992_1.R1084	Score	887
Exons	13678..13817, 13900..13968, 14655..14801, 14885..15026		
GI Descrip.	'3426064/emb|CAA07575.1| 7.0e-18 (AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]'		

Seq. No.	678	Seq. ID	OJ990423_08.9924.C1
Gene No.	1396	Strand	-
Start	7915	End	18242
Name	OJ990423_08.9924.C1.o5.gs	Method	GENSCAN
Start	16521	End	18242
GI	none	Score	.79
Exons	16521..17047, 17139..17367, 17452..17617, 17766..17834, 17887..18063, 18157..18242		

Seq. No.	679	Seq. ID	OJ990423_08.9924.C2
Gene No.	1397	Strand	-
Start	1	End	1031
Name	OJ990423_08.9924.C2.o1.np	Method	AAT/NAP
Start	1	End	1031
GI	6006359	Score	74
Exons	1..36, 661..780, 992..1031		
GI Descrip.	(AP000559) hypothetical protein [Oryza sativa]		

Seq. No.	679	Seq. ID	OJ990423_08.9924.C2
Gene No.	1397	Strand	-
Start	1	End	1031
Name	OJ990423_08.9924.C2.o1.gs	Method	GENSCAN
Start	602	End	832
GI	none	Score	.44
Exons	602..832		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o1.tm	Method	TBLASTX:Maize
Start	2982	End	3348

GI	none	Score	115
Exons	2982..3302, 2992..3165, 3000..3182, 3252..3347, 3252..3344, 3292..3348		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o1.np	Method	AAT/NAP
Start	2985	End	6013
GI	3426064	Score	791
Exons	2985..3505, 3598..3826, 3904..4112, 5559..5723, 5934..6013		
GI Descrip.	(AJ007588) monooxygenase [Arabidopsis thaliana] gi|4467141|emb|CAB37510| (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o2.gs	Method	GENSCAN
Start	2988	End	6034
GI	none	Score	.95
Exons	2988..3505, 3598..3826, 3904..4102, 4158..4226, 5577..5723, 5934..6034		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o1.tc	Method	TBLASTX:Cress
Start	2991	End	6005
GI	none	Score	69
Exons	2991..3188, 2995..3162, 3165..3344, 3289..3345, 3602..3835, 3618..3833, 3901..4059, 5579..5725, 5616..5726, 5925..6005		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o2.ts	Method	TBLASTX:Soybean
Start	2991	End	3420
GI	none	Score	69
Exons	2991..3077, 3171..3344, 3286..3420		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o1.ts	Method	TBLASTX:Soybean
Start	3605	End	3945
GI	none	Score	111
Exons	3605..3835, 3609..3710, 3614..3829, 3729..3833, 3901..3945		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o2.tm	Method	TBLASTX:Maize
Start	3621	End	3856
GI	none	Score	143
Exons	3621..3827, 3623..3856		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o1.tw	Method	TBLASTX:Wheat
Start	3764	End	4072
GI	none	Score	71
Exons	3764..3835, 3765..3866, 3901..4068, 3902..4072		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o3.tm	Method	TBLASTX:Maize
Start	3955	End	5999
GI	none	Score	147
Exons	3955..4068, 3983..4072, 5588..5725, 5604..5726, 5934..5999		

Seq. No.	680	Seq. ID	OJ990423_08.9924.C3
Gene No.	1398	Strand	-
Start	2988	End	6034
Name	OJ990423_08.9924.C3.o2.tw	Method	TBLASTX:Wheat
Start	4160	End	5987
GI	none	Score	151
Exons	4160..4234, 5588..5725, 5601..5726, 5934..5987		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1399	Strand	+
Start	61	End	2762
Name	OJ990423_08.9924.C4.o1.gp	Method	AAT/GAP
Start	61	End	421
GI	5004678	Score	629
Exons	61..421		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1399	Strand	+
Start	61	End	2762
Name	OJ990423_08.9924.C4.o1.gs	Method	GENSCAN
Start	140	End	2762
GI	none	Score	.4
Exons	140..214, 1338..1508, 2745..2762		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1400	Strand	+
Start	4737	End	10003
Name	OJ990423_08.9924.C4.o1.np	Method	AAT/NAP
Start	4737	End	10003
GI	5295971	Score	3012
Exons	4737..4932, 5206..5393, 5618..10003		
GI Descrip.	(AB026295) EST D24315(R1718) corresponds to a region of the predicted gene.; Similar to Tobacco DNA for retroviral-like transposon Tnt 1-94.(X13777) [Oryza sativa]		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1400	Strand	+
Start	4737	End	10003
Name	OJ990423_08.9924.C4.o3.gs	Method	GENSCAN
Start	5697	End	9997
GI	none	Score	.56

Exons	5697..7300, 7348..9997		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1401	Strand	-
Start	4530	End	5353
Name	OJ990423_08.9924.C4.o2.gs	Method	GENSCAN
Start	4530	End	5353
GI	none	Score	.97
Exons	4530..5047, 5129..5264, 5318..5353		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o5.tm	Method	TBLASTX:Maize
Start	4524	End	4889
GI	none	Score	112
Exons	4524..4712, 4534..4707, 4542..4724, 4794..4889, 4794..4871		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o3.tc	Method	TBLASTX:Cress
Start	4533	End	12654
GI	none	Score	62
Exons	4533..4712, 4776..4886, 4831..4887, 10466..10636, 10468..10644, 11499..11657, 12507..12653, 12544..12654		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o4.ts	Method	TBLASTX:Soybean
Start	5136	End	10644
GI	none	Score	61
Exons	5136..5192, 5140..5199, 10468..10644, 10469..10519, 10538..10636		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o9.tm	Method	TBLASTX:Maize
Start	5154	End	10644
GI	none	Score	111
Exons	5154..5201, 10468..10644, 10469..10636		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o8.tm	Method	TBLASTX:Maize
Start	5599	End	5977
GI	none	Score	47
Exons	5599..5709, 5641..5667, 5739..5975, 5765..5977		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o4.tw	Method	TBLASTX:Wheat
Start	5871	End	6266
GI	none	Score	235

Exons	5871..6266, 5973..6209		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o4.tm	Method	TBLASTX:Maize
Start	5991	End	6380
GI	none	Score	200
Exons	5991..6194, 5996..6190, 6206..6262, 6207..6317, 6297..6380		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o7.tm	Method	TBLASTX:Maize
Start	6797	End	7208
GI	none	Score	188
Exons	6797..6973, 6798..7016, 7077..7208		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o5.tw	Method	TBLASTX:Wheat
Start	6818	End	7247
GI	none	Score	169
Exons	6818..7021, 6819..7064, 7080..7187, 7188..7247		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o5.ts	Method	TBLASTX:Soybean
Start	7256	End	7540
GI	none	Score	184
Exons	7256..7540		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o1.tw	Method	TBLASTX:Wheat
Start	7361	End	7906
GI	none	Score	338
Exons	7361..7807, 7561..7800, 7811..7906		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o2.tm	Method	TBLASTX:Maize
Start	7553	End	7978
GI	none	Score	384
Exons	7553..7894, 7561..7884, 7907..7978		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o2.ts	Method	TBLASTX:Soybean
Start	7580	End	8056
GI	none	Score	399
Exons	7580..8056, 7588..7881		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o2.tc	Method	TBLASTX:Cress
Start	7595	End	8044
GI	none	Score	287
Exons	7595..8044, 7597..7680, 7705..7878, 7907..8041		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o3.ts	Method	TBLASTX:Soybean
Start	8468	End	8956
GI	5509260	Score	362
Exons	8468..8956, 8533..8706, 8791..8928		
GI Descrip.	-		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o3.tm	Method	TBLASTX:Maize
Start	8486	End	8800
GI	none	Score	318
Exons	8486..8800, 8504..8785		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o4.tc	Method	TBLASTX:Cress
Start	8575	End	8839
GI	none	Score	224
Exons	8575..8706, 8576..8839		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o2.tw	Method	TBLASTX:Wheat
Start	8620	End	9175
GI	none	Score	253
Exons	8620..8706, 8621..8965, 8621..8968, 8951..9175		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o6.tm	Method	TBLASTX:Maize
Start	9002	End	9265
GI	none	Score	245
Exons	9002..9265, 9002..9244, 9004..9264		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o1.tm	Method	TBLASTX:Maize
Start	9269	End	9721
GI	none	Score	425
Exons	9269..9721, 9304..9648, 9521..9700		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o1.tc	Method	TBLASTX:Cress
Start	9307	End	9970
GI	none	Score	274
Exons	9307..9576, 9308..9601, 9605..9721, 9719..9970, 9761..9913, 9772..9918		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o1.ts	Method	TBLASTX:Soybean
Start	9329	End	9979
GI	none	Score	151
Exons	9329..9490, 9358..9495, 9503..9979, 9790..9918		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o3.tw	Method	TBLASTX:Wheat
Start	9497	End	9940
GI	none	Score	146
Exons	9497..9724, 9746..9940, 9772..9939		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o10.tm	Method	TBLASTX:Maize
Start	9727	End	9946
GI	none	Score	186
Exons	9727..9918, 9728..9946		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o4.gs	Method	GENSCAN
Start	10456	End	12907
GI	none	Score	.7
Exons	10456..10635, 11502..11667, 11744..11812, 12505..12651, 12801..12907		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o6.tw	Method	TBLASTX:Wheat
Start	10572	End	11670
GI	none	Score	81
Exons	10572..10622, 10573..10644, 10574..10636, 11499..11666, 11500..11670		

Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o11.tm	Method	TBLASTX:Maize
Start	11553	End	12654

GI	none	Score	162
Exons	11553..11666, 12516..12653, 12532..12654		
Seq. No.	681	Seq. ID	OJ990423_08.9924.C4
Gene No.	1402	Strand	-
Start	10456	End	12907
Name	OJ990423_08.9924.C4.o7.tw	Method	TBLASTX:Wheat
Start	11746	End	12654
GI	none	Score	157
Exons	11746..11814, 12516..12653, 12529..12654		
Seq. No.	682	Seq. ID	OJ990423_08.9924.C5
Gene No.	1403	Strand	+
Start	2849	End	3412
Name	OJ990423_08.9924.C5.o1.gs	Method	GENSCAN
Start	2849	End	3412
GI	none	Score	.81
Exons	2849..3412		
Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1404	Strand	+
Start	423	End	6878
Name	OJ990423_08.9924.C6.o1.np	Method	AAT/NAP
Start	423	End	6635
GI	3757522	Score	815
Exons	423..497, 593..649, 842..897, 2123..2336, 2497..2625, 2661..2735, 2838..2921, 3117..3194, 4607..4870, 5006..5094, 6396..6510, 6591..6635		
GI Descrip.	(AC005167) putative splicing factor [Arabidopsis thaliana]		
Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1404	Strand	+
Start	423	End	6878
Name	OJ990423_08.9924.C6.o1.gs	Method	GENSCAN
Start	425	End	6534
GI	none	Score	.79
Exons	425..497, 842..897, 2123..2336, 2838..2921, 3555..3619, 4651..4870, 5006..5094, 5562..5674, 5679..5863, 5872..6071, 6396..6534		
Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1404	Strand	+
Start	423	End	6878
Name	OJ990423_08.9924.C6.o1.gp	Method	AAT/GAP
Start	6472	End	6878
GI	3759173	Score	586
Exons	6472..6510, 6591..6878		
Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o1.tm	Method	TBLASTX:Maize
Start	408	End	2583
GI	none	Score	108
Exons	408..497, 423..500, 590..649, 592..651, 838..897, 839..901, 842..898, 849..899, 2111..2338, 2115..2339, 2482..2583		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o1.ts	Method	TBLASTX:Soybean
Start	408	End	2339
GI	none	Score	110
Exons	408..500, 426..500, 590..649, 598..663, 841..900, 842..898, 2106..2240, 2123..2242, 2124..2246, 2280..2339, 2282..2320		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o3.tm	Method	TBLASTX:Maize
Start	2645	End	6623
GI	none	Score	92
Exons	2645..2737, 2659..2721, 2660..2734, 2661..2741, 2835..2876, 2837..2923, 3554..3625, 3555..3617, 4564..4596, 4690..4779, 4691..4780, 4698..4802, 4765..4815, 4787..4870, 4821..4880, 4822..4869, 4829..4882, 4997..5092, 4999..5094, 5000..5095, 5013..5093, 6393..6509, 6393..6509, 6394..6510, 6591..6623		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o4.tm	Method	TBLASTX:Maize
Start	4181	End	4409
GI	none	Score	193
Exons	4181..4345, 4182..4346, 4207..4359, 4361..4408, 4362..4409		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o5.tm	Method	TBLASTX:Maize
Start	7038	End	7329
GI	none	Score	111
Exons	7038..7184, 7039..7182, 7040..7183, 7302..7328, 7303..7329		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o2.gs	Method	GENSCAN
Start	7040	End	15469
GI	none	Score	.88
Exons	7040..7182, 7301..7429, 7984..8127, 8887..9012, 9346..9471, 9809..9901, 9988..10117, 10198..10323, 10427..10534, 10898..11077, 11224..11358, 11694..11906, 12560..12648, 12815..12964, 13050..13203, 13290..13511, 14205..14318, 14633..14797, 14891..14981, 15244..15469		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o3.ts	Method	TBLASTX:Soybean
Start	7043	End	8128
GI	none	Score	87
Exons	7043..7183, 7302..7430, 7309..7431, 7974..8099, 7982..8128		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o2.np	Method	AAT/NAP
Start	7052	End	15513
GI	5541717	Score	1889
Exons	7052..7182, 7301..7429, 7984..8127, 8887..9012, 9346..9471, 9809..9901, 9988..10550, 10908..11077, 11224..11358, 11694..11906, 12560..12648, 12815..12960, 13046..13186, 13287..13511, 14133..14317, 14674..14797, 14891..15005, 15314..15513		
GI Descrip.	(AL049655) kinesin-like protein [Arabidopsis thaliana]		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o6.tm	Method	TBLASTX:Maize
Start	9962	End	10303
GI	none	Score	153
Exons	9962..10120, 9975..10118, 9976..10119, 10226..10303, 10228..10302		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o2.tm	Method	TBLASTX:Maize
Start	11720	End	12646
GI	none	Score	38
Exons	11720..11905, 11721..11909, 11778..11828, 11824..11907, 12550..12615, 12560..12646, 12563..12640, 12564..12641		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o7.tm	Method	TBLASTX:Maize
Start	12855	End	13123
GI	none	Score	88
Exons	12855..12956, 12879..12965, 12880..12966, 13027..13116, 13046..13123, 13058..13117		

Seq. No.	683	Seq. ID	OJ990423_08.9924.C6
Gene No.	1405	Strand	-
Start	7040	End	15513
Name	OJ990423_08.9924.C6.o2.ts	Method	TBLASTX:Soybean
Start	13287	End	13512
GI	none	Score	159
Exons	13287..13511, 13288..13512		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1406	Strand	+
Start	13554	End	17613
Name	OJ990423_08.9924.C7.o2.gs	Method	GENSCAN
Start	13554	End	17613
GI	none	Score	.83
Exons	13554..13782, 14055..14155, 15398..15499, 17458..17613		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7

Gene No.	1407	Strand	-
Start	1645	End	12155
Name	OJ990423_08.9924.C7.o1.gp	Method	AAT/GAP
Start	1156	End	1635
GI	17795_1.R1084	Score	908
Exons	1156..1635		
GI Descrip.	'3426064/emb|CAA07575.1| 7.0e-18 (AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]'		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1407	Strand	-
Start	1645	End	12155
Name	OJ990423_08.9924.C7.o1.gs	Method	GENSCAN
Start	1645	End	12155
GI	none	Score	.81
Exons	1645..1715, 1956..2059, 2289..2590, 2672..2805, 2891..3096, 3436..3590, 3806..3954, 4120..4265, 4722..5379, 5453..5530, 5775..6062, 7247..7308, 8366..8421, 9234..9290, 9990..10140, 10511..10559, 10645..10738, 10852..10918, 11035..11135, 11397..11476, 11606..12155		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1407	Strand	-
Start	1645	End	12155
Name	OJ990423_08.9924.C7.o2.gp	Method	AAT/GAP
Start	1979	End	2707
GI	28299_1.R1084	Score	783
Exons	1979..2058, 2287..2590, 2672..2707		
GI Descrip.	'1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence'		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1407	Strand	-
Start	1645	End	12155
Name	OJ990423_08.9924.C7.o3.gp	Method	AAT/GAP
Start	2877	End	3589
GI	none	Score	668
Exons	2877..3096, 3436..3589		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1407	Strand	-
Start	1645	End	12155
Name	OJ990423_08.9924.C7.o4.gp	Method	AAT/GAP
Start	7365	End	7594
GI	5005358	Score	392
Exons	7365..7594		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1407	Strand	-
Start	1645	End	12155
Name	OJ990423_08.9924.C7.o1.np	Method	AAT/NAP
Start	7829	End	10076
GI	3402691	Score	190
Exons	7829..7886, 8366..8421, 9234..9290, 9990..10076		
GI Descrip.	(AC004697) unknown protein [Arabidopsis thaliana]		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1407	Strand	-
Start	1645	End	12155
Name	OJ990423_08.9924.C7.o2.np	Method	AAT/NAP
Start	10510	End	12143
GI	3402689	Score	578
Exons	10510..10559, 10645..10738, 10852..10918, 11035..11135, 11397..11476, 11606..12143		
GI Descrip.	(AC004697) unknown protein [Arabidopsis thaliana]		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o1.tm	Method	TBLASTX:Maize
Start	1578	End	3614
GI	none	Score	95
Exons	1578..1604, 1641..1718, 1942..2058, 1956..2060, 1957..2061, 2284..2373, 2286..2375, 2286..2375, 2288..2377, 2330..2593, 2362..2574, 2382..2585, 2660..2833, 2669..2806, 2673..2807, 2673..2906, 2674..2808, 2892..3098, 2892..3098, 2893..3108, 3435..3614, 3436..3570		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o1.ts	Method	TBLASTX:Soybean
Start	2670	End	3593
GI	none	Score	101
Exons	2670..2807, 2672..2803, 2847..2948, 2893..2934, 2973..3098, 3058..3108, 3435..3593, 3436..3591		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o4.tm	Method	TBLASTX:Maize
Start	3671	End	3798
GI	none	Score	166
Exons	3671..3796, 3680..3784, 3681..3797, 3682..3798		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o5.tm	Method	TBLASTX:Maize
Start	4184	End	4867
GI	none	Score	92
Exons	4184..4270, 4187..4270, 4188..4271, 4688..4867, 4689..4787, 4690..4833		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o2.tm	Method	TBLASTX:Maize
Start	4868	End	5531
GI	none	Score	71
Exons	4868..5050, 4869..4928, 4873..5061, 4874..5050, 5162..5365, 5226..5363, 5228..5365, 5449..5529, 5454..5525, 5457..5531		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o1.tc	Method	TBLASTX:Cress
Start	9996	End	11456
GI	none	Score	90
Exons	9996..10139, 10024..10140, 10508..10561, 10510..10572, 10637..10738, 10638..10736, 10852..10899, 11034..11135, 11035..11136, 11037..11138, 11397..11456		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o3.tm	Method	TBLASTX:Maize
Start	15187	End	16107
GI	none	Score	172
Exons	15187..15324, 15206..15325, 15206..15325, 15395..15511, 15398..15502, 15889..16065, 15911..16105, 15928..16107, 15930..16106		

Seq. No.	684	Seq. ID	OJ990423_08.9924.C7
Gene No.	1408	Strand	-
Start	18525	End	21534
Name	OJ990423_08.9924.C7.o3.gs	Method	GENSCAN
Start	18525	End	21534
GI	none	Score	.61
Exons	18525..18649, 20213..20380, 20478..20598, 20635..20997, 21267..21534		

Seq. No.	685	Seq. ID	OJ990423_08.9924.C8
Gene No.	1409	Strand	-
Start	1	End	2980
Name	OJ990423_08.9924.C8.o1.np	Method	AAT/NAP
Start	1	End	2668
GI	5441880	Score	883
Exons	1..21, 611..907, 1169..1218, 1660..2668		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	685	Seq. ID	OJ990423_08.9924.C8
Gene No.	1409	Strand	-
Start	1	End	2980
Name	OJ990423_08.9924.C8.o1.gs	Method	GENSCAN
Start	455	End	2980
GI	none	Score	.48
Exons	455..705, 823..1550, 1713..2915, 2961..2980		

Seq. No.	685	Seq. ID	OJ990423_08.9924.C8
Gene No.	1409	Strand	-
Start	1	End	2980
Name	OJ990423_08.9924.C8.o1.tw	Method	TBLASTX:Wheat
Start	1421	End	1808
GI	none	Score	66
Exons	1421..1618, 1498..1581, 1517..1606, 1563..1610, 1631..1807, 1658..1807, 1659..1808		

Seq. No.	685	Seq. ID	OJ990423_08.9924.C8
Gene No.	1409	Strand	-
Start	1	End	2980
Name	OJ990423_08.9924.C8.o1.tm	Method	TBLASTX:Maize
Start	1517	End	2099
GI	none	Score	44
Exons	1517..1597, 1569..1595, 1637..1945, 1641..1946, 1946..2098, 1977..2099		

Seq. No.	686	Seq. ID	OJ990423_08.9924.C9
Gene No.	1410	Strand	+
Start	468	End	1870
Name	OJ990423_08.9924.C9.o1.gs	Method	GENSCAN
Start	468	End	1690
GI	none	Score	.68
Exons	468..928, 948..1432, 1674..1690		

Seq. No.	686	Seq. ID	OJ990423_08.9924.C9
Gene No.	1410	Strand	+
Start	468	End	1870
Name	OJ990423_08.9924.C9.o1.np	Method	AAT/NAP
Start	498	End	1870
GI	4678345	Score	719
Exons	498..1111, 1138..1432, 1519..1597, 1674..1743, 1839..1870		
GI Descrip.	(AL049659) putative zinc finger protein [Arabidopsis thaliana]		

Seq. No.	686	Seq. ID	OJ990423_08.9924.C9
Gene No.	1410	Strand	+
Start	468	End	1870
Name	OJ990423_08.9924.C9.o1.ts	Method	TBLASTX:Soybean
Start	534	End	1580
GI	none	Score	125
Exons	534..662, 1150..1410, 1159..1422, 1542..1580		

Seq. No.	686	Seq. ID	OJ990423_08.9924.C9
Gene No.	1410	Strand	+
Start	468	End	1870
Name	OJ990423_08.9924.C9.o1.tm	Method	TBLASTX:Maize
Start	1150	End	1378
GI	none	Score	216
Exons	1150..1374, 1230..1373, 1238..1378, 1244..1378		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1411	Strand	+
Start	1322	End	6202
Name	OJ990423_08.9924.C10.o1.gs	Method	GENSCAN
Start	1322	End	6202
GI	none	Score	.67
Exons	1322..1398, 2037..2644, 3308..3727, 4032..4636, 4685..6202		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1411	Strand	+
Start	1322	End	6202
Name	OJ990423_08.9924.C10.o1.gp	Method	AAT/GAP
Start	3678	End	4877
GI	24575_1.R1084	Score	1709
Exons	3678..3727, 4032..4877		

GI Descrip. '4678345/emb|CAB41155.1| 1.0e-09 (AL049659) putative zinc finger protein [Arabidopsis thaliana]'

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1411	Strand	+
Start	1322	End	6202
Name	OJ990423_08.9924.C10.o2.gp	Method	AAT/GAP
Start	5433	End	5782
GI	2310851	Score	637
Exons	5433..5782		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1412	Strand	+
Start	8990	End	9811
Name	OJ990423_08.9924.C10.o3.gs	Method	GENSCAN
Start	8990	End	9811
GI	none	Score	.81
Exons	8990..9811		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1413	Strand	+
Start	10687	End	16482
Name	OJ990423_08.9924.C10.o4.gs	Method	GENSCAN
Start	10687	End	16482
GI	none	Score	.94
Exons	10687..10932, 11035..11250, 11333..12424, 12833..12955, 13112..13228, 13366..13547, 13631..13862, 13964..14173, 14295..14423, 15297..15365, 15869..15991, 16075..16125, 16219..16357, 16409..16482		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1413	Strand	+
Start	10687	End	16482
Name	OJ990423_08.9924.C10.o5.gp	Method	AAT/GAP
Start	13396	End	14016
GI	2428176	Score	801
Exons	13396..13547, 13631..13862, 13964..14016		
GI Descrip.	5803221/ref|NP_006775.1|pWDR3| 6.0e-50 WD repeat domain 3 >gi_5639663_gb_AAD45865.1_AF083217_1 (AF083217) WD repeat protein WDR3 [Homo sapiens]		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1414	Strand	+
Start	19755	End	19821
Name	OJ990423_08.9924.C10.o9.gp	Method	AAT/GAP
Start	19755	End	19821
GI	uC-osf1M202134e04a1	Score	90
Exons	19755..19821		
GI Descrip.	'3915008/sp|P93407|SODP_ORYSA 2.0e-24 SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR >gi_1805502_dbj_BAA12745.1_ (D85239) superoxide dismutase precusor [Oryza sativa]'		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1415	Strand	-
Start	5831	End	6593
Name	OJ990423_08.9924.C10.o3.gp	Method	AAT/GAP
Start	5831	End	6593

GI	45631_1.R1084	Score	1458
Exons	5831..6593		
GI Descrip.	'4678345/emb|CAB41155.1| 5.0e-34 (AL049659) putative zinc finger protein [Arabidopsis thaliana]'		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1416	Strand	-
Start	6909	End	7786
Name	OJ990423_08.9924.C10.o2.gs	Method	GENSCAN
Start	6909	End	7786
GI	none	Score	1
Exons	6909..7380, 7707..7786		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1417	Strand	-
Start	9429	End	9728
Name	OJ990423_08.9924.C10.o4.gp	Method	AAT/GAP
Start	9429	End	9728
GI	2442409	Score	527
Exons	9429..9728		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o2.tc	Method	TBLASTX:Cress
Start	5714	End	6199
GI	none	Score	63
Exons	5714..5773, 5870..6199, 5893..6180		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o6.tm	Method	TBLASTX:Maize
Start	5861	End	6118
GI	none	Score	149
Exons	5861..6025, 5875..5988, 6029..6118, 6031..6114		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o8.tm	Method	TBLASTX:Maize
Start	8841	End	9146
GI	none	Score	36
Exons	8841..8876, 8920..8952, 8993..9145, 8994..9146		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o2.ts	Method	TBLASTX:Soybean
Start	9038	End	9338
GI	none	Score	179
Exons	9038..9337, 9054..9338		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o3.tm	Method	TBLASTX:Maize

Start	9148	End	9686
GI	none	Score	213
Exons	9148..9195, 9149..9280, 9150..9338, 9278..9421, 9279..9467, 9528..9686, 9530..9685		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o9.tm	Method	TBLASTX:Maize
Start	11035	End	13509
GI	none	Score	64
Exons	11035..11205, 11360..11539, 12310..12426, 12311..12430, 12832..12960, 12833..12958, 12835..12960, 13360..13509, 13365..13493		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o4.ts	Method	TBLASTX:Soybean
Start	11444	End	14044
GI	none	Score	63
Exons	11444..11527, 13399..13497, 13734..13862, 13737..13865, 13742..13864, 13742..13873, 13948..14043, 13958..14044		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o2.tm	Method	TBLASTX:Maize
Start	11613	End	12142
GI	none	Score	127
Exons	11613..11729, 11615..12142, 11615..11995, 11653..12141		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o3.tc	Method	TBLASTX:Cress
Start	11846	End	12274
GI	none	Score	70
Exons	11846..11920, 11909..12274, 11929..12234		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o3.ts	Method	TBLASTX:Soybean
Start	12019	End	12270
GI	none	Score	312
Exons	12019..12237, 12029..12268, 12031..12270, 12032..12268		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o4.tm	Method	TBLASTX:Maize
Start	13754	End	16403
GI	none	Score	186
Exons	13754..13873, 13755..13862, 13948..14196, 13958..14176, 14291..14416, 14293..14415, 14294..14422, 14295..14423, 15297..15371, 15299..15367, 15860..15997, 15867..15992,		

15904..15993, 16072..16134, 16074..16124, 16075..16125,
16218..16343, 16219..16350, 16308..16403

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o6.gp	Method	AAT/GAP
Start	17426	End	17812
GI	5038606	Score	718
Exons	17426..17812		
GI Descrip.	1705677/sp|P54609|CC48_ARATH 9.0e-20 CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >gi_2118115_pir__S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell division cycle protein [Arabidopsis thaliana]		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o5.gs	Method	GENSCAN
Start	17564	End	28023
GI	none	Score	.81
Exons	17564..17860, 17956..18315, 18399..18680, 18752..18823, 18916..19137, 19223..19989, 20324..20552, 21145..21307, 21316..21404, 21431..21551, 21662..21914, 22755..22812, 23064..23150, 23235..23324, 23693..23768, 23995..24089, 24208..24291, 24388..24461, 24826..24883, 27838..28023		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o2.np	Method	AAT/NAP
Start	17567	End	21468
GI	6630743	Score	3545
Exons	17567..17860, 17956..18315, 18399..18680, 18752..18823, 18916..19137, 19223..19989, 20324..20552, 21145..21301, 21431..21468		
GI Descrip.	(AL132958) CDC48-like protein [Arabidopsis thaliana]		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o1.tm	Method	TBLASTX:Maize
Start	17638	End	21319
GI	none	Score	167
Exons	17638..17721, 17639..17827, 17657..17863, 17661..17843, 17668..17862, 17951..18118, 17956..18318, 17956..18270, 17959..18270, 17960..18076, 18013..18258, 18167..18262, 18399..18683, 18403..18681, 18405..18683, 18406..18636, 18746..18823, 18752..18823, 18783..18824, 18913..19149, 18915..19106, 19033..19137, 19193..19417, 19196..19987, 19216..19431, 19218..19649, 19220..19987, 19220..19450, 19284..19997, 19302..19421, 19445..19828, 19446..19649, 19481..19792, 19848..19997, 20323..20499, 20325..20555, 20326..20553, 21143..21202, 21144..21233, 21145..21255, 21145..21294, 21146..21295, 21251..21319		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10

Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o1.tc	Method	TBLASTX:Cress
Start	17648	End	21295
GI	none	Score	153
Exons	17648..17818, 17653..17742, 17657..17863, 17946..18065, 17951..18106, 17953..18270, 17954..18103, 17956..18315, 17956..18270, 17960..18076, 18167..18262, 18197..18274, 18216..18314, 18399..18683, 18403..18681, 18405..18683, 18406..18669, 18746..18823, 18752..18823, 18913..19149, 18915..19112, 19033..19149, 19196..20011, 19220..20008, 19220..19450, 19302..19421, 19463..19792, 19463..19828, 20323..20499, 20324..20440, 20325..20555, 20326..20553, 21145..21294, 21146..21295		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o1.ts	Method	TBLASTX:Soybean
Start	17655	End	21304
GI	none	Score	132
Exons	17655..17762, 17657..17845, 17795..17863, 17815..17868, 17951..18106, 17953..18270, 17954..18112, 17956..18318, 17956..18270, 17960..18067, 18100..18264, 18179..18277, 18399..18683, 18403..18681, 18405..18683, 18406..18690, 18746..18823, 18752..18823, 18913..19149, 18915..19121, 19033..19149, 19154..19195, 19196..19987, 19216..19431, 19220..19450, 19221..19649, 19235..19987, 19302..19421, 19445..19828, 19446..19649, 19666..20043, 20323..20499, 20325..20555, 20326..20553, 21143..21202, 21145..21294, 21146..21295, 21248..21304		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o7.gp	Method	AAT/GAP
Start	17804	End	18058
GI	uC-osflcyp092g03b1	Score	199
Exons	17804..17860, 17956..18058		
GI Descrip.	'5803221/ref|NP_006775.1|pWDR3| 6.0e-50 WD repeat domain 3 >gi_5639663_gb_AAD45865.1_AF083217_1 (AF083217) WD repeat protein WDR3 [Homo sapiens]'		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o1.tw	Method	TBLASTX:Wheat
Start	17959	End	19828
GI	none	Score	71
Exons	17959..18267, 18100..18264, 18618..18683, 18619..18681, 18624..18683, 18746..18823, 18752..18823, 18787..18849, 18913..19149, 18915..19136, 19196..19426, 19220..19423, 19685..19828		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023

Name	OJ990423_08.9924.C10.o8.gp	Method	AAT/GAP
Start	18069	End	19399
GI	11986_1.R1084	Score	1856
Exons	18069..18315, 18399..18680, 18752..18823, 18916..19137, 19223..19399		
GI Descrip.	'1705678/sp|P54774|CC48_SOYBN 1.0e-176 CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]'		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o2.tw	Method	TBLASTX:Wheat
Start	18405	End	19685
GI	none	Score	128
Exons	18405..18617, 18406..18618, 19444..19683, 19445..19684, 19446..19685		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o3.tw	Method	TBLASTX:Wheat
Start	20310	End	21292
GI	none	Score	216
Exons	20310..20555, 20364..20555, 21143..21199, 21144..21233, 21145..21288, 21146..21292, 21251..21289		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o10.gp	Method	AAT/GAP
Start	20350	End	21583
GI	24991_1.R1084	Score	978
Exons	20350..20552, 21145..21307, 21431..21583		
GI Descrip.	'1705678/sp|P54774|CC48_SOYBN 7.0e-61 CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) >gi_862480 (U20213) valosin-containing protein [Glycine max]'		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o11.gp	Method	AAT/GAP
Start	22069	End	25113
GI	148_1.R1084	Score	1860
Exons	22069..22369, 23064..23150, 23235..23324, 23693..23798, 23995..24089, 24208..24291, 24388..24461, 24921..25113		
GI Descrip.	'5931625/dbj|BAA84717.1| 1.0e-106 (AB032761) rab5B [Oryza sativa]'		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o7.tm	Method	TBLASTX:Maize
Start	22290	End	23358
GI	none	Score	65
Exons	22290..22370, 22316..22372, 22331..22378, 23062..23151, 23063..23155, 23064..23153, 23233..23325, 23235..23351,		

23235..23342, 23239..23358

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o3.np	Method	AAT/NAP
Start	22334	End	24945
GI	5931625	Score	792
Exons	22334..22369, 23064..23150, 23235..23324, 23693..23798, 23995..24089, 24208..24291, 24388..24461, 24921..24945		
GI Descrip.	(AB032761) rab5B [Oryza sativa]		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o5.ts	Method	TBLASTX:Soybean
Start	23055	End	24311
GI	none	Score	63
Exons	23055..23120, 23062..23154, 23064..23156, 23225..23326, 23235..23330, 23245..23325, 23691..23741, 23693..23800, 23991..24092, 23992..24090, 24184..24279, 24185..24304, 24219..24311		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o4.tc	Method	TBLASTX:Cress
Start	23062	End	24343
GI	none	Score	81
Exons	23062..23151, 23064..23153, 23228..23326, 23229..23327, 23235..23330, 23691..23741, 23693..23800, 23988..24092, 23992..24090, 24184..24279, 24187..24279, 24203..24343		

Seq. No.	687	Seq. ID	OJ990423_08.9924.C10
Gene No.	1418	Strand	-
Start	17564	End	28023
Name	OJ990423_08.9924.C10.o5.tm	Method	TBLASTX:Maize
Start	23991	End	24971
GI	none	Score	154
Exons	23991..24092, 23992..24090, 24183..24293, 24184..24279, 24185..24343, 24198..24293, 24389..24409, 24418..24465, 24419..24466, 24918..24971		

Seq. No.	688	Seq. ID	OJ990423_08.9924.C11
Gene No.	1419	Strand	+
Start	2510	End	2808
Name	OJ990423_08.9924.C11.o1.gs	Method	GENSCAN
Start	2510	End	2808
GI	none	Score	.51
Exons	2510..2568, 2622..2808		

Seq. No.	688	Seq. ID	OJ990423_08.9924.C11
Gene No.	1420	Strand	-
Start	3190	End	3302
Name	OJ990423_08.9924.C11.o2.gs	Method	GENSCAN
Start	3190	End	3302
GI	none	Score	.97

Exons	3190..3302		
Seq. No.	689	Seq. ID	OJ990423_08.9924.C12
Gene No.	1421	Strand	+
Start	2596	End	8726
Name	OJ990423_08.9924.C12.o2.gs	Method	GENSCAN
Start	2596	End	5352
GI	none	Score	.91
Exons	2596..2601, 3100..3476, 4075..4151, 4261..4304, 5167..5352		
Seq. No.	689	Seq. ID	OJ990423_08.9924.C12
Gene No.	1421	Strand	+
Start	2596	End	8726
Name	OJ990423_08.9924.C12.o1.np	Method	AAT/NAP
Start	3251	End	8587
GI	5454112	Score	213
Exons	3251..3425, 4095..4151, 4261..4304, 5016..5075, 5167..5326, 5414..5469, 5643..5763, 8543..8587		
GI Descrip.	transcription factor Dp-2 (E2F dimerization partner 2) gi|604479 (U18422) DP2 [Homo sapiens]		
Seq. No.	689	Seq. ID	OJ990423_08.9924.C12
Gene No.	1421	Strand	+
Start	2596	End	8726
Name	OJ990423_08.9924.C12.o3.gs	Method	GENSCAN
Start	8163	End	8726
GI	none	Score	.4
Exons	8163..8228, 8592..8726		
Seq. No.	689	Seq. ID	OJ990423_08.9924.C12
Gene No.	1422	Strand	-
Start	221	End	795
Name	OJ990423_08.9924.C12.o1.gs	Method	GENSCAN
Start	221	End	742
GI	none	Score	.74
Exons	221..488, 622..742		
Seq. No.	689	Seq. ID	OJ990423_08.9924.C12
Gene No.	1422	Strand	-
Start	221	End	795
Name	OJ990423_08.9924.C12.o1.gp	Method	AAT/GAP
Start	427	End	795
GI	5038563	Score	709
Exons	427..795		
Seq. No.	689	Seq. ID	OJ990423_08.9924.C12
Gene No.	1423	Strand	
Start	3370	End	7886
Name	OJ990423_08.9924.C12.o1.ts	Method	TBLASTX:Soybean
Start	3370	End	7587
GI	none	Score	76
Exons	3370..3459, 4072..4161, 4091..4150, 4251..4310, 4259..4306, 5010..5042, 5013..5075, 5163..5306, 5164..5325, 5164..5331, 5395..5493, 5400..5465, 5640..5741, 5642..5737, 5828..5908, 5831..5908, 5838..5909, 7456..7587		
Seq. No.	689	Seq. ID	OJ990423_08.9924.C12

Gene No.	1423	Strand	
Start	3370	End	7886
Name	OJ990423_08.9924.C12.o1.tm	Method	TBLASTX:Maize
Start	5169	End	7886
GI	none	Score	151
Exons	5169..5306, 5169..5306, 5170..5313, 5170..5358, 5395..5493, 5399..5542, 5400..5468, 5633..5740, 5640..5741, 5640..5741, 5641..5742, 5831..5908, 5834..5908, 7434..7709, 7456..7713, 7458..7712, 7459..7713, 7460..7747, 7782..7874, 7839..7886		

Seq. No.	689	Seq. ID	OJ990423_08.9924.C12
Gene No.	1423	Strand	
Start	3370	End	7886
Name	OJ990423_08.9924.C12.o1.tc	Method	TBLASTX:Cress
Start	5197	End	7521
GI	none	Score	179
Exons	5197..5325, 5203..5304, 5395..5493, 5612..5737, 5640..5741, 5640..5741, 5642..5767, 5831..5908, 5837..5908, 7456..7521		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1424	Strand	+
Start	1847	End	3410
Name	OJ990423_08.9924.C13.o1.gs	Method	GENSCAN
Start	1847	End	3410
GI	none	Score	.97
Exons	1847..2062, 2166..3410		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1424	Strand	+
Start	1847	End	3410
Name	OJ990423_08.9924.C13.o1.np	Method	AAT/NAP
Start	1859	End	2897
GI	4538930	Score	569
Exons	1859..2072, 2149..2897		
GI Descrip.	(AL049483) putative peroxidase [Arabidopsis thaliana]		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o1.tm	Method	TBLASTX:Maize
Start	1924	End	2984
GI	none	Score	156
Exons	1924..2079, 1934..2062, 2162..2626, 2166..2627, 2631..2984, 2688..2966, 2708..2977		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o1.ts	Method	TBLASTX:Soybean
Start	1934	End	2894
GI	none	Score	100
Exons	1934..2062, 2166..2234, 2238..2429, 2505..2549, 2628..2894		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o1.tc	Method	TBLASTX:Cress

Start	2018	End	2897
GI	none	Score	48
Exons	2018..2056, 2165..2386, 2166..2411, 2427..2549, 2432..2542, 2649..2897		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o1.tw	Method	TBLASTX:Wheat
Start	2271	End	2621
GI	none	Score	218
Exons	2271..2426, 2291..2386, 2318..2434, 2368..2433, 2406..2621, 2415..2540, 2432..2620		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o2.gs	Method	GENSCAN
Start	4367	End	10856
GI	none	Score	.79
Exons	4367..4777, 6253..6384, 6738..6840, 6979..7046, 7778..7920, 8258..8450, 9825..10856		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o2.np	Method	AAT/NAP
Start	6238	End	10889
GI	1361982	Score	747
Exons	6238..6348, 6738..6840, 6979..7046, 7778..7920, 8258..8450, 9825..10889		
GI Descrip.	4-coumarate--CoA ligase (EC 6.2.1.12) - Arabidopsis thaliana gi|609340 (U18675) 4-coumarate--coenzyme A ligase [Arabidopsis thaliana] gi|5702184|gb|AAD47191.1|AF106084_1 (AF106084) 4-coumarate:CoA ligase 1 [Arabidopsis thaliana]		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o2.ts	Method	TBLASTX:Soybean
Start	6241	End	10572
GI	none	Score	65
Exons	6241..6351, 6251..6349, 6278..6352, 6735..6833, 6736..6834, 7775..7879, 8256..8378, 8412..8462, 9825..10139, 9844..10065, 10192..10248, 10197..10334, 10419..10556, 10423..10572		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o2.tc	Method	TBLASTX:Cress
Start	6250	End	10560
GI	none	Score	81
Exons	6250..6351, 6735..6824, 6736..6834, 7775..7873, 7775..7912, 8256..8420, 8412..8459, 9825..10139, 9844..10065, 10185..10280, 10407..10532, 10411..10560		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13

Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o3.tm	Method	TBLASTX:Maize
Start	7856	End	10043
GI	none	Score	125
Exons	7856..7921, 7857..7922, 7858..7923, 8233..8451, 8256..8462, 8259..8453, 9823..10041, 9825..10043, 9844..10041		

Seq. No.	690	Seq. ID	OJ990423_08.9924.C13
Gene No.	1425	Strand	-
Start	4367	End	10889
Name	OJ990423_08.9924.C13.o2.tm	Method	TBLASTX:Maize
Start	10044	End	10658
GI	none	Score	121
Exons	10044..10232, 10044..10343, 10063..10344, 10393..10551, 10395..10550, 10549..10575, 10573..10656, 10575..10658		

Seq. No.	691	Seq. ID	OJ990423_08.9924.C14
Gene No.	1426	Strand	+
Start	336	End	523
Name	OJ990423_08.9924.C14.o1.gs	Method	GENSCAN
Start	336	End	523
GI	none	Score	.47
Exons	336..523		

Seq. No.	692	Seq. ID	OJ990423_08.9924.C16
Gene No.	1427	Strand	-
Start	146	End	556
Name	OJ990423_08.9924.C16.o1.gs	Method	GENSCAN
Start	146	End	553
GI	none	Score	.76
Exons	146..219, 271..409, 503..553		

Seq. No.	692	Seq. ID	OJ990423_08.9924.C16
Gene No.	1427	Strand	-
Start	146	End	556
Name	OJ990423_08.9924.C16.o1.tm	Method	TBLASTX:Maize
Start	224	End	556
GI	none	Score	74
Exons	224..346, 225..320, 278..409, 285..410, 494..556, 503..553		

Seq. No.	693	Seq. ID	OJ990423_08.9924.C17
Gene No.	1428	Strand	-
Start	307	End	784
Name	OJ990423_08.9924.C17.o1.tm	Method	TBLASTX:Maize
Start	304	End	696
GI	none	Score	96
Exons	304..516, 314..469, 322..504, 526..696, 593..631		

Seq. No.	693	Seq. ID	OJ990423_08.9924.C17
Gene No.	1428	Strand	-
Start	307	End	784
Name	OJ990423_08.9924.C17.o1.np	Method	AAT/NAP
Start	307	End	784
GI	3426064	Score	286
Exons	307..784		
GI Descrip.	(AJ007588) monooxygenase [Arabidopsis thaliana]		

gi|4467141|emb|CAB37510| (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]

Seq. No.	693	Seq. ID	OJ990423_08.9924.C17
Gene No.	1428	Strand	-
Start	307	End	784
Name	OJ990423_08.9924.C17.o1.ts	Method	TBLASTX:Soybean
Start	307	End	510
GI	none	Score	179
Exons	307..510		

Seq. No.	694	Seq. ID	OJ990423_08.9924.C18
Gene No.	1429	Strand	-
Start	266	End	906
Name	OJ990423_08.9924.C18.o1.gs	Method	GENSCAN
Start	266	End	849
GI	none	Score	.93
Exons	266..849		

Seq. No.	694	Seq. ID	OJ990423_08.9924.C18
Gene No.	1429	Strand	-
Start	266	End	906
Name	OJ990423_08.9924.C18.o1.np	Method	AAT/NAP
Start	269	End	906
GI	4097571	Score	219
Exons	269..487, 531..906		
GI Descrip.	(U64916) GMFP5 [Glycine max]		

Seq. No.	695	Seq. ID	OJ990423_08.9924.C19
Gene No.	1430	Strand	+
Start	1	End	733
Name	OJ990423_08.9924.C19.o1.np	Method	AAT/NAP
Start	1	End	733
GI	5541717	Score	167
Exons	1..78, 155..368, 702..733		
GI Descrip.	(AL049655) kinesin-like protein [Arabidopsis thaliana]		

Seq. No.	695	Seq. ID	OJ990423_08.9924.C19
Gene No.	1430	Strand	+
Start	1	End	733
Name	OJ990423_08.9924.C19.o1.gs	Method	GENSCAN
Start	185	End	268
GI	none	Score	.42
Exons	185..268		

Seq. No.	696	Seq. ID	OJ990423_08.9924.C20
Gene No.	1431	Strand	-
Start	1	End	1618
Name	OJ990423_08.9924.C20.o1.gp	Method	AAT/GAP
Start	1	End	1618
GI	5144_1.R1084	Score	478
Exons	1..168, 1508..1618		
GI Descrip.	'3426064/emb|CAA07575.1| 7.0e-18 (AJ007588) monooxygenase [Arabidopsis thaliana] >gi_4467141_emb_CAB37510_ (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]'		

Seq. No.	696	Seq. ID	OJ990423_08.9924.C20

Gene No.	1431	Strand	-
Start	1	End	1618
Name	OJ990423_08.9924.C20.o1.np	Method	AAT/NAP
Start	1	End	196
GI	6440857	Score	204
Exons	1..196		
GI Descrip.	(AU066528) 40S ribosomal protein S9 [Chlamydomonas sp.]		

Seq. No.	696	Seq. ID	OJ990423_08.9924.C20
Gene No.	1431	Strand	-
Start	1	End	1618
Name	OJ990423_08.9924.C20.o1.tc	Method	TBLASTX:Cress
Start	2	End	187
GI	none	Score	117
Exons	2..178, 2..187		

Seq. No.	696	Seq. ID	OJ990423_08.9924.C20
Gene No.	1431	Strand	-
Start	1	End	1618
Name	OJ990423_08.9924.C20.o1.ts	Method	TBLASTX:Soybean
Start	2	End	186
GI	none	Score	108
Exons	2..166, 3..167, 28..168, 28..186		

Seq. No.	696	Seq. ID	OJ990423_08.9924.C20
Gene No.	1431	Strand	-
Start	1	End	1618
Name	OJ990423_08.9924.C20.o1.tm	Method	TBLASTX:Maize
Start	2	End	182
GI	none	Score	176
Exons	2..169, 2..166, 4..168, 9..182		

Seq. No.	696	Seq. ID	OJ990423_08.9924.C20
Gene No.	1431	Strand	-
Start	1	End	1618
Name	OJ990423_08.9924.C20.o1.tw	Method	TBLASTX:Wheat
Start	2	End	182
GI	none	Score	199
Exons	2..169, 2..166, 6..182		

Seq. No.	696	Seq. ID	OJ990423_08.9924.C20
Gene No.	1431	Strand	-
Start	1	End	1618
Name	OJ990423_08.9924.C20.o1.gs	Method	GENSCAN
Start	97	End	1596
GI	none	Score	.71
Exons	97..168, 1422..1596		

Seq. No.	697	Seq. ID	OJ990423_08.9924.C21
Gene No.	1432	Strand	+
Start	1	End	615
Name	OJ990423_08.9924.C21.o1.np	Method	AAT/NAP
Start	1	End	615
GI	5257259	Score	105
Exons	1..74, 538..615		
GI Descrip.	(AP000364) hypothetical protein [Oryza sativa]		

Seq. No.	697	Seq. ID	OJ990423_08.9924.C21
Gene No.	1433	Strand	+
Start	2914	End	3522
Name	OJ990423_08.9924.C21.o1.gs	Method	GENSCAN
Start	2914	End	3522
GI	none	Score	.9
Exons	2914..3005, 3366..3522		

Seq. No.	697	Seq. ID	OJ990423_08.9924.C21
Gene No.	1434	Strand	+
Start	4567	End	6404
Name	OJ990423_08.9924.C21.o2.gs	Method	GENSCAN
Start	4567	End	6404
GI	none	Score	.56
Exons	4567..4648, 4816..5044, 5202..5345, 5739..5808, 6288..6404		

Seq. No.	697	Seq. ID	OJ990423_08.9924.C21
Gene No.	1435	Strand	-
Start	3408	End	3946
Name	OJ990423_08.9924.C21.o1.tm	Method	TBLASTX:Maize
Start	3385	End	3940
GI	none	Score	106
Exons	3385..3495, 3392..3538, 3691..3771, 3693..3803, 3697..3792, 3773..3940, 3788..3937		

Seq. No.	697	Seq. ID	OJ990423_08.9924.C21
Gene No.	1435	Strand	-
Start	3408	End	3946
Name	OJ990423_08.9924.C21.o2.np	Method	AAT/NAP
Start	3408	End	3939
GI	4884932	Score	199
Exons	3408..3482, 3693..3939		
GI Descrip.	(AF141659) AtHVA22a [Arabidopsis thaliana] gi|4884944|gb|AAD31885.1|AF141977_1 (AF141977) AtHVA22a [Arabidopsis thaliana] gi|6539254|gb|AAF15924.1|AC011765_20 (AC011765) AtHVA22a [Arabidopsis thaliana]		

Seq. No.	697	Seq. ID	OJ990423_08.9924.C21
Gene No.	1435	Strand	-
Start	3408	End	3946
Name	OJ990423_08.9924.C21.o1.tw	Method	TBLASTX:Wheat
Start	3700	End	3946
GI	none	Score	44
Exons	3700..3750, 3782..3937, 3800..3946		

Seq. No.	698	Seq. ID	OJ990423_08.9924.C22
Gene No.	1436	Strand	-
Start	1	End	547
Name	OJ990423_08.9924.C22.o1.np	Method	AAT/NAP
Start	1	End	547
GI	5541717	Score	79
Exons	1..64, 140..265, 457..547		
GI Descrip.	(AL049655) kinesin-like protein [Arabidopsis thaliana]		

Seq. No.	698	Seq. ID	OJ990423_08.9924.C22
Gene No.	1436	Strand	-
Start	1	End	547

Name	OJ990423_08.9924.C22.o1.gs	Method	GENSCAN
Start	140	End	265
GI	none	Score	.45
Exons	140..265		

Seq. No.	699	Seq. ID	OJ990423_08.9924.C23
Gene No.	1437	Strand	+
Start	118	End	686
Name	OJ990423_08.9924.C23.o1.gs	Method	GENSCAN
Start	118	End	686
GI	none	Score	.66
Exons	118..686		

Seq. No.	699	Seq. ID	OJ990423_08.9924.C23
Gene No.	1437	Strand	+
Start	118	End	686
Name	OJ990423_08.9924.C23.o1.tm	Method	TBLASTX:Maize
Start	132	End	629
GI	none	Score	219
Exons	132..335, 134..271, 436..624,	447..629,	447..623, 569..628

Seq. No.	700	Seq. ID	OJ990423_08.9924.C24
Gene No.	1438	Strand	+
Start	1	End	1328
Name	OJ990423_08.9924.C24.o1.np	Method	AAT/NAP
Start	1	End	1328
GI	4678345	Score	201
Exons	1..141, 856..1010, 1309..1328		
GI Descrip.	(AL049659) putative zinc finger protein [Arabidopsis thaliana]		

Seq. No.	700	Seq. ID	OJ990423_08.9924.C24
Gene No.	1439	Strand	-
Start	123	End	140
Name	OJ990423_08.9924.C24.o1.gs	Method	GENSCAN
Start	123	End	140
GI	none	Score	.94
Exons	123..140		

Seq. No.	701	Seq. ID	OJ990423_08.9924.C26
Gene No.	1440	Strand	-
Start	56	End	669
Name	OJ990423_08.9924.C26.o1.gp	Method	AAT/GAP
Start	56	End	669
GI	24575_1.R1084	Score	570
Exons	56..315, 620..669		
GI Descrip.	'4678345/emb|CAB41155.1| 1.0e-09 (AL049659) putative zinc finger protein [Arabidopsis thaliana]'		

Seq. No.	701	Seq. ID	OJ990423_08.9924.C26
Gene No.	1440	Strand	-
Start	56	End	669
Name	OJ990423_08.9924.C26.o1.gs	Method	GENSCAN
Start	94	End	315
GI	none	Score	.48
Exons	94..315		

Seq. No.	702	Seq. ID	OJ990423_08.9924.C27

Gene No.	1441	Strand	-
Start	1	End	729
Name	OJ990423_08.9924.C27.o1.np	Method	AAT/NAP
Start	1	End	729
GI	3426064	Score	120
Exons	1..142, 276..470, 604..729		
GI Descrip.	(AJ007588) monooxygenase [Arabidopsis thaliana] gi|4467141|emb|CAB37510| (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]		

Seq. No.	702	Seq. ID	OJ990423_08.9924.C27
Gene No.	1441	Strand	-
Start	1	End	729
Name	OJ990423_08.9924.C27.o1.gs	Method	GENSCAN
Start	289	End	474
GI	none	Score	.59
Exons	289..474		

Seq. No.	702	Seq. ID	OJ990423_08.9924.C27
Gene No.	1441	Strand	-
Start	1	End	729
Name	OJ990423_08.9924.C27.o1.tm	Method	TBLASTX:Maize
Start	301	End	477
GI	none	Score	111
Exons	301..477, 302..469		

Seq. No.	702	Seq. ID	OJ990423_08.9924.C27
Gene No.	1441	Strand	-
Start	1	End	729
Name	OJ990423_08.9924.C27.o1.ts	Method	TBLASTX:Soybean
Start	301	End	477
GI	none	Score	60
Exons	301..477, 302..352, 371..469		

Seq. No.	703	Seq. ID	OJ990423_08.9924.C30
Gene No.	1442	Strand	-
Start	1	End	706
Name	OJ990423_08.9924.C30.o1.np	Method	AAT/NAP
Start	1	End	706
GI	3426064	Score	282
Exons	1..393, 470..706		
GI Descrip.	(AJ007588) monooxygenase [Arabidopsis thaliana] gi|4467141|emb|CAB37510| (AL035540) monooxygenase 2 (MO2) [Arabidopsis thaliana]		

Seq. No.	703	Seq. ID	OJ990423_08.9924.C30
Gene No.	1442	Strand	-
Start	1	End	706
Name	OJ990423_08.9924.C30.o1.gs	Method	GENSCAN
Start	94	End	635
GI	none	Score	.92
Exons	94..393, 470..635		

Seq. No.	703	Seq. ID	OJ990423_08.9924.C30
Gene No.	1442	Strand	-
Start	1	End	706
Name	OJ990423_08.9924.C30.o1.ts	Method	TBLASTX:Soybean

Start	172	End	511
GI	none	Score	93
Exons	172..396, 185..277, 296..400,	467..511	

Seq. No.	703	Seq. ID	OJ990423_08.9924.C30
Gene No.	1442	Strand	-
Start	1	End	706
Name	OJ990423_08.9924.C30.o1.tc	Method	TBLASTX:Cress
Start	184	End	628
GI	none	Score	168
Exons	184..396, 185..406, 467..628		

Seq. No.	703	Seq. ID	OJ990423_08.9924.C30
Gene No.	1442	Strand	-
Start	1	End	706
Name	OJ990423_08.9924.C30.o1.tm	Method	TBLASTX:Maize
Start	186	End	396
GI	none	Score	170
Exons	186..311, 188..394, 190..396		

Seq. No.	703	Seq. ID	OJ990423_08.9924.C30
Gene No.	1442	Strand	-
Start	1	End	706
Name	OJ990423_08.9924.C30.o1.tw	Method	TBLASTX:Wheat
Start	331	End	640
GI	none	Score	75
Exons	331..393, 332..394, 340..396,	467..640,	468..638

Seq. No.	703	Seq. ID	OJ990423_08.9924.C30
Gene No.	1442	Strand	-
Start	1	End	706
Name	OJ990423_08.9924.C30.o1.gp	Method	AAT/GAP
Start	347	End	706
GI	2312132	Score	502
Exons	347..393, 470..706		

Seq. No.	704	Seq. ID	OJ990423_08.9924.C31
Gene No.	1443	Strand	-
Start	1	End	428
Name	OJ990423_08.9924.C31.o1.np	Method	AAT/NAP
Start	1	End	428
GI	3875727	Score	111
Exons	1..79, 259..428		
GI Descrip.	(Z70751) similar to 4-coumarate-CoA ligase; cDNA EST EMBL:C07240 comes from this gene; cDNA EST EMBL:C08540 comes from this gene [Caenorhabditis elegans]		

Seq. No.	704	Seq. ID	OJ990423_08.9924.C31
Gene No.	1443	Strand	-
Start	1	End	428
Name	OJ990423_08.9924.C31.o1.tm	Method	TBLASTX:Maize
Start	277	End	426
GI	none	Score	179
Exons	277..423, 280..426, 281..424		

Seq. No.	704	Seq. ID	OJ990423_08.9924.C31
Gene No.	1443	Strand	-

Start	1	End	428
Name	OJ990423_08.9924.C31.o1.gs	Method	GENSCAN
Start	280	End	422
GI	none	Score	.99
Exons	280..422		

Seq. No.	705	Seq. ID	OJ990423_08.9924.C35
Gene No.	1444	Strand	
Start	234	End	1155
Name	OJ990423_08.9924.C35.o1.tm	Method	TBLASTX:Maize
Start	234	End	1155
GI	none	Score	172
Exons	234..371, 253..372, 253..372, 442..558, 445..549, 935..1048, 957..1055, 974..1057, 976..1056, 1047..1154, 1047..1112, 1048..1155, 1049..1153		

Seq. No.	706	Seq. ID	OJ990423_08.9924.C36
Gene No.	1445	Strand	-
Start	1	End	704
Name	OJ990423_08.9924.C36.o1.np	Method	AAT/NAP
Start	1	End	704
GI	5541717	Score	163
Exons	1..228, 652..704		
GI Descrip.	(AL049655) kinesin-like protein [Arabidopsis thaliana]		

Seq. No.	706	Seq. ID	OJ990423_08.9924.C36
Gene No.	1445	Strand	-
Start	1	End	704
Name	OJ990423_08.9924.C36.o1.tm	Method	TBLASTX:Maize
Start	66	End	231
GI	none	Score	38
Exons	66..227, 88..231, 100..150, 134..229		

Seq. No.	706	Seq. ID	OJ990423_08.9924.C36
Gene No.	1445	Strand	-
Start	1	End	704
Name	OJ990423_08.9924.C36.o1.gs	Method	GENSCAN
Start	102	End	225
GI	none	Score	.51
Exons	102..225		

Seq. No.	707	Seq. ID	OJ990423_08.9924.C37
Gene No.	1446	Strand	+
Start	382	End	745
Name	OJ990423_08.9924.C37.o1.gs	Method	GENSCAN
Start	382	End	712
GI	none	Score	.4
Exons	382..712		

Seq. No.	707	Seq. ID	OJ990423_08.9924.C37
Gene No.	1446	Strand	+
Start	382	End	745
Name	OJ990423_08.9924.C37.o1.tm	Method	TBLASTX:Maize
Start	513	End	740
GI	none	Score	205
Exons	513..740, 515..619		

Seq. No.	707	Seq. ID	OJ990423_08.9924.C37
Gene No.	1446	Strand	+
Start	382	End	745
Name	OJ990423_08.9924.C37.o1.np	Method	AAT/NAP
Start	518	End	745
GI	2832244	Score	111
Exons	518..745		
GI Descrip.	(AF031569) hypothetical protein [Zea mays]		

Seq. No.	708	Seq. ID	OJ990423_08.9924.C38
Gene No.	1447	Strand	-
Start	1	End	270
Name	OJ990423_08.9924.C38.o1.np	Method	AAT/NAP
Start	1	End	270
GI	2982456	Score	156
Exons	1..270		
GI Descrip.	(AL022223) putative protein [Arabidopsis thaliana]		

Seq. No.	708	Seq. ID	OJ990423_08.9924.C38
Gene No.	1447	Strand	-
Start	1	End	270
Name	OJ990423_08.9924.C38.o1.gs	Method	GENSCAN
Start	53	End	247
GI	none	Score	.6
Exons	53..247		

Seq. No.	709	Seq. ID	OJ990513_03.9924.C1
Gene No.	1448	Strand	-
Start	15	End	172
Name	OJ990513_03.9924.C1.o1.gs	Method	GENSCAN
Start	15	End	172
GI	none	Score	.71
Exons	15..172		

Seq. No.	710	Seq. ID	OJ990513_03.9924.C3
Gene No.	1449	Strand	-
Start	1	End	227
Name	OJ990513_03.9924.C3.o1.gp	Method	AAT/GAP
Start	1	End	227
GI	uC-osflcyp106a12a1	Score	312
Exons	1..227		
GI Descrip.	'2811029/sp|O04866|ARGD_ALNGL 1.0e-09 ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]'		

Seq. No.	710	Seq. ID	OJ990513_03.9924.C3
Gene No.	1450	Strand	-
Start	171	End	551
Name	OJ990513_03.9924.C3.o1.np	Method	AAT/NAP
Start	171	End	551
GI	4454472	Score	189
Exons	171..551		
GI Descrip.	(AC006234) unknown protein [Arabidopsis thaliana]		

Seq. No.	710	Seq. ID	OJ990513_03.9924.C3
Gene No.	1450	Strand	-

Start	171	End	551
Name	OJ990513_03.9924.C3.o1.gs	Method	GENSCAN
Start	237	End	425
GI	none	Score	.48
Exons	237..425		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1451	Strand	+
Start	7616	End	8068
Name	OJ990513_03.9924.C4.o3.gp	Method	AAT/GAP
Start	7616	End	8068
GI	none	Score	821
Exons	7616..8068		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1452	Strand	+
Start	16658	End	17982
Name	OJ990513_03.9924.C4.o3.gs	Method	GENSCAN
Start	16658	End	17982
GI	none	Score	.5
Exons	16658..16977, 17046..17310, 17464..17982		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o2.np	Method	AAT/NAP
Start	3	End	17385
GI	6523547	Score	252
Exons	3..138, 1318..1536, 3669..3815, 4382..4435, 4547..4878, 17031..17385		
GI Descrip.	(AJ242540) hydroxyproline-rich glycoprotein DZ-HRGP [Volvox carteri f. nagariensis]		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o1.tm	Method	TBLASTX:Maize
Start	1323	End	4395
GI	none	Score	104
Exons	1323..1490, 3705..3806, 3706..3810, 3825..3995, 3832..3960, 4044..4148, 4049..4126, 4342..4395		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o1.gp	Method	AAT/GAP
Start	3171	End	3473
GI	uC-osflcyp106a12a1	Score	460
Exons	3171..3473		
GI Descrip.	'2811029/sp|O04866|ARGD_ALNGL 1.0e-09 ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]'		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385

Name	OJ990513_03.9924.C4.o1.np	Method	AAT/NAP
Start	3417	End	4773
GI	4454472	Score	450
Exons	3417..3950, 4052..4205, 4343..4418, 4515..4773		
GI Descrip.	(AC006234) unknown protein [Arabidopsis thaliana]		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o1.gs	Method	GENSCAN
Start	3483	End	4812
GI	none	Score	.9
Exons	3483..4251, 4343..4812		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o1.ts	Method	TBLASTX:Soybean
Start	3705	End	4148
GI	none	Score	78
Exons	3705..3800, 3706..3795, 3828..3995, 3850..3960, 4049..4126, 4053..4148		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o1.tc	Method	TBLASTX:Cress
Start	3706	End	3953
GI	none	Score	66
Exons	3706..3795, 3711..3800, 3825..3953, 3826..3951		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o2.gp	Method	AAT/GAP
Start	4481	End	4854
GI	none	Score	732
Exons	4481..4854		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o2.gs	Method	GENSCAN
Start	8079	End	15931
GI	none	Score	.4
Exons	8079..9818, 10284..10413, 10491..10651, 11486..11603, 12206..12319, 15894..15931		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o4.tm	Method	TBLASTX:Maize
Start	8483	End	9362
GI	none	Score	128
Exons	8483..8650, 8485..8649, 8487..8654, 8487..8654, 8646..8771, 8649..8774, 8662..8778, 8772..8804, 9027..9074, 9067..9135, 9171..9362, 9174..9341		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o4.gp	Method	AAT/GAP
Start	8715	End	9705
GI	none	Score	1937
Exons	8715..9705		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o3.tm	Method	TBLASTX:Maize
Start	9750	End	14784
GI	none	Score	136
Exons	9750..9869, 9758..9859, 9958..10023, 10150..10218, 10151..10219, 10188..10259, 10242..10418, 10255..10434, 10263..10448, 10476..10643, 10479..10649, 10487..10654, 10490..10651, 11481..11576, 11483..11599, 12061..12129, 12064..12132, 12184..12318, 12206..12319, 12206..12319, 12207..12320, 14727..14783, 14728..14784		

Seq. No.	711	Seq. ID	OJ990513_03.9924.C4
Gene No.	1453	Strand	-
Start	3	End	17385
Name	OJ990513_03.9924.C4.o2.tm	Method	TBLASTX:Maize
Start	15133	End	15376
GI	none	Score	193
Exons	15133..15369, 15143..15376, 15146..15376		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1454	Strand	+
Start	1	End	2057
Name	OJ990513_03.9924.C5.o1.np	Method	AAT/NAP
Start	1	End	2057
GI	6539581	Score	450
Exons	1..1049, 2019..2057		
GI Descrip.	(AP000837) Similar to Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10; hypothetical protein (AL035538) [Oryza sativa]		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1454	Strand	+
Start	1	End	2057
Name	OJ990513_03.9924.C5.o1.gs	Method	GENSCAN
Start	160	End	834
GI	none	Score	.53
Exons	160..834		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o2.tm	Method	TBLASTX:Maize
Start	2	End	573
GI	none	Score	67
Exons	2..79, 82..276, 133..243, 289..573, 322..462, 327..524		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5

Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o2.ts	Method	TBLASTX:Soybean
Start	2	End	486
GI	none	Score	86
Exons	2..70, 11..79, 13..78, 84..242, 97..486, 100..438		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o1.tw	Method	TBLASTX:Wheat
Start	88	End	525
GI	none	Score	296
Exons	88..525, 90..269, 339..434		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o2.np	Method	AAT/NAP
Start	978	End	2057
GI	2811029	Score	735
Exons	978..1510, 1872..2057		
GI Descrip.	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) gi|1944511|emb|CAA69936| (Y08680) acetylornithine aminotransferase [Alnus glutinosa]		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o2.gs	Method	GENSCAN
Start	1043	End	1970
GI	none	Score	.98
Exons	1043..1510, 1872..1970		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o1.tc	Method	TBLASTX:Cress
Start	1050	End	1513
GI	none	Score	189
Exons	1050..1349, 1070..1351, 1070..1351, 1352..1429, 1353..1445, 1403..1483, 1407..1460, 1481..1513, 1485..1511		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o1.tm	Method	TBLASTX:Maize
Start	1070	End	1524
GI	none	Score	536
Exons	1070..1516, 1071..1517, 1423..1524		

Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o1.ts	Method	TBLASTX:Soybean
Start	1070	End	1396
GI	none	Score	253

Exons	1070..1396, 1071..1394		
Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o1.gp	Method	AAT/GAP
Start	1325	End	1496
GI	2796278	Score	311
Exons	1325..1496		
GI Descrip.	2811029/sp|O04866|ARGD_ALNGL 1.0e-09 ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]		
Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o3.ts	Method	TBLASTX:Soybean
Start	1400	End	2057
GI	none	Score	128
Exons	1400..1513, 1401..1511, 1869..2057, 1870..2001		
Seq. No.	712	Seq. ID	OJ990513_03.9924.C5
Gene No.	1455	Strand	-
Start	978	End	2057
Name	OJ990513_03.9924.C5.o3.tm	Method	TBLASTX:Maize
Start	1875	End	2057
GI	none	Score	68
Exons	1875..1994, 1875..2057, 1877..2053		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1456	Strand	+
Start	360	End	431
Name	OJ990513_03.9924.C6.o1.gs	Method	GENSCAN
Start	360	End	431
GI	none	Score	.52
Exons	360..431		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1457	Strand	+
Start	2302	End	2766
Name	OJ990513_03.9924.C6.o1.gp	Method	AAT/GAP
Start	2302	End	2766
GI	2800691	Score	701
Exons	2302..2766		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1458	Strand	+
Start	7168	End	8202
Name	OJ990513_03.9924.C6.o3.gs	Method	GENSCAN
Start	7168	End	8202
GI	none	Score	.88
Exons	7168..7212, 7518..7682, 7706..7873, 7885..8202		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1459	Strand	+
Start	8899	End	13777

Name	OJ990513_03.9924.C6.o2.np	Method	AAT/NAP
Start	8887	End	10712
GI	4467124	Score	788
Exons	8887..10712		
GI Descrip.	(AL035538) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1459	Strand	+
Start	8899	End	13777
Name	OJ990513_03.9924.C6.o4.gs	Method	GENSCAN
Start	8899	End	13777
GI	none	Score	.64
Exons	8899..9167, 9195..10785, 10936..10958, 11246..11370, 11400..11520, 12465..12533, 12556..12620, 12902..13183, 13656..13777		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1460	Strand	-
Start	2631	End	6877
Name	OJ990513_03.9924.C6.o2.gs	Method	GENSCAN
Start	2631	End	6643
GI	none	Score	.83
Exons	2631..2737, 3066..3135, 3231..3311, 3531..3623, 3801..3881, 3976..4065, 4183..4276, 4433..4527, 4915..4998, 5125..5217, 5365..5472, 5667..5817, 6396..6643		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1460	Strand	-
Start	2631	End	6877
Name	OJ990513_03.9924.C6.o2.gp	Method	AAT/GAP
Start	2653	End	4613
GI	13141_1.R1084	Score	1507
Exons	2653..2926, 3066..3135, 3231..3311, 3531..3623, 3801..3881, 3976..4065, 4183..4276, 4433..4501, 4575..4613		
GI Descrip.	'2811029/sp|O04866|ARGD_ALNGL 1.0e-09 ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]'		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1460	Strand	-
Start	2631	End	6877
Name	OJ990513_03.9924.C6.o1.np	Method	AAT/NAP
Start	2841	End	6877
GI	3913791	Score	1593
Exons	2841..2926, 3066..3135, 3231..3311, 3531..3623, 3801..3881, 3976..4065, 4183..4276, 4433..4501, 4575..4645, 4739..4807, 4915..4998, 5125..5217, 5365..5472, 5667..5817, 6396..6656, 6809..6877		
GI Descrip.	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYLCYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) gi|2407615 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon esculentum]		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1461	Strand	-
Start	15264	End	15726
Name	OJ990513_03.9924.C6.o3.gp	Method	AAT/GAP

Start	15264	End	15726
GI	3768859	Score	761
Exons	15264..15726		
GI Descrip.	755772/emb|X85747|OS1A1COX 1.0e-158 O.sativa mRNA for 1-aminocyclopropane-1-carboxylate oxidase		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o1.tm	Method	TBLASTX:Maize
Start	2460	End	6464
GI	none	Score	50
Exons	2460..2504, 2470..2505, 2502..2564, 2532..2561, 2833..2928, 2835..2927, 2837..2929, 3062..3136, 3064..3144, 3231..3311, 3232..3312, 3519..3623, 3528..3623, 3529..3624, 3798..3884, 3799..3882, 3973..4068, 3974..4066, 3974..4069, 4178..4276, 4183..4278, 4183..4275, 4427..4504, 4432..4503, 4575..4646, 4577..4660, 4724..4813, 4731..4841, 4906..4998, 4910..5002, 4913..4999, 4914..5000, 5124..5219, 5125..5220, 5125..5217, 5357..5410, 5362..5475, 5372..5476, 5666..5818, 5667..5819, 5667..5819, 5668..5820, 6389..6463, 6390..6464		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o1.tc	Method	TBLASTX:Cress
Start	2838	End	6496
GI	none	Score	66
Exons	2838..2927, 2842..2928, 3064..3144, 3066..3134, 3231..3311, 3244..3312, 3528..3623, 3529..3624, 3798..3884, 3799..3882, 3971..4054, 3973..4068, 4183..4278, 4183..4275, 4184..4276, 4427..4531, 4432..4503, 4575..4646, 4577..4660, 4730..4813, 4731..4841, 4906..4998, 4910..5002, 4913..4999, 5125..5220, 5125..5217, 5350..5475, 5351..5476, 5667..5822, 5668..5820, 6383..6496, 6384..6494		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o1.tw	Method	TBLASTX:Wheat
Start	3270	End	4275
GI	none	Score	71
Exons	3270..3311, 3271..3312, 3528..3623, 3529..3624, 3530..3625, 3530..3640, 3798..3884, 3799..3882, 3973..4068, 3974..4066, 3974..4069, 3975..4067, 4178..4273, 4182..4274, 4183..4275, 4183..4272		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o3.ts	Method	TBLASTX:Soybean
Start	3798	End	4068
GI	none	Score	101
Exons	3798..3884, 3799..3882, 3973..4068, 3974..4066, 3975..4067		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-

Start	15759	End	19448
Name	OJ990513_03.9924.C6.o2.ts	Method	TBLASTX:Soybean
Start	4181	End	6496
GI	none	Score	95
Exons	4181..4270, 4183..4275, 4196..4267, 4417..4506, 4430..4513, 4432..4503, 4575..4646, 4577..4660, 4730..4813, 4731..4835, 4906..4998, 4910..4999, 4914..5000, 4915..5001, 5125..5220, 5125..5217, 5350..5475, 5351..5476, 5667..5819, 5667..5819, 5668..5820, 6383..6496, 6384..6494		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o4.tw	Method	TBLASTX:Wheat
Start	9622	End	9849
GI	none	Score	198
Exons	9622..9849, 9642..9848		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o2.tc	Method	TBLASTX:Cress
Start	9658	End	9999
GI	none	Score	227
Exons	9658..9999, 9774..9974		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o1.ts	Method	TBLASTX:Soybean
Start	9744	End	10311
GI	none	Score	451
Exons	9744..10067, 9745..10311, 9745..10263		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o3.tm	Method	TBLASTX:Maize
Start	9787	End	10398
GI	none	Score	217
Exons	9787..10068, 9804..10073, 9805..10101, 10114..10398, 10147..10287, 10152..10349		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o3.tw	Method	TBLASTX:Wheat
Start	9913	End	10350
GI	none	Score	296
Exons	9913..10350, 9915..10094, 10164..10259		

Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o2.tm	Method	TBLASTX:Maize
Start	15517	End	19005
GI	none	Score	222

Exons	15517..15570, 15603..15632, 15723..16001, 15723..15983, 18922..19005, 18945..19004		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o2.tw	Method	TBLASTX:Wheat
Start	15721	End	19032
GI	none	Score	67
Exons	15721..15822, 15723..15983, 15731..15793, 15760..15984, 15869..15994, 18922..19032, 18945..19025		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o4.ts	Method	TBLASTX:Soybean
Start	15723	End	19336
GI	none	Score	96
Exons	15723..15977, 15790..15978, 15795..16007, 18945..19025, 18958..19035, 19092..19151, 19259..19336		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o3.np	Method	AAT/NAP
Start	15759	End	19342
GI	6862951	Score	496
Exons	15759..15984, 18946..19151, 19253..19342		
GI Descrip.	(AC019018) unknown protein [Arabidopsis thaliana]		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o3.tc	Method	TBLASTX:Cress
Start	15759	End	19336
GI	none	Score	66
Exons	15759..15878, 15759..15902, 15903..15977, 15906..16007, 18945..19145, 18955..19035, 19259..19336		
Seq. No.	713	Seq. ID	OJ990513_03.9924.C6
Gene No.	1462	Strand	-
Start	15759	End	19448
Name	OJ990513_03.9924.C6.o5.gp	Method	AAT/GAP
Start	19010	End	19448
GI	none	Score	641
Exons	19010..19151, 19253..19448		
Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1463	Strand	+
Start	1306	End	1971
Name	OJ990513_03.9924.C7.o1.gs	Method	GENSCAN
Start	1306	End	1971
GI	none	Score	.76
Exons	1306..1360, 1858..1971		
Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1464	Strand	+

Start	4806	End	7735
Name	OJ990513_03.9924.C7.o1.np	Method	AAT/NAP
Start	4806	End	7723
GI	6691716	Score	2469
Exons	4806..5690, 5888..6066, 6149..6251, 6328..6507, 6585..6772, 6847..6948, 7098..7212, 7286..7723		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1464	Strand	+
Start	4806	End	7735
Name	OJ990513_03.9924.C7.o2.gs	Method	GENSCAN
Start	4806	End	7735
GI	none	Score	.97
Exons	4806..5690, 5747..6066, 6149..6507, 6585..6772, 6847..7036, 7286..7501, 7581..7735		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o5.tw	Method	TBLASTX:Wheat
Start	4926	End	5216
GI	none	Score	213
Exons	4926..5216		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o3.gs	Method	GENSCAN
Start	8066	End	10495
GI	none	Score	.66
Exons	8066..8389, 8540..8879, 8897..9030, 9323..9516, 9619..9886, 10181..10495		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o2.np	Method	AAT/NAP
Start	8069	End	10704
GI	5902445	Score	4003
Exons	8069..10704		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o3.tw	Method	TBLASTX:Wheat
Start	8078	End	8692
GI	none	Score	84
Exons	8078..8209, 8201..8692, 8403..8531, 8586..8672		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o3.tm	Method	TBLASTX:Maize

Start	8117	End	8371
GI	none	Score	97
Exons	8117..8218, 8118..8219, 8198..8371, 8199..8273		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o4.tm	Method	TBLASTX:Maize
Start	8462	End	8735
GI	none	Score	48
Exons	8462..8548, 8558..8641, 8586..8645, 8628..8735, 8636..8734		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o2.tw	Method	TBLASTX:Wheat
Start	8805	End	9194
GI	none	Score	173
Exons	8805..9194, 8807..9193		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o1.tm	Method	TBLASTX:Maize
Start	8837	End	9193
GI	none	Score	232
Exons	8837..8884, 8876..9193, 8877..9179		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o6.tw	Method	TBLASTX:Wheat
Start	9197	End	9496
GI	none	Score	134
Exons	9197..9295, 9338..9496		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o4.tw	Method	TBLASTX:Wheat
Start	9512	End	9934
GI	none	Score	217
Exons	9512..9934, 9588..9929		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o2.ts	Method	TBLASTX:Soybean
Start	9555	End	9943
GI	none	Score	121
Exons	9555..9803, 9557..9799, 9839..9943		

Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o5.tm	Method	TBLASTX:Maize
Start	9608	End	9880

GI	none	Score	122
Exons	9608..9706, 9710..9880		
Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o1.tw	Method	TBLASTX:Wheat
Start	9971	End	10406
GI	none	Score	40
Exons	9971..10399, 9972..10130, 9990..10406, 10191..10400		
Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o2.tm	Method	TBLASTX:Maize
Start	10082	End	10498
GI	none	Score	149
Exons	10082..10225, 10247..10498, 10248..10469		
Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o1.ts	Method	TBLASTX:Soybean
Start	10169	End	10608
GI	none	Score	79
Exons	10169..10498, 10256..10498, 10510..10608, 10511..10561		
Seq. No.	714	Seq. ID	OJ990513_03.9924.C7
Gene No.	1465	Strand	-
Start	8066	End	10704
Name	OJ990513_03.9924.C7.o7.tw	Method	TBLASTX:Wheat
Start	10409	End	10648
GI	none	Score	82
Exons	10409..10498, 10510..10611, 10520..10648		
Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1466	Strand	+
Start	2348	End	9142
Name	OJ990513_03.9924.C8.o2.gs	Method	GENSCAN
Start	2348	End	8844
GI	none	Score	.55
Exons	2348..2587, 3227..3755, 3792..4748, 5127..5392, 5824..5978, 6315..7157, 7215..7306, 8237..8844		
Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1466	Strand	+
Start	2348	End	9142
Name	OJ990513_03.9924.C8.o2.np	Method	AAT/NAP
Start	2688	End	9142
GI	6691193	Score	825
Exons	2688..2744, 5989..7437, 7734..7867, 8032..9142		
GI Descrip.	(AC007534) F7F22.17 [Arabidopsis thaliana]		
Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1466	Strand	+
Start	2348	End	9142
Name	OJ990513_03.9924.C8.o1.np	Method	AAT/NAP

Start	4208	End	9096
GI	4206306	Score	1298
Exons	4208..4234, 4547..4628, 5307..5768, 5884..9096		
GI Descrip.	(AF049110) prpol [Zea mays]		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1467	Strand	+
Start	16370	End	26596
Name	OJ990513_03.9924.C8.o5.gs	Method	GENSCAN
Start	16370	End	25013
GI	none	Score	.61
Exons	16370..16456, 17648..17695, 17700..18569, 18591..18945, 19053..20592, 20689..21202, 21653..22062, 22364..22765, 22794..22918, 23048..23115, 23213..23347, 24308..24461, 24907..25013		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1467	Strand	+
Start	16370	End	26596
Name	OJ990513_03.9924.C8.o3.np	Method	AAT/NAP
Start	17652	End	26596
GI	5922631	Score	4589
Exons	17652..17776, 18035..18294, 18562..18731, 18777..19345, 19388..19547, 19674..20600, 21207..22200, 23161..23347, 26545..26596		
GI Descrip.	(AP000492) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] gi|6016864|dbj|BAA85207.1| (AP000570) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativ		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1467	Strand	+
Start	16370	End	26596
Name	OJ990513_03.9924.C8.o4.np	Method	AAT/NAP
Start	24308	End	24513
GI	4680186	Score	255
Exons	24308..24513		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1468	Strand	-
Start	129	End	814
Name	OJ990513_03.9924.C8.o1.gs	Method	GENSCAN
Start	129	End	814
GI	none	Score	.91
Exons	129..215, 308..380, 479..585, 713..814		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1469	Strand	-
Start	9449	End	11701
Name	OJ990513_03.9924.C8.o3.gs	Method	GENSCAN
Start	9449	End	11701
GI	none	Score	.82
Exons	9449..10129, 10208..10321, 10643..10948, 11030..11701		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1470	Strand	-
Start	11870	End	15788
Name	OJ990513_03.9924.C8.o4.gs	Method	GENSCAN
Start	11870	End	15788
GI	none	Score	.75
Exons	11870..12487, 12586..12741, 12989..13066, 13158..13230, 13329..13435, 15340..15492, 15762..15788		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1471	Strand	-
Start	24060	End	24441
Name	OJ990513_03.9924.C8.o1.gp	Method	AAT/GAP
Start	24060	End	24441
GI	uC-osflcyp033a04b1	Score	671
Exons	24060..24441		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o4.tw	Method	TBLASTX:Wheat
Start	5989	End	20737
GI	none	Score	83
Exons	5989..6141, 19940..20116, 20161..20397, 20165..20395, 20501..20737, 20509..20733		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o5.ts	Method	TBLASTX:Soybean
Start	6064	End	21022
GI	none	Score	124
Exons	6064..6288, 6295..6429, 20657..20881, 20888..21022		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o2.tm	Method	TBLASTX:Maize
Start	6154	End	21091
GI	none	Score	251
Exons	6154..6483, 6168..6383, 20747..21091, 20794..21090		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o1.tw	Method	TBLASTX:Wheat
Start	6226	End	21193
GI	none	Score	73
Exons	6226..6282, 6277..6630, 6285..6587, 6289..6630, 20870..21076, 21080..21193		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805

Name	OJ990513_03.9924.C8.o1.tm	Method	TBLASTX:Maize
Start	6499	End	21535
GI	none	Score	410
Exons	6499..6831, 6499..6762, 6832..6957, 6837..6956, 21092..21535, 21100..21150, 21235..21411		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o2.tw	Method	TBLASTX:Wheat
Start	6631	End	21607
GI	none	Score	139
Exons	6631..6825, 6648..6758, 6925..7026, 21232..21606, 21233..21607		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o2.ts	Method	TBLASTX:Soybean
Start	6646	End	21633
GI	none	Score	160
Exons	6646..6834, 6684..6758, 6814..6924, 6925..7113, 6969..7100, 21236..21622, 21283..21408, 21463..21633		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o3.tw	Method	TBLASTX:Wheat
Start	7195	End	22183
GI	none	Score	91
Exons	7195..7398, 7296..7397, 7437..7517, 7438..7578, 21775..22005, 21776..22006, 22036..22182, 22037..22183		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o1.ts	Method	TBLASTX:Soybean
Start	7263	End	22198
GI	none	Score	147
Exons	7263..7415, 7264..7401, 7422..7589, 7423..7674, 21893..21997, 21901..21996, 22033..22182, 22037..22198		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o3.ts	Method	TBLASTX:Soybean
Start	8113	End	8514
GI	none	Score	243
Exons	8113..8514, 8220..8270, 8295..8426		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o3.tm	Method	TBLASTX:Maize
Start	8128	End	8493
GI	none	Score	82
Exons	8128..8271, 8269..8493		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o6.tw	Method	TBLASTX:Wheat
Start	8665	End	9081
GI	none	Score	219
Exons	8665..9081, 8874..9047		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o4.ts	Method	TBLASTX:Soybean
Start	8857	End	9107
GI	none	Score	235
Exons	8857..9102, 8859..9029, 9066..9107		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o5.tw	Method	TBLASTX:Wheat
Start	18983	End	19360
GI	none	Score	259
Exons	18983..19360		

Seq. No.	715	Seq. ID	OJ990513_03.9924.C8
Gene No.	1472	Strand	-
Start	24906	End	26805
Name	OJ990513_03.9924.C8.o5.np	Method	AAT/NAP
Start	24906	End	26805
GI	6907087	Score	1225
Exons	24906..25007, 25548..26225, 26435..26805		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1473	Strand	+
Start	1	End	1722
Name	OJ990513_03.9924.C9.o1.np	Method	AAT/NAP
Start	1	End	1719
GI	5902445	Score	1963
Exons	1..48, 361..1719		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1473	Strand	+
Start	1	End	1722
Name	OJ990513_03.9924.C9.o1.gs	Method	GENSCAN
Start	529	End	1722
GI	none	Score	.89
Exons	529..1722		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1474	Strand	+
Start	14384	End	16622
Name	OJ990513_03.9924.C9.o3.np	Method	AAT/NAP
Start	14384	End	16622

GI	2213632	Score	751
Exons	14384..15138, 16598..16622		
GI Descrip.	(AC000103) F21J9.24 [Arabidopsis thaliana]		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1475	Strand	-
Start	2038	End	8169
Name	OJ990513_03.9924.C9.o2.gs	Method	GENSCAN
Start	2038	End	6597
GI	none	Score	.76
Exons	2038..2483, 2557..2673, 2734..2923, 2997..3079, 3263..3448, 3521..3651, 5461..5503, 5917..6129, 6256..6327, 6489..6597		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1475	Strand	-
Start	2038	End	8169
Name	OJ990513_03.9924.C9.o2.np	Method	AAT/NAP
Start	2044	End	8169
GI	6691716	Score	2382
Exons	2044..2483, 2557..2673, 2824..2923, 2997..3184, 3263..3444, 3521..3621, 3705..3759, 7008..7154, 7343..8169		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1475	Strand	-
Start	2038	End	8169
Name	OJ990513_03.9924.C9.o3.gs	Method	GENSCAN
Start	7816	End	8169
GI	none	Score	.65
Exons	7816..8169		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1476	Strand	-
Start	9435	End	9680
Name	OJ990513_03.9924.C9.o4.gs	Method	GENSCAN
Start	9435	End	9680
GI	none	Score	.97
Exons	9435..9680		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1477	Strand	-
Start	11886	End	13448
Name	OJ990513_03.9924.C9.o5.gs	Method	GENSCAN
Start	11886	End	13448
GI	none	Score	.93
Exons	11886..12351, 12605..12715, 13243..13448		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o3.tm	Method	TBLASTX:Maize
Start	645	End	980
GI	none	Score	423
Exons	645..980, 646..978		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o2.tw	Method	TBLASTX:Wheat
Start	651	End	1040
GI	none	Score	395
Exons	651..1040, 652..1038		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o4.tw	Method	TBLASTX:Wheat
Start	1069	End	1359
GI	none	Score	250
Exons	1069..1359, 1080..1355		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o5.tm	Method	TBLASTX:Maize
Start	1110	End	1383
GI	none	Score	91
Exons	1110..1217, 1111..1209, 1200..1274, 1204..1284, 1297..1383		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o4.tm	Method	TBLASTX:Maize
Start	1417	End	1671
GI	none	Score	156
Exons	1417..1590, 1530..1589, 1569..1670, 1570..1671		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o5.tw	Method	TBLASTX:Wheat
Start	1474	End	1725
GI	none	Score	172
Exons	1474..1653, 1480..1647, 1687..1725		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o2.tm	Method	TBLASTX:Maize
Start	4713	End	14608
GI	none	Score	430
Exons	4713..4760, 4743..4838, 14129..14608, 14144..14608		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o3.tw	Method	TBLASTX:Wheat
Start	14126	End	14550
GI	none	Score	42
Exons	14126..14167, 14174..14548, 14185..14463, 14396..14548, 14494..14550		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o1.tm	Method	TBLASTX:Maize
Start	14626	End	15103
GI	none	Score	461
Exons	14626..14997, 14627..14998, 14848..15009, 14995..15036, 14996..15034, 15032..15103, 15038..15103		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o1.tw	Method	TBLASTX:Wheat
Start	14669	End	15091
GI	none	Score	216
Exons	14669..14854, 14680..14844, 14857..15009, 14864..15091, 14866..15081		

Seq. No.	716	Seq. ID	OJ990513_03.9924.C9
Gene No.	1478	Strand	-
Start	15660	End	16182
Name	OJ990513_03.9924.C9.o7.gs	Method	GENSCAN
Start	15660	End	16182
GI	none	Score	.63
Exons	15660..15710, 15847..16182		

Seq. No.	717	Seq. ID	OJ990513_03.9924.C10
Gene No.	1479	Strand	+
Start	1013	End	2238
Name	OJ990513_03.9924.C10.o1.gs	Method	GENSCAN
Start	1013	End	2238
GI	none	Score	.86
Exons	1013..1075, 1322..1343, 2099..2238		

Seq. No.	718	Seq. ID	OJ990513_03.9924.C11
Gene No.	1480	Strand	+
Start	114	End	269
Name	OJ990513_03.9924.C11.o1.gs	Method	GENSCAN
Start	114	End	269
GI	none	Score	.95
Exons	114..269		

Seq. No.	719	Seq. ID	OJ990513_03.9924.C15
Gene No.	1481	Strand	-
Start	1	End	764
Name	OJ990513_03.9924.C15.o1.np	Method	AAT/NAP
Start	1	End	764
GI	6691716	Score	315
Exons	1..149, 228..409, 486..586, 670..764		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	719	Seq. ID	OJ990513_03.9924.C15
Gene No.	1481	Strand	-
Start	1	End	764
Name	OJ990513_03.9924.C15.o1.gs	Method	GENSCAN

Start	228	End	613
GI	none	Score	.73
Exons	228..413, 486..613		

Seq. No.	720	Seq. ID	OJ990513_03.9924.C16
Gene No.	1482	Strand	+
Start	189	End	434
Name	OJ990513_03.9924.C16.o1.gs	Method	GENSCAN
Start	189	End	434
GI	none	Score	.98
Exons	189..434		

Seq. No.	721	Seq. ID	OJ990513_03.9924.C17
Gene No.	1483	Strand	-
Start	431	End	718
Name	OJ990513_03.9924.C17.o1.np	Method	AAT/NAP
Start	431	End	718
GI	3292836	Score	78
Exons	431..516, 656..718		
GI Descrip.	(AL031018) gamma-glutamylcysteine synthetase [Arabidopsis thaliana] gi|4262277|gb|AAD14544| (AF068299) gamma-glutamylcysteine synthetase [Arabidopsis thaliana]		

Seq. No.	722	Seq. ID	OJ990513_03.9924.C20
Gene No.	1484	Strand	-
Start	1	End	569
Name	OJ990513_03.9924.C20.o1.np	Method	AAT/NAP
Start	1	End	569
GI	6651031	Score	80
Exons	1..43, 469..569		
GI Descrip.	(AF128455) gamma-glutamylcysteinyl synthetase precursor [Pisum sativum]		

Seq. No.	723	Seq. ID	OJ990513_03.9924.C21
Gene No.	1485	Strand	-
Start	54	End	566
Name	OJ990513_03.9924.C21.o1.np	Method	AAT/NAP
Start	54	End	566
GI	5902447	Score	279
Exons	54..566		
GI Descrip.	(AB030283) orf4 [Oryza sativa]		

Seq. No.	723	Seq. ID	OJ990513_03.9924.C21
Gene No.	1485	Strand	-
Start	54	End	566
Name	OJ990513_03.9924.C21.o1.gs	Method	GENSCAN
Start	85	End	507
GI	none	Score	.81
Exons	85..270, 459..507		

Seq. No.	724	Seq. ID	OJ990513_03.9924.C22
Gene No.	1486	Strand	-
Start	57	End	407
Name	OJ990513_03.9924.C22.o1.gs	Method	GENSCAN
Start	57	End	407
GI	none	Score	.55
Exons	57..407		

Seq. No.	725	Seq. ID	OJ990513_03.9924.C23
Gene No.	1487	Strand	+
Start	445	End	498
Name	OJ990513_03.9924.C23.o1.gs	Method	GENSCAN
Start	445	End	498
GI	none	Score	.58
Exons	445..498		

Seq. No.	725	Seq. ID	OJ990513_03.9924.C23
Gene No.	1488	Strand	-
Start	1	End	553
Name	OJ990513_03.9924.C23.o1.np	Method	AAT/NAP
Start	1	End	553
GI	4680180	Score	189
Exons	1..22, 364..553		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	726	Seq. ID	OJ990513_03.9924.C24
Gene No.	1489	Strand	-
Start	301	End	343
Name	OJ990513_03.9924.C24.o1.gs	Method	GENSCAN
Start	301	End	343
GI	none	Score	.44
Exons	301..343		

Seq. No.	727	Seq. ID	OJ990513_03.9924.C26
Gene No.	1490	Strand	-
Start	1	End	256
Name	OJ990513_03.9924.C26.o1.np	Method	AAT/NAP
Start	1	End	256
GI	1196998	Score	448
Exons	1..256		
GI Descrip.	(J01829) unknown protein [Transposon Tn10] gi|5103202|dbj|BAA78838.1| (AP000342) transposase of Tn10 [Plasmid R100] gi|5706382|dbj|BAA83097.1| (AB026428) transposase [Methylomonas aminofaciens] gi|5738092|gb|AAD50250.1|AF162223_9 (AF162223) IS10-right transposase [Shigella flexneri] gi|6721110|gb|AAF26764.1|AC007396_13 (AC007396) T4O12.21 [Arabidopsis thaliana]		

Seq. No.	728	Seq. ID	OJ990503_08.9924.C5
Gene No.	1491	Strand	+
Start	151	End	542
Name	OJ990503_08.9924.C5.o1.gs	Method	GENSCAN
Start	151	End	542
GI	none	Score	.46
Exons	151..542		

Seq. No.	729	Seq. ID	OJ990503_08.9924.C6
Gene No.	1492	Strand	-
Start	29	End	84
Name	OJ990503_08.9924.C6.o1.gs	Method	GENSCAN
Start	29	End	84
GI	none	Score	.62
Exons	29..84		

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o1.gp	Method	AAT/GAP
Start	96	End	980
GI	292_1.R1084	Score	1146
Exons	96..369, 524..697, 799..980		
GI Descrip.	'2429290 1.0e-156 (AF014469) peroxidase [Oryza sativa]'		

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o1.gs	Method	GENSCAN
Start	163	End	967
GI	none	Score	.83
Exons	163..373, 423..463, 524..805,	868..967	

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o1.np	Method	AAT/NAP
Start	163	End	1044
GI	2429290	Score	828
Exons	163..369, 524..697, 799..1044		
GI Descrip.	(AF014469) peroxidase [Oryza sativa]		

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o1.ts	Method	TBLASTX:Soybean
Start	189	End	975
GI	none	Score	145
Exons	189..365, 229..369, 521..547, 801..971	550..693, 551..694, 799..975,	

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o2.tm	Method	TBLASTX:Maize
Start	204	End	370
GI	none	Score	104
Exons	204..368, 219..368, 232..369,	320..370	

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o1.tc	Method	TBLASTX:Cress
Start	243	End	981
GI	none	Score	114
Exons	243..365, 244..369, 521..547, 877..981	554..691, 556..690, 802..840,	

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o1.tm	Method	TBLASTX:Maize
Start	517	End	981

GI	none	Score	50
Exons	517..576, 518..547, 556..690, 557..691, 766..846, 801..887, 865..981		

Seq. No.	730	Seq. ID	OJ990503_08.9924.C9
Gene No.	1493	Strand	+
Start	96	End	1044
Name	OJ990503_08.9924.C9.o1.tw	Method	TBLASTX:Wheat
Start	580	End	981
GI	none	Score	154
Exons	580..696, 581..700, 789..851, 799..861, 835..981		

Seq. No.	731	Seq. ID	OJ990503_08.9924.C10
Gene No.	1494	Strand	+
Start	547	End	921
Name	OJ990503_08.9924.C10.o1.gs	Method	GENSCAN
Start	547	End	921
GI	none	Score	.63
Exons	547..645, 722..921		

Seq. No.	732	Seq. ID	OJ990503_08.9924.C11
Gene No.	1495	Strand	+
Start	1	End	1514
Name	OJ990503_08.9924.C11.o1.np	Method	AAT/NAP
Start	1	End	1511
GI	82613	Score	1130
Exons	1..171, 426..602, 889..1054, 1126..1511		
GI Descrip.	peroxidase (EC 1.11.1.7) precursor, pathogen-induced - wheat gi|21829|emb|CAA39486| (X56011) peroxidase [Triticum aestivum]		

Seq. No.	732	Seq. ID	OJ990503_08.9924.C11
Gene No.	1495	Strand	+
Start	1	End	1514
Name	OJ990503_08.9924.C11.o1.gs	Method	GENSCAN
Start	426	End	1514
GI	none	Score	.57
Exons	426..602, 1146..1514		

Seq. No.	732	Seq. ID	OJ990503_08.9924.C11
Gene No.	1496	Strand	-
Start	2111	End	2271
Name	OJ990503_08.9924.C11.o1.tm	Method	TBLASTX:Maize
Start	12	End	1511
GI	none	Score	89
Exons	12..83, 46..108, 60..107, 112..171, 120..170, 420..452, 450..572, 503..616, 888..974, 889..975, 953..1054, 957..1055, 961..1056, 1088..1273, 1119..1244, 1127..1273, 1235..1510, 1239..1511		

Seq. No.	732	Seq. ID	OJ990503_08.9924.C11
Gene No.	1496	Strand	-
Start	2111	End	2271
Name	OJ990503_08.9924.C11.o1.tc	Method	TBLASTX:Cress
Start	46	End	1508
GI	none	Score	138
Exons	46..168, 420..449, 456..572, 888..1055, 892..1056, 1119..1181, 1161..1358, 1265..1351, 1367..1504, 1434..1508		

Seq. No.	732	Seq. ID	OJ990503_08.9924.C11
Gene No.	1496	Strand	-
Start	2111	End	2271
Name	OJ990503_08.9924.C11.o1.ts	Method	TBLASTX:Soybean
Start	46	End	1508
GI	none	Score	137
Exons	46..168, 60..167, 459..572, 467..595, 889..1056, 891..1055, 1119..1244, 1133..1243, 1238..1381, 1239..1508, 1323..1487		

Seq. No.	732	Seq. ID	OJ990503_08.9924.C11
Gene No.	1496	Strand	-
Start	2111	End	2271
Name	OJ990503_08.9924.C11.o1.tw	Method	TBLASTX:Wheat
Start	891	End	1367
GI	none	Score	169
Exons	891..1055, 892..1056, 1119..1247, 1131..1247, 1244..1351, 1245..1367		

Seq. No.	732	Seq. ID	OJ990503_08.9924.C11
Gene No.	1496	Strand	-
Start	2111	End	2271
Name	OJ990503_08.9924.C11.o1.gp	Method	AAT/GAP
Start	2111	End	2271
GI	uC-osrocyp036g09b1	Score	263
Exons	2111..2271		
GI Descrip.	'5453379/gb|AAD43561.1|AF155124_1 7.0e-19 (AF155124) bacterial-induced peroxidase precursor [Gossypium hirsutum]'		

Seq. No.	733	Seq. ID	OJ990503_08.9924.C14
Gene No.	1497	Strand	+
Start	745	End	820
Name	OJ990503_08.9924.C14.o1.gp	Method	AAT/GAP
Start	745	End	820
GI	none	Score	144
Exons	745..820		

Seq. No.	733	Seq. ID	OJ990503_08.9924.C14
Gene No.	1498	Strand	-
Start	503	End	816
Name	OJ990503_08.9924.C14.o1.gs	Method	GENSCAN
Start	503	End	816
GI	none	Score	.67
Exons	503..691, 808..816		

Seq. No.	734	Seq. ID	OJ990503_08.9924.C18
Gene No.	1499	Strand	+
Start	1	End	677
Name	OJ990503_08.9924.C18.o1.np	Method	AAT/NAP
Start	1	End	677
GI	6016693	Score	96
Exons	1..64, 530..677		
GI Descrip.	(AC009991) putative disease resistance protein [Arabidopsis thaliana]		

Seq. No.	735	Seq. ID	OJ990503_08.9924.C20
Gene No.	1500	Strand	-

Start	56	End	270
Name	OJ990503_08.9924.C20.o1.gs	Method	GENSCAN
Start	56	End	270
GI	none	Score	.97
Exons	56..270		

Seq. No.	735	Seq. ID	OJ990503_08.9924.C20
Gene No.	1501	Strand	-
Start	220	End	451
Name	OJ990503_08.9924.C20.o1.gp	Method	AAT/GAP
Start	220	End	451
GI	9836_1.R1084	Score	401
Exons	220..451		
GI Descrip.	'5922603/dbj|AP000492.1|AP000492 3.0e-52 Oryza sativa genomic DNA, chromosome 1, clone:P0705D01'		

Seq. No.	736	Seq. ID	OJ990503_08.9924.C21
Gene No.	1502	Strand	+
Start	6	End	179
Name	OJ990503_08.9924.C21.o1.gs	Method	GENSCAN
Start	6	End	179
GI	none	Score	.96
Exons	6..179		

Seq. No.	737	Seq. ID	OJ990503_08.9924.C22
Gene No.	1503	Strand	+
Start	1	End	322
Name	OJ990503_08.9924.C22.o1.np	Method	AAT/NAP
Start	1	End	303
GI	2492782	Score	119
Exons	1..132, 231..303		
GI Descrip.	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) gi|504489 (L27992) alpha-galactosidase [Coffea arabica]		

Seq. No.	737	Seq. ID	OJ990503_08.9924.C22
Gene No.	1503	Strand	+
Start	1	End	322
Name	OJ990503_08.9924.C22.o1.tm	Method	TBLASTX:Maize
Start	16	End	322
GI	none	Score	179
Exons	16..132, 27..137, 29..133, 229..318, 235..297, 245..322		

Seq. No.	737	Seq. ID	OJ990503_08.9924.C22
Gene No.	1503	Strand	+
Start	1	End	322
Name	OJ990503_08.9924.C22.o1.tw	Method	TBLASTX:Wheat
Start	35	End	303
GI	none	Score	141
Exons	35..133, 37..132, 44..157, 241..303		

Seq. No.	738	Seq. ID	OJ990503_08.9924.C24
Gene No.	1504	Strand	-
Start	12	End	396
Name	OJ990503_08.9924.C24.o1.gs	Method	GENSCAN
Start	12	End	396
GI	none	Score	.8

Exons	12..58, 334..396		
Seq. No.	739	Seq. ID	OJ990503_08.9924.C28
Gene No.	1505	Strand	-
Start	211	End	719
Name	OJ990503_08.9924.C28.o1.gs	Method	GENSCAN
Start	211	End	719
GI	none	Score	.45
Exons	211..448, 712..719		
Seq. No.	740	Seq. ID	OJ990503_08.9924.C29
Gene No.	1506	Strand	-
Start	170	End	438
Name	OJ990503_08.9924.C29.o1.gs	Method	GENSCAN
Start	170	End	438
GI	none	Score	.78
Exons	170..438		
Seq. No.	741	Seq. ID	OJ990503_08.9924.C32
Gene No.	1507	Strand	+
Start	1	End	621
Name	OJ990503_08.9924.C32.o1.gp	Method	AAT/GAP
Start	1	End	621
GI	292_1.R1084	Score	1112
Exons	1..621		
GI Descrip.	'2429290 1.0e-156 (AF014469) peroxidase [Oryza sativa]'		
Seq. No.	741	Seq. ID	OJ990503_08.9924.C32
Gene No.	1507	Strand	+
Start	1	End	621
Name	OJ990503_08.9924.C32.o1.np	Method	AAT/NAP
Start	1	End	244
GI	2429290	Score	391
Exons	1..244		
GI Descrip.	(AF014469) peroxidase [Oryza sativa]		
Seq. No.	741	Seq. ID	OJ990503_08.9924.C32
Gene No.	1507	Strand	+
Start	1	End	621
Name	OJ990503_08.9924.C32.o1.gs	Method	GENSCAN
Start	59	End	247
GI	none	Score	.78
Exons	59..247		
Seq. No.	741	Seq. ID	OJ990503_08.9924.C32
Gene No.	1508	Strand	-
Start	792	End	866
Name	OJ990503_08.9924.C32.o1.tm	Method	TBLASTX:Maize
Start	1	End	243
GI	none	Score	270
Exons	1..72, 2..241, 21..77, 56..232, 163..243, 166..237		
Seq. No.	741	Seq. ID	OJ990503_08.9924.C32
Gene No.	1508	Strand	-
Start	792	End	866
Name	OJ990503_08.9924.C32.o1.ts	Method	TBLASTX:Soybean
Start	1	End	259

GI	none	Score	154
Exons	1..114, 1..72, 2..259, 6..77,	56..244,	166..246

Seq. No.	741	Seq. ID	OJ990503_08.9924.C32
Gene No.	1508	Strand	-
Start	792	End	866
Name	OJ990503_08.9924.C32.o2.gs	Method	GENSCAN
Start	792	End	866
GI	none	Score	.86
Exons	792..866		

Seq. No.	742	Seq. ID	OJ990503_08.9924.C33
Gene No.	1509	Strand	+
Start	456	End	619
Name	OJ990503_08.9924.C33.o1.gp	Method	AAT/GAP
Start	456	End	619
GI	23307_1.R1084	Score	280
Exons	456..619		
GI Descrip.	'1777312/dbj|BAA06311| 3.0e-67 (D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]'		

Seq. No.	743	Seq. ID	OJ990503_08.9924.C34
Gene No.	1510	Strand	+
Start	87	End	171
Name	OJ990503_08.9924.C34.o1.gs	Method	GENSCAN
Start	87	End	171
GI	none	Score	.43
Exons	87..171		

Seq. No.	744	Seq. ID	OJ990503_08.9924.C35
Gene No.	1511	Strand	+
Start	205	End	525
Name	OJ990503_08.9924.C35.o1.gs	Method	GENSCAN
Start	205	End	525
GI	none	Score	.8
Exons	205..276, 400..525		

Seq. No.	745	Seq. ID	OJ990503_08.9924.C42
Gene No.	1512	Strand	+
Start	1	End	314
Name	OJ990503_08.9924.C42.o1.gp	Method	AAT/GAP
Start	1	End	314
GI	23307_1.R1084	Score	563
Exons	1..314		
GI Descrip.	'1777312/dbj|BAA06311| 3.0e-67 (D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]'		

Seq. No.	745	Seq. ID	OJ990503_08.9924.C42
Gene No.	1512	Strand	+
Start	1	End	314
Name	OJ990503_08.9924.C42.o1.np	Method	AAT/NAP
Start	1	End	314
GI	4539389	Score	329
Exons	1..314		
GI Descrip.	(AL035526) putative protein kinase [Arabidopsis thaliana]		

Seq. No.	745	Seq. ID	OJ990503_08.9924.C42

Gene No.	1512	Strand	+
Start	1	End	314
Name	OJ990503_08.9924.C42.o1.tm	Method	TBLASTX:Maize
Start	3	End	314
GI	none	Score	154
Exons	3..188, 4..189, 4..183, 6..188, 191..313, 191..313, 195..314		

Seq. No.	745	Seq. ID	OJ990503_08.9924.C42
Gene No.	1512	Strand	+
Start	1	End	314
Name	OJ990503_08.9924.C42.o1.tc	Method	TBLASTX:Cress
Start	4	End	313
GI	none	Score	221
Exons	4..189, 9..197, 191..313, 191..277		

Seq. No.	745	Seq. ID	OJ990503_08.9924.C42
Gene No.	1512	Strand	+
Start	1	End	314
Name	OJ990503_08.9924.C42.o1.tw	Method	TBLASTX:Wheat
Start	4	End	189
GI	none	Score	186
Exons	4..189, 6..185		

Seq. No.	745	Seq. ID	OJ990503_08.9924.C42
Gene No.	1512	Strand	+
Start	1	End	314
Name	OJ990503_08.9924.C42.o1.ts	Method	TBLASTX:Soybean
Start	4	End	310
GI	none	Score	212
Exons	4..189, 9..188, 190..237, 191..310		

Seq. No.	745	Seq. ID	OJ990503_08.9924.C42
Gene No.	1512	Strand	+
Start	1	End	314
Name	OJ990503_08.9924.C42.o1.gs	Method	GENSCAN
Start	13	End	171
GI	none	Score	.83
Exons	13..171		

Seq. No.	746	Seq. ID	OJ990503_08.9924.C44
Gene No.	1513	Strand	-
Start	227	End	307
Name	OJ990503_08.9924.C44.o1.gs	Method	GENSCAN
Start	227	End	307
GI	none	Score	.62
Exons	227..307		

Seq. No.	747	Seq. ID	OJ990503_08.9924.C45
Gene No.	1514	Strand	-
Start	339	End	482
Name	OJ990503_08.9924.C45.o1.gs	Method	GENSCAN
Start	339	End	482
GI	none	Score	.78
Exons	339..482		

Seq. No.	748	Seq. ID	OJ990503_08.9924.C48
Gene No.	1515	Strand	+

Start	1	End	611
Name	OJ990503_08.9924.C48.o1.np	Method	AAT/NAP
Start	1	End	611
GI	6815099	Score	85
Exons	1..43, 491..611		
GI Descrip.	(AP001081) hypothetical protein [Oryza sativa]		

Seq. No.	749	Seq. ID	OJ990503_08.9924.C49
Gene No.	1516	Strand	+
Start	52	End	303
Name	OJ990503_08.9924.C49.o1.gs	Method	GENSCAN
Start	52	End	303
GI	none	Score	.52
Exons	52..145, 207..303		

Seq. No.	750	Seq. ID	OJ990503_08.9924.C50
Gene No.	1517	Strand	+
Start	230	End	477
Name	OJ990503_08.9924.C50.o1.gs	Method	GENSCAN
Start	230	End	477
GI	none	Score	.55
Exons	230..349, 360..477		

Seq. No.	751	Seq. ID	OJ990503_08.9924.C51
Gene No.	1518	Strand	+
Start	133	End	522
Name	OJ990503_08.9924.C51.o1.gp	Method	AAT/GAP
Start	133	End	522
GI	LIB3433-003-Q6-K6-B7	Score	697
Exons	133..522		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 6.0e-28 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	751	Seq. ID	OJ990503_08.9924.C51
Gene No.	1519	Strand	+
Start	991	End	1072
Name	OJ990503_08.9924.C51.o1.gs	Method	GENSCAN
Start	991	End	1072
GI	none	Score	.83
Exons	991..1072		

Seq. No.	751	Seq. ID	OJ990503_08.9924.C51
Gene No.	1520	Strand	-
Start	1717	End	1856
Name	OJ990503_08.9924.C51.o1.np	Method	AAT/NAP
Start	1605	End	1856
GI	6069646	Score	142
Exons	1605..1856		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	751	Seq. ID	OJ990503_08.9924.C51
Gene No.	1520	Strand	-
Start	1717	End	1856

Name	OJ990503_08.9924.C51.o2.gs	Method	GENSCAN
Start	1717	End	1802
GI	none	Score	.75
Exons	1717..1802		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1521	Strand	+
Start	5947	End	8568
Name	OJ990503_08.9924.C52.o2.gs	Method	GENSCAN
Start	5947	End	7275
GI	none	Score	.9
Exons	5947..6754, 6878..7275		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1521	Strand	+
Start	5947	End	8568
Name	OJ990503_08.9924.C52.o1.np	Method	AAT/NAP
Start	6325	End	8568
GI	2213632	Score	775
Exons	6325..7067, 8535..8568		
GI Descrip.	(AC000103) F21J9.24 [Arabidopsis thaliana]		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947
Name	OJ990503_08.9924.C52.o3.tw	Method	TBLASTX:Wheat
Start	6115	End	6435
GI	none	Score	182
Exons	6115..6435, 6189..6380		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947
Name	OJ990503_08.9924.C52.o1.tm	Method	TBLASTX:Maize
Start	6280	End	6708
GI	none	Score	370
Exons	6280..6606, 6288..6605, 6610..6708, 6624..6707		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947
Name	OJ990503_08.9924.C52.o1.tw	Method	TBLASTX:Wheat
Start	6439	End	6846
GI	none	Score	223
Exons	6439..6603, 6441..6599, 6610..6846, 6627..6845		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947
Name	OJ990503_08.9924.C52.o2.tm	Method	TBLASTX:Maize
Start	6709	End	7047
GI	none	Score	222
Exons	6709..6942, 6801..6941, 6982..7047, 6982..7044		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947

Name	OJ990503_08.9924.C52.o2.tw	Method	TBLASTX:Wheat
Start	6847	End	7059
GI	none	Score	198
Exons	6847..7059, 6849..7043, 6922..7044		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947
Name	OJ990503_08.9924.C52.o2.np	Method	AAT/NAP
Start	8652	End	10901
GI	2317934	Score	136
Exons	8652..8743, 9550..10054, 10110..10901		
GI Descrip.	(U97553) unknown [murine herpesvirus 68]		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947
Name	OJ990503_08.9924.C52.o3.np	Method	AAT/NAP
Start	8697	End	14947
GI	4895218	Score	68
Exons	8697..8717, 12866..12986, 13995..14100, 14885..14947		
GI Descrip.	(AC007660) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	752	Seq. ID	OJ990503_08.9924.C52
Gene No.	1522	Strand	-
Start	9237	End	14947
Name	OJ990503_08.9924.C52.o3.gs	Method	GENSCAN
Start	9237	End	14518
GI	none	Score	.71
Exons	9237..9301, 9583..9708, 9916..10009, 10078..10182, 10320..10465, 10602..10791, 12365..12986, 13995..14132, 14229..14518		

Seq. No.	753	Seq. ID	OJ990503_08.9924.C54
Gene No.	1523	Strand	-
Start	9	End	1085
Name	OJ990503_08.9924.C54.o1.gs	Method	GENSCAN
Start	9	End	1085
GI	none	Score	.57
Exons	9..1085		

Seq. No.	754	Seq. ID	OJ990503_08.9924.C56
Gene No.	1524	Strand	+
Start	418	End	497
Name	OJ990503_08.9924.C56.o1.gs	Method	GENSCAN
Start	418	End	497
GI	none	Score	.77
Exons	418..497		

Seq. No.	755	Seq. ID	OJ990503_08.9924.C58
Gene No.	1525	Strand	+
Start	1	End	831
Name	OJ990503_08.9924.C58.o1.np	Method	AAT/NAP
Start	1	End	831
GI	4539658	Score	106
Exons	1..54, 573..726, 787..831		
GI Descrip.	(AF061282) serine carboxypeptidase-like protein [Sorghum bicolor]		

Seq. No.	755	Seq. ID	OJ990503_08.9924.C58
Gene No.	1526	Strand	-
Start	199	End	478
Name	OJ990503_08.9924.C58.o1.gs	Method	GENSCAN
Start	199	End	478
GI	none	Score	.43
Exons	199..478		

Seq. No.	756	Seq. ID	OJ990503_08.9924.C60
Gene No.	1527	Strand	+
Start	1	End	630
Name	OJ990503_08.9924.C60.o1.np	Method	AAT/NAP
Start	1	End	630
GI	6069659	Score	94
Exons	1..83, 179..373, 560..630		
GI Descrip.	(AP000616) hypothetical protein [Oryza sativa]		

Seq. No.	757	Seq. ID	OJ990503_08.9924.C61
Gene No.	1528	Strand	+
Start	56	End	169
Name	OJ990503_08.9924.C61.o1.gs	Method	GENSCAN
Start	56	End	169
GI	none	Score	.76
Exons	56..169		

Seq. No.	758	Seq. ID	OJ990503_08.9924.C63
Gene No.	1529	Strand	-
Start	870	End	1229
Name	OJ990503_08.9924.C63.o1.gs	Method	GENSCAN
Start	870	End	1229
GI	none	Score	.99
Exons	870..1229		

Seq. No.	759	Seq. ID	OJ990503_08.9924.C68
Gene No.	1530	Strand	-
Start	129	End	857
Name	OJ990503_08.9924.C68.o1.tc	Method	TBLASTX:Cress
Start	75	End	857
GI	none	Score	62
Exons	75..278, 132..407, 132..845, 132..500, 465..851, 522..686, 523..696, 525..854, 525..851, 525..845, 525..851, 525..851, 526..831, 528..854, 801..857		

Seq. No.	759	Seq. ID	OJ990503_08.9924.C68
Gene No.	1530	Strand	-
Start	129	End	857
Name	OJ990503_08.9924.C68.o1.ts	Method	TBLASTX:Soybean
Start	120	End	857
GI	none	Score	142
Exons	120..335, 132..503, 132..407, 132..245, 132..359, 159..413, 168..503, 504..851, 504..836, 525..857, 525..845, 525..797, 525..845, 525..851, 567..851, 588..674, 594..851		

Seq. No.	759	Seq. ID	OJ990503_08.9924.C68
Gene No.	1530	Strand	-
Start	129	End	857

Name	OJ990503_08.9924.C68.o1.np	Method	AAT/NAP
Start	129	End	857
GI	1684913	Score	333
Exons	129..857		
GI Descrip.	(U77888) receptor-like protein kinase [Ipomoea nil]		

Seq. No.	759	Seq. ID	OJ990503_08.9924.C68
Gene No.	1530	Strand	-
Start	129	End	857
Name	OJ990503_08.9924.C68.o1.tm	Method	TBLASTX:Maize
Start	132	End	857
GI	none	Score	79
Exons	132..383, 141..407, 159..410, 159..413, 162..401, 168..377, 225..407, 231..836, 492..635, 504..857, 505..615, 511..831, 525..857, 585..845, 588..845, 660..857, 681..854, 738..851		

Seq. No.	760	Seq. ID	OJ990503_08.9924.C70
Gene No.	1531	Strand	-
Start	262	End	2947
Name	OJ990503_08.9924.C70.o1.gs	Method	GENSCAN
Start	262	End	2947
GI	none	Score	.9
Exons	262..755, 1345..1460, 2193..2244, 2668..2947		

Seq. No.	760	Seq. ID	OJ990503_08.9924.C70
Gene No.	1531	Strand	-
Start	262	End	2947
Name	OJ990503_08.9924.C70.o1.np	Method	AAT/NAP
Start	497	End	1937
GI	6907088	Score	671
Exons	497..891, 1386..1624, 1800..1937		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	761	Seq. ID	OJ990503_08.9924.C71
Gene No.	1532	Strand	+
Start	148	End	2673
Name	OJ990503_08.9924.C71.o1.gs	Method	GENSCAN
Start	148	End	2673
GI	none	Score	.4
Exons	148..241, 792..929, 1127..1344, 1895..2007, 2577..2673		

Seq. No.	762	Seq. ID	OJ990503_08.9924.C72
Gene No.	1533	Strand	+
Start	459	End	532
Name	OJ990503_08.9924.C72.o1.gs	Method	GENSCAN
Start	459	End	532
GI	none	Score	.5
Exons	459..532		

Seq. No.	762	Seq. ID	OJ990503_08.9924.C72
Gene No.	1534	Strand	-
Start	3222	End	3402
Name	OJ990503_08.9924.C72.o2.gs	Method	GENSCAN
Start	3222	End	3402
GI	none	Score	.84
Exons	3222..3402		

Seq. No.	763	Seq. ID	OJ990503_08.9924.C73
Gene No.	1535	Strand	-
Start	1319	End	1616
Name	OJ990503_08.9924.C73.o1.gs	Method	GENSCAN
Start	1319	End	1616
GI	none	Score	1
Exons	1319..1616		

Seq. No.	764	Seq. ID	OJ990503_08.9924.C74
Gene No.	1536	Strand	+
Start	70	End	1253
Name	OJ990503_08.9924.C74.o1.np	Method	AAT/NAP
Start	70	End	1253
GI	6472921	Score	115
Exons	70..254, 1145..1253		
GI Descrip.	(AB035271) elicitor-induced DNA-binding protein homolog [Matricaria chamomilla]		

Seq. No.	764	Seq. ID	OJ990503_08.9924.C74
Gene No.	1536	Strand	+
Start	70	End	1253
Name	OJ990503_08.9924.C74.o1.gs	Method	GENSCAN
Start	81	End	633
GI	none	Score	.94
Exons	81..633		

Seq. No.	764	Seq. ID	OJ990503_08.9924.C74
Gene No.	1537	Strand	+
Start	1182	End	1603
Name	OJ990503_08.9924.C74.o2.gp	Method	AAT/GAP
Start	1182	End	1603
GI	37688_1.R1084	Score	840
Exons	1182..1603		
GI Descrip.	'1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence'		

Seq. No.	764	Seq. ID	OJ990503_08.9924.C74
Gene No.	1538	Strand	-
Start	868	End	1195
Name	OJ990503_08.9924.C74.o1.gp	Method	AAT/GAP
Start	868	End	1195
GI	6025053	Score	565
Exons	868..1195		

Seq. No.	765	Seq. ID	OJ990503_08.9924.C76
Gene No.	1539	Strand	-
Start	1	End	305
Name	OJ990503_08.9924.C76.o1.np	Method	AAT/NAP
Start	1	End	305
GI	5803259	Score	419
Exons	1..305		
GI Descrip.	(AP000399) hypothetical protein [Oryza sativa]		

Seq. No.	765	Seq. ID	OJ990503_08.9924.C76
Gene No.	1539	Strand	-
Start	1	End	305
Name	OJ990503_08.9924.C76.o1.gs	Method	GENSCAN

Start	6	End	272
GI	none	Score	.96
Exons	6..272		

Seq. No.	766	Seq. ID	OJ990503_08.9924.C77
Gene No.	1540	Strand	-
Start	75	End	188
Name	OJ990503_08.9924.C77.o1.gs	Method	GENSCAN
Start	75	End	188
GI	none	Score	.51
Exons	75..188		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1541	Strand	+
Start	548	End	692
Name	OJ990503_08.9924.C79.o1.gs	Method	GENSCAN
Start	548	End	692
GI	none	Score	.68
Exons	548..692		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1542	Strand	+
Start	3058	End	3464
Name	OJ990503_08.9924.C79.o2.gp	Method	AAT/GAP
Start	3058	End	3464
GI	none	Score	798
Exons	3058..3464		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1543	Strand	-
Start	419	End	7382
Name	OJ990503_08.9924.C79.o1.gp	Method	AAT/GAP
Start	419	End	2396
GI	599_2.R1084	Score	1010
Exons	419..681, 1667..1797, 1979..2063, 2165..2257, 2347..2396		
GI Descrip.	'1350969/sp|P49216|RS26_ORYSA 2.0e-41 40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_ (D38011) ribosomal protein S31 [Oryza sativa]'		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1543	Strand	-
Start	419	End	7382
Name	OJ990503_08.9924.C79.o1.np	Method	AAT/NAP
Start	595	End	2260
GI	1350969	Score	581
Exons	595..681, 1667..1797, 1979..2063, 2165..2260		
GI Descrip.	40S RIBOSOMAL PROTEIN S26 (S31) gi|971284|dbj|BAA07208| (D38011) ribosomal protein S31 [Oryza sativa]		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1543	Strand	-
Start	419	End	7382
Name	OJ990503_08.9924.C79.o2.gs	Method	GENSCAN
Start	1645	End	7376
GI	none	Score	.54
Exons	1645..1667, 1714..1797, 1979..2063, 2165..2257, 2347..2457, 4019..4180, 5475..5597, 6186..6535, 7262..7376		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1543	Strand	-
Start	419	End	7382
Name	OJ990503_08.9924.C79.o2.np	Method	AAT/NAP
Start	3307	End	7382
GI	1946372	Score	547
Exons	3307..3424, 3663..3895, 5535..5659, 7262..7382		
GI Descrip.	(U93215) putative integral membrane protein [Arabidopsis thaliana]		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1544	Strand	-
Start	9291	End	10601
Name	OJ990503_08.9924.C79.o3.gp	Method	AAT/GAP
Start	8790	End	10601
GI	993_1.R1084	Score	2646
Exons	8790..9594, 9955..10267, 10375..10601		
GI Descrip.	'1041710 1.0e-121 (U30477) expansin Os-EXP2 [Oryza sativa]'		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1544	Strand	-
Start	9291	End	10601
Name	OJ990503_08.9924.C79.o3.gs	Method	GENSCAN
Start	9291	End	10513
GI	none	Score	.99
Exons	9291..9594, 9955..10267, 10375..10513		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1544	Strand	-
Start	9291	End	10601
Name	OJ990503_08.9924.C79.o3.np	Method	AAT/NAP
Start	9294	End	10513
GI	1041710	Score	1301
Exons	9294..9594, 9955..10267, 10375..10513		
GI Descrip.	(U30477) expansin Os-EXP2 [Oryza sativa]		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o3.tm	Method	TBLASTX:Maize
Start	1656	End	2259
GI	none	Score	117
Exons	1656..1802, 1695..1796, 1721..1798, 1977..2066, 1978..2064, 2142..2213, 2163..2258, 2164..2259		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o3.ts	Method	TBLASTX:Soybean
Start	1721	End	2259
GI	none	Score	92
Exons	1721..1795, 1980..2066, 1987..2064, 2154..2213, 2160..2258, 2164..2259		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-

Start	11330	End	13896
Name	OJ990503_08.9924.C79.o2.tm	Method	TBLASTX:Maize
Start	3629	End	7355
GI	none	Score	276
Exons	3629..3928, 3645..3926, 3680..3928, 3711..3935, 3754..3963, 4010..4180, 4011..4181, 4647..4829, 4682..4825, 5052..5150, 5472..5657, 5476..5664, 5476..5688, 7263..7355		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o2.ts	Method	TBLASTX:Soybean
Start	3641	End	4181
GI	none	Score	231
Exons	3641..3931, 3645..3932, 4010..4180, 4011..4181		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o1.tw	Method	TBLASTX:Wheat
Start	3701	End	4184
GI	none	Score	240
Exons	3701..3928, 3711..3926, 3711..3935, 3761..3928, 4010..4180, 4032..4184		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o4.tm	Method	TBLASTX:Maize
Start	8937	End	9408
GI	none	Score	43
Exons	8937..8957, 8968..9054, 8978..9010, 9101..9148, 9118..9189, 9121..9153, 9142..9207, 9149..9208, 9292..9324, 9293..9325, 9295..9408, 9327..9407		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o2.tc	Method	TBLASTX:Cress
Start	9292	End	9485
GI	none	Score	197
Exons	9292..9483, 9327..9485		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o1.ts	Method	TBLASTX:Soybean
Start	9295	End	10436
GI	none	Score	361
Exons	9295..9597, 9327..9596, 9954..10268, 9955..10269, 10201..10281, 10373..10435, 10374..10436		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o1.tm	Method	TBLASTX:Maize
Start	9409	End	10442

GI	none	Score	310
Exons	9409..9597, 9414..9596, 9922..10269, 9954..10022, 9954..10166, 9954..10268, 9955..10167, 10134..10181, 10201..10281, 10373..10441, 10374..10442		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o2.tw	Method	TBLASTX:Wheat
Start	9423	End	10097
GI	none	Score	132
Exons	9423..9596, 9424..9648, 9954..10097		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o1.tc	Method	TBLASTX:Cress
Start	9489	End	10585
GI	none	Score	142
Exons	9489..9596, 9496..9600, 9954..10268, 9955..10269, 10373..10435, 10374..10436, 10511..10585		

Seq. No.	767	Seq. ID	OJ990503_08.9924.C79
Gene No.	1545	Strand	-
Start	11330	End	13896
Name	OJ990503_08.9924.C79.o4.gs	Method	GENSCAN
Start	11330	End	13896
GI	none	Score	.46
Exons	11330..11529, 12096..12239, 13848..13896		

Seq. No.	768	Seq. ID	OJ990503_08.9924.C80
Gene No.	1546	Strand	-
Start	214	End	1499
Name	OJ990503_08.9924.C80.o1.gs	Method	GENSCAN
Start	214	End	1499
GI	none	Score	.85
Exons	214..440, 843..1051, 1122..1327, 1335..1499		

Seq. No.	768	Seq. ID	OJ990503_08.9924.C80
Gene No.	1547	Strand	-
Start	2728	End	3036
Name	OJ990503_08.9924.C80.o3.gs	Method	GENSCAN
Start	2728	End	3036
GI	none	Score	.6
Exons	2728..3036		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1548	Strand	+
Start	6533	End	8805
Name	OJ990503_08.9924.C81.o3.gs	Method	GENSCAN
Start	6533	End	7127
GI	none	Score	.93
Exons	6533..6600, 6905..7127		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1548	Strand	+
Start	6533	End	8805

Name	OJ990503_08.9924.C81.o1.np	Method	AAT/NAP
Start	6820	End	8502
GI	6539588	Score	207
Exons	6820..7132, 8480..8502		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1548	Strand	+
Start	6533	End	8805
Name	OJ990503_08.9924.C81.o1.gp	Method	AAT/GAP
Start	7756	End	8805
GI	26857_1.R1084	Score	1821
Exons	7756..8207, 8294..8805		
GI Descrip.	'6093512/sp|Q39950|NLTP_HELAN 1.0e-16 NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (LTP) (NSLTP) (SDI-9) >gi_1050918_emb_CAA63340_ (X92648) lipid transfer protein [Helianthus annuus]'		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1548	Strand	+
Start	6533	End	8805
Name	OJ990503_08.9924.C81.o2.np	Method	AAT/NAP
Start	7852	End	8214
GI	6492243	Score	453
Exons	7852..8214		
GI Descrip.	(AF109195) lipid transfer protein [Hordeum vulgare]		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1548	Strand	+
Start	6533	End	8805
Name	OJ990503_08.9924.C81.o4.gs	Method	GENSCAN
Start	7855	End	8223
GI	none	Score	.97
Exons	7855..8223		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1549	Strand	-
Start	720	End	3367
Name	OJ990503_08.9924.C81.o1.gs	Method	GENSCAN
Start	720	End	3367
GI	none	Score	.54
Exons	720..832, 860..913, 1111..1219, 2039..2097, 3172..3367		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1550	Strand	-
Start	4695	End	5919
Name	OJ990503_08.9924.C81.o2.gs	Method	GENSCAN
Start	4695	End	5919
GI	none	Score	.48
Exons	4695..4713, 4958..5019, 5422..5504, 5754..5919		

Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1551	Strand	
Start	7857	End	8208
Name	OJ990503_08.9924.C81.o1.tm	Method	TBLASTX:Maize
Start	7857	End	8205
GI	none	Score	108

Exons	7857..8009, 7939..8028, 7995..8117, 7996..8118, 8118..8204, 8119..8205		
Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1551	Strand	
Start	7857	End	8208
Name	OJ990503_08.9924.C81.o1.ts	Method	TBLASTX:Soybean
Start	7938	End	8202
GI	none	Score	235
Exons	7938..8105, 7939..8202, 8136..8201		
Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1551	Strand	
Start	7857	End	8208
Name	OJ990503_08.9924.C81.o1.tw	Method	TBLASTX:Wheat
Start	7938	End	8208
GI	none	Score	97
Exons	7938..8036, 7938..8204, 7939..8208		
Seq. No.	769	Seq. ID	OJ990503_08.9924.C81
Gene No.	1551	Strand	
Start	7857	End	8208
Name	OJ990503_08.9924.C81.o1.tc	Method	TBLASTX:Cress
Start	7939	End	8204
GI	none	Score	228
Exons	7939..8202, 7953..8204		
Seq. No.	770	Seq. ID	OJ990503_08.9924.C82
Gene No.	1552	Strand	+
Start	132	End	408
Name	OJ990503_08.9924.C82.o1.gs	Method	GENSCAN
Start	132	End	408
GI	none	Score	.5
Exons	132..408		
Seq. No.	770	Seq. ID	OJ990503_08.9924.C82
Gene No.	1553	Strand	+
Start	2805	End	3030
Name	OJ990503_08.9924.C82.o1.np	Method	AAT/NAP
Start	2805	End	3030
GI	6069646	Score	222
Exons	2805..3030		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		
Seq. No.	770	Seq. ID	OJ990503_08.9924.C82
Gene No.	1554	Strand	-
Start	1232	End	4519
Name	OJ990503_08.9924.C82.o2.gs	Method	GENSCAN
Start	1232	End	4519
GI	none	Score	.46
Exons	1232..1345, 1873..2006, 4477..4519		
Seq. No.	771	Seq. ID	OJ990503_08.9924.C83

Gene No.	1555	Strand	-
Start	1	End	143
Name	OJ990503_08.9924.C83.o1.gp	Method	AAT/GAP
Start	1	End	143
GI	LIB3431-026-P1-N1-F3	Score	274
Exons	1..143		
GI Descrip.	'5922603/dbj|AP000492.1|AP000492 3.0e-52 Oryza sativa genomic DNA, chromosome 1, clone:P0705D01'		

Seq. No.	772	Seq. ID	OJ990503_08.9924.C85
Gene No.	1556	Strand	+
Start	144	End	1237
Name	OJ990503_08.9924.C85.o1.gs	Method	GENSCAN
Start	144	End	1237
GI	none	Score	.9
Exons	144..570, 752..830, 1117..1237		

Seq. No.	772	Seq. ID	OJ990503_08.9924.C85
Gene No.	1557	Strand	+
Start	1738	End	7260
Name	OJ990503_08.9924.C85.o2.gs	Method	GENSCAN
Start	1738	End	6938
GI	none	Score	.48
Exons	1738..1842, 3285..3413, 4445..5027, 5503..5821, 5898..6071, 6190..6610, 6691..6833, 6857..6938		

Seq. No.	772	Seq. ID	OJ990503_08.9924.C85
Gene No.	1557	Strand	+
Start	1738	End	7260
Name	OJ990503_08.9924.C85.o2.np	Method	AAT/NAP
Start	1738	End	1824
GI	6721561	Score	94
Exons	1738..1824		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	772	Seq. ID	OJ990503_08.9924.C85
Gene No.	1557	Strand	+
Start	1738	End	7260
Name	OJ990503_08.9924.C85.o3.np	Method	AAT/NAP
Start	5809	End	7260
GI	5922636	Score	402
Exons	5809..6120, 6410..6543, 6780..6856, 7180..7260		
GI Descrip.	(AP000492) ESTs C99517(E20319),AU078130(E20319) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6016869|dbj|BAA85212.1| (AP000570) ESTs C99517(E20319),AU078130(E20319) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	772	Seq. ID	OJ990503_08.9924.C85
Gene No.	1557	Strand	+
Start	1738	End	7260
Name	OJ990503_08.9924.C85.o2.gp	Method	AAT/GAP
Start	6597	End	6772

GI	5771106	Score	245
Exons	6597..6772		
GI Descrip.	5922603/dbj|AP000492.1|AP000492 3.0e-52 Oryza sativa genomic DNA, chromosome 1, clone:P0705D01		

Seq. No.	772	Seq. ID	OJ990503_08.9924.C85
Gene No.	1557	Strand	+
Start	1738	End	7260
Name	OJ990503_08.9924.C85.o4.np	Method	AAT/NAP
Start	6811	End	7260
GI	5777631	Score	47
Exons	6811..6945, 7192..7260		
GI Descrip.	(AJ245900) CAA303719.1 protein [Oryza sativa]		

Seq. No.	772	Seq. ID	OJ990503_08.9924.C85
Gene No.	1558	Strand	-
Start	1616	End	5666
Name	OJ990503_08.9924.C85.o1.np	Method	AAT/NAP
Start	1616	End	5666
GI	4680183	Score	137
Exons	1616..1707, 5624..5666		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1559	Strand	+
Start	1704	End	4795
Name	OJ990503_08.9924.C86.o1.gs	Method	GENSCAN
Start	1704	End	4795
GI	none	Score	.54
Exons	1704..1848, 3676..3871, 4012..4168, 4358..4429, 4571..4795		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1560	Strand	+
Start	6774	End	9123
Name	OJ990503_08.9924.C86.o2.gs	Method	GENSCAN
Start	6774	End	9123
GI	none	Score	.68
Exons	6774..6934, 6988..7125, 8399..8594, 9004..9123		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1561	Strand	+
Start	10917	End	13761
Name	OJ990503_08.9924.C86.o1.gp	Method	AAT/GAP
Start	9625	End	11261
GI	none	Score	1026
Exons	9625..9801, 10896..11261		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1561	Strand	+
Start	10917	End	13761
Name	OJ990503_08.9924.C86.o1.np	Method	AAT/NAP
Start	10911	End	13758
GI	6714377	Score	1173
Exons	10911..11546, 12372..12629, 12765..12881, 13144..13758		
GI Descrip.	(AC012562) putative protein kinase [Arabidopsis thaliana]		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86

Gene No.	1561	Strand	+
Start	10917	End	13761
Name	OJ990503_08.9924.C86.o3.gs	Method	GENSCAN
Start	10917	End	13761
GI	none	Score	.77
Exons	10917..11546, 12372..12629, 12765..12884, 13144..13761		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1562	Strand	+
Start	17098	End	21179
Name	OJ990503_08.9924.C86.o5.gs	Method	GENSCAN
Start	17098	End	21179
GI	none	Score	.91
Exons	17098..17216, 19691..19780, 19985..20096, 20538..20750, 21096..21179		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o1.tm	Method	TBLASTX:Maize
Start	11015	End	13260
GI	none	Score	116
Exons	11015..11104, 11016..11120, 11017..11109, 11064..11357, 11108..11356, 11155..11358, 11198..11365, 11387..11431, 11388..11435, 11451..11552, 11467..11544, 12364..12618, 12365..12661, 12369..12662, 12369..12629, 12548..12634, 12758..12862, 12761..12862, 12762..12863, 12762..12866, 13144..13260, 13146..13259, 13150..13260		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o2.ts	Method	TBLASTX:Soybean
Start	11219	End	12452
GI	none	Score	50
Exons	11219..11275, 11333..11359, 11334..11360, 11348..11530, 11349..11552, 12369..12452, 12374..12445		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o1.tc	Method	TBLASTX:Cress
Start	12362	End	12839
GI	none	Score	77
Exons	12362..12484, 12365..12607, 12369..12608, 12762..12839		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o1.ts	Method	TBLASTX:Soybean
Start	12513	End	13610
GI	none	Score	147
Exons	12513..12629, 12513..12629, 12524..12631, 12548..12634, 12735..12881, 12735..12860, 12758..12880, 13143..13610, 13144..13608, 13146..13610		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86

Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o1.tw	Method	TBLASTX:Wheat
Start	13164	End	13469
GI	none	Score	196
Exons	13164..13247, 13165..13467, 13338..13469		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o2.tc	Method	TBLASTX:Cress
Start	13308	End	13665
GI	none	Score	233
Exons	13308..13517, 13309..13521, 13581..13616, 13582..13665		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o2.tm	Method	TBLASTX:Maize
Start	13534	End	13931
GI	none	Score	244
Exons	13534..13755, 13536..13868, 13896..13931		

Seq. No.	773	Seq. ID	OJ990503_08.9924.C86
Gene No.	1563	Strand	-
Start	23340	End	23645
Name	OJ990503_08.9924.C86.o6.gs	Method	GENSCAN
Start	23340	End	23645
GI	none	Score	.5
Exons	23340..23426, 23487..23645		

Seq. No.	774	Seq. ID	OJ990503_08.9924.C87
Gene No.	1564	Strand	+
Start	679	End	981
Name	OJ990503_08.9924.C87.o1.np	Method	AAT/NAP
Start	679	End	981
GI	2642433	Score	111
Exons	679..981		
GI Descrip.	(AC002391) putative receptor-like protein kinase [Arabidopsis thaliana]		

Seq. No.	774	Seq. ID	OJ990503_08.9924.C87
Gene No.	1564	Strand	+
Start	679	End	981
Name	OJ990503_08.9924.C87.o1.gs	Method	GENSCAN
Start	691	End	884
GI	none	Score	.96
Exons	691..884		

Seq. No.	774	Seq. ID	OJ990503_08.9924.C87
Gene No.	1564	Strand	+
Start	679	End	981
Name	OJ990503_08.9924.C87.o1.tm	Method	TBLASTX:Maize
Start	776	End	981
GI	none	Score	87
Exons	776..853, 798..944, 799..981, 922..981		

Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1565	Strand	+
Start	1	End	3109
Name	OJ990503_08.9924.C88.o1.np	Method	AAT/NAP
Start	1	End	3109
GI	4585876	Score	376
Exons	1..140, 1178..1957, 2984..3109		
GI Descrip.	(AC005850) Putative serine/threonine kinase [Arabidopsis thaliana]		

Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1565	Strand	+
Start	1	End	3109
Name	OJ990503_08.9924.C88.o1.gs	Method	GENSCAN
Start	582	End	2017
GI	none	Score	.62
Exons	582..2017		

Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o3.ts	Method	TBLASTX:Soybean
Start	530	End	969
GI	none	Score	279
Exons	530..871, 544..771, 545..742, 612..881, 899..937, 949..969	557..736, 559..867, 560..736,	

Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o3.tc	Method	TBLASTX:Cress
Start	557	End	984
GI	none	Score	61
Exons	557..664, 589..867, 590..865,	910..984	

Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o2.tm	Method	TBLASTX:Maize
Start	640	End	880
GI	none	Score	171
Exons	640..795, 641..802, 809..880,	833..874	

Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o3.tm	Method	TBLASTX:Maize
Start	1015	End	1153
GI	none	Score	90
Exons	1015..1152, 1050..1151, 1058..1153		

Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o2.ts	Method	TBLASTX:Soybean
Start	1088	End	1426
GI	none	Score	45

Exons	1088..1117, 1123..1413, 1124..1402, 1403..1426		
Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o1.tm	Method	TBLASTX:Maize
Start	1154	End	2084
GI	none	Score	1017
Exons	1154..2017, 1157..2014, 1773..2084, 1941..2021		
Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o1.tc	Method	TBLASTX:Cress
Start	1231	End	1615
GI	none	Score	189
Exons	1231..1425, 1280..1444, 1436..1615, 1436..1612		
Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o1.tw	Method	TBLASTX:Wheat
Start	1283	End	1675
GI	none	Score	144
Exons	1283..1510, 1517..1621, 1637..1675		
Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o1.ts	Method	TBLASTX:Soybean
Start	1439	End	1969
GI	none	Score	475
Exons	1439..1762, 1439..1963, 1566..1883, 1567..1932, 1808..1969, 1861..1965		
Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o2.tc	Method	TBLASTX:Cress
Start	1616	End	1870
GI	none	Score	251
Exons	1616..1870, 1616..1840		
Seq. No.	775	Seq. ID	OJ990503_08.9924.C88
Gene No.	1566	Strand	-
Start	2685	End	2809
Name	OJ990503_08.9924.C88.o2.np	Method	AAT/NAP
Start	2685	End	2809
GI	6815099	Score	88
Exons	2685..2809		
GI Descrip.	(AP001081) hypothetical protein [Oryza sativa]		
Seq. No.	776	Seq. ID	OJ990503_08.9924.C89
Gene No.	1567	Strand	-
Start	51	End	222
Name	OJ990503_08.9924.C89.o1.gs	Method	GENSCAN
Start	51	End	222

GI	none	Score	.91
Exons	51..222		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1568	Strand	+
Start	908	End	11230
Name	OJ990503_08.9924.C90.o1.gs	Method	GENSCAN
Start	908	End	11230
GI	none	Score	.64
Exons	908..1187, 1629..1789, 2883..2987, 4874..4981, 5940..6020, 6096..6266, 6364..6429, 6950..7018, 7421..7537, 7869..8092, 8189..8279, 8396..8464, 8863..8954, 9373..9436, 9731..9831, 10943..11230		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1568	Strand	+
Start	908	End	11230
Name	OJ990503_08.9924.C90.o3.np	Method	AAT/NAP
Start	4756	End	9832
GI	4895232	Score	699
Exons	4756..4981, 5943..6041, 6096..6270, 6368..6455, 7381..7523, 7906..8092, 8189..8279, 8396..8464, 8863..8954, 9373..9436, 9731..9832		
GI Descrip.	(AC007660) putative methionyl-tRNA synthetase [Arabidopsis thaliana]		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1568	Strand	+
Start	908	End	11230
Name	OJ990503_08.9924.C90.o2.gp	Method	AAT/GAP
Start	4861	End	6425
GI	41356_1.R1084	Score	758
Exons	4861..4981, 5940..6020, 6096..6266, 6364..6425		
GI Descrip.	'1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence'		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1568	Strand	+
Start	908	End	11230
Name	OJ990503_08.9924.C90.o3.gp	Method	AAT/GAP
Start	6962	End	8421
GI	uC-osflcyp172h10b1	Score	874
Exons	6962..7018, 7421..7537, 7869..8092, 8189..8278, 8396..8421		
GI Descrip.	'4895232/gb|AAD32818.1|AC007660_19 8.0e-22 (AC007660) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1568	Strand	+
Start	908	End	11230
Name	OJ990503_08.9924.C90.o4.gp	Method	AAT/GAP
Start	9357	End	10045
GI	38905_1.R1084	Score	715
Exons	9357..9436, 9731..10045		
GI Descrip.	'4895232/gb|AAD32818.1|AC007660_19 8.0e-21 (AC007660) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90

Gene No.	1569	Strand	-
Start	1020	End	3005
Name	OJ990503_08.9924.C90.o1.np	Method	AAT/NAP
Start	1020	End	3005
GI	6539570	Score	183
Exons	1020..1072, 2547..2626, 2803..3005		
GI Descrip.	(AP000836) hypothetical protein [Oryza sativa]		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1570	Strand	-
Start	3133	End	3215
Name	OJ990503_08.9924.C90.o2.np	Method	AAT/NAP
Start	3133	End	3215
GI	6630699	Score	82
Exons	3133..3215		
GI Descrip.	(AP000969) hypothetical protein [Oryza sativa] gi|6721536|dbj|BAA89566.1| (AP001073) hypothetical protein [Oryza sativa]		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1571	Strand	-
Start	3823	End	3881
Name	OJ990503_08.9924.C90.o1.gp	Method	AAT/GAP
Start	3823	End	3881
GI	2312838	Score	66
Exons	3823..3881		
GI Descrip.	1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1572	Strand	
Start	6096	End	9852
Name	OJ990503_08.9924.C90.o1.tm	Method	TBLASTX:Maize
Start	6096	End	9850
GI	none	Score	183
Exons	6096..6269, 6113..6265, 6355..6498, 6358..6429, 6368..6457, 6947..7018, 6949..7017, 7421..7537, 7422..7535, 7876..7980, 7878..7991, 7916..7963, 7923..8015, 7949..8092, 7983..8090, 7988..8092, 8177..8272, 8186..8269, 8208..8276, 8380..8472, 8396..8467, 8862..8978, 8863..8955, 9373..9444, 9374..9436, 9724..9837, 9725..9838, 9725..9850		

Seq. No.	777	Seq. ID	OJ990503_08.9924.C90
Gene No.	1572	Strand	
Start	6096	End	9852
Name	OJ990503_08.9924.C90.o1.tc	Method	TBLASTX:Cress
Start	6141	End	9852
GI	none	Score	96
Exons	6141..6275, 6170..6268, 6370..6429, 6388..6429, 7972..8082, 7989..8090, 8003..8092, 8177..8272, 8208..8276, 8380..8472, 8396..8467, 8862..8978, 8863..8994, 9376..9435, 9377..9436, 9724..9852, 9725..9835		

Seq. No.	778	Seq. ID	OJ990503_08.9924.C91
Gene No.	1573	Strand	+
Start	451	End	1649
Name	OJ990503_08.9924.C91.o1.tm	Method	TBLASTX:Maize

Start	407	End	1544
GI	none	Score	39
Exons	407..475, 413..481, 466..750, 480..752, 520..777, 528..752, 746..796, 754..807, 756..794, 757..795, 975..1145, 976..1146, 978..1097, 998..1144, 1006..1146, 1494..1544		

Seq. No.	778	Seq. ID	OJ990503_08.9924.C91
Gene No.	1573	Strand	+
Start	451	End	1649
Name	OJ990503_08.9924.C91.o1.gs	Method	GENSCAN
Start	451	End	1147
GI	none	Score	.56
Exons	451..793, 977..1147		

Seq. No.	778	Seq. ID	OJ990503_08.9924.C91
Gene No.	1573	Strand	+
Start	451	End	1649
Name	OJ990503_08.9924.C91.o1.np	Method	AAT/NAP
Start	467	End	1649
GI	1143711	Score	300
Exons	467..793, 977..1147, 1499..1541, 1616..1649		
GI Descrip.	(U13631) non-green plastid inner envelope membrane protein precursor [Brassica oleracea]		

Seq. No.	778	Seq. ID	OJ990503_08.9924.C91
Gene No.	1573	Strand	+
Start	451	End	1649
Name	OJ990503_08.9924.C91.o1.tc	Method	TBLASTX:Cress
Start	484	End	737
GI	none	Score	184
Exons	484..732, 501..737		

Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o1.np	Method	AAT/NAP
Start	1313	End	4472
GI	6498441	Score	3789
Exons	1313..2377, 2706..3169, 3233..3606, 3790..3924, 4099..4472		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o4.tw	Method	TBLASTX:Wheat
Start	1465	End	1854
GI	none	Score	44
Exons	1465..1509, 1516..1614, 1533..1613, 1581..1820, 1597..1854		

Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o3.tm	Method	TBLASTX:Maize
Start	1489	End	1752
GI	none	Score	200

Exons	1489..1752, 1506..1751		
Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o3.tw	Method	TBLASTX:Wheat
Start	2590	End	3076
GI	none	Score	400
Exons	2590..2763, 2591..3076, 2785..3045		
Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o1.tw	Method	TBLASTX:Wheat
Start	3240	End	3703
GI	none	Score	194
Exons	3240..3683, 3241..3696, 3242..3703, 3242..3697		
Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o2.ts	Method	TBLASTX:Soybean
Start	3281	End	3646
GI	none	Score	114
Exons	3281..3505, 3512..3646		
Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o2.gs	Method	GENSCAN
Start	3296	End	4446
GI	none	Score	.96
Exons	3296..4446		
Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o1.tm	Method	TBLASTX:Maize
Start	3371	End	3727
GI	none	Score	388
Exons	3371..3727, 3406..3717, 3611..3727		
Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o2.tm	Method	TBLASTX:Maize
Start	3754	End	4138
GI	none	Score	361
Exons	3754..4119, 3755..4138		
Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o2.tw	Method	TBLASTX:Wheat
Start	3811	End	4231
GI	none	Score	491
Exons	3811..4206, 3812..4231		

Seq. No.	779	Seq. ID	OJ990503_08.9924.C94
Gene No.	1574	Strand	+
Start	1313	End	4472
Name	OJ990503_08.9924.C94.o1.ts	Method	TBLASTX:Soybean
Start	3890	End	4261
GI	none	Score	281
Exons	3890..4261, 3907..4050		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1575	Strand	+
Start	1	End	1094
Name	OJ990503_08.9924.C95.o1.np	Method	AAT/NAP
Start	1	End	1091
GI	6498441	Score	1640
Exons	1..716, 810..1091		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1575	Strand	+
Start	1	End	1094
Name	OJ990503_08.9924.C95.o1.gs	Method	GENSCAN
Start	99	End	1094
GI	none	Score	.53
Exons	99..638, 648..1094		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1576	Strand	-
Start	1717	End	2433
Name	OJ990503_08.9924.C95.o1.tm	Method	TBLASTX:Maize
Start	3	End	304
GI	none	Score	312
Exons	3..284, 5..271, 155..304		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1576	Strand	-
Start	1717	End	2433
Name	OJ990503_08.9924.C95.o1.tw	Method	TBLASTX:Wheat
Start	98	End	479
GI	none	Score	351
Exons	98..175, 99..479, 203..448		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1576	Strand	-
Start	1717	End	2433
Name	OJ990503_08.9924.C95.o2.tw	Method	TBLASTX:Wheat
Start	480	End	1082
GI	none	Score	247
Exons	480..770, 485..763, 956..1078, 957..1082		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1576	Strand	-
Start	1717	End	2433
Name	OJ990503_08.9924.C95.o2.tm	Method	TBLASTX:Maize
Start	951	End	1094

GI	none	Score	180
Exons	951..1094, 956..1090		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1576	Strand	-
Start	1717	End	2433
Name	OJ990503_08.9924.C95.o2.gs	Method	GENSCAN
Start	1717	End	2261
GI	none	Score	.45
Exons	1717..2261		

Seq. No.	780	Seq. ID	OJ990503_08.9924.C95
Gene No.	1576	Strand	-
Start	1717	End	2433
Name	OJ990503_08.9924.C95.o2.np	Method	AAT/NAP
Start	1720	End	2433
GI	6907089	Score	1017
Exons	1720..2433		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	781	Seq. ID	OJ990503_08.9924.C96
Gene No.	1577	Strand	+
Start	3084	End	5156
Name	OJ990503_08.9924.C96.o3.np	Method	AAT/NAP
Start	3084	End	5156
GI	4895218	Score	40
Exons	3084..3112, 4510..4617, 5134..5156		
GI Descrip.	(AC007660) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	781	Seq. ID	OJ990503_08.9924.C96
Gene No.	1577	Strand	+
Start	3084	End	5156
Name	OJ990503_08.9924.C96.o2.gs	Method	GENSCAN
Start	3955	End	4740
GI	none	Score	.91
Exons	3955..4334, 4515..4601, 4635..4740		

Seq. No.	781	Seq. ID	OJ990503_08.9924.C96
Gene No.	1578	Strand	-
Start	1	End	3313
Name	OJ990503_08.9924.C96.o1.np	Method	AAT/NAP
Start	1	End	1510
GI	6907089	Score	2186
Exons	1..155, 250..1510		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	781	Seq. ID	OJ990503_08.9924.C96
Gene No.	1578	Strand	-
Start	1	End	3313
Name	OJ990503_08.9924.C96.o2.np	Method	AAT/NAP
Start	611	End	3313
GI	5922623	Score	180
Exons	611..647, 2326..2402, 2590..2742, 3228..3313		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016856|dbj|BAA85199.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	782	Seq. ID	OJ990503_08.9924.C97
Gene No.	1579	Strand	+
Start	1	End	1021
Name	OJ990503_08.9924.C97.o1.gs	Method	GENSCAN
Start	1	End	983
GI	none	Score	.55
Exons	1..983		

Seq. No.	782	Seq. ID	OJ990503_08.9924.C97
Gene No.	1579	Strand	+
Start	1	End	1021
Name	OJ990503_08.9924.C97.o1.tw	Method	TBLASTX:Wheat
Start	1	End	432
GI	none	Score	230
Exons	1..249, 13..195, 63..248, 283..432, 294..431		

Seq. No.	782	Seq. ID	OJ990503_08.9924.C97
Gene No.	1579	Strand	+
Start	1	End	1021
Name	OJ990503_08.9924.C97.o1.np	Method	AAT/NAP
Start	1	End	1021
GI	6498441	Score	1324
Exons	1..126, 298..1021		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	782	Seq. ID	OJ990503_08.9924.C97
Gene No.	1579	Strand	+
Start	1	End	1021
Name	OJ990503_08.9924.C97.o1.ts	Method	TBLASTX:Soybean
Start	121	End	687
GI	5666795	Score	67
Exons	121..219, 295..432, 487..687		
GI Descrip.	4206306 2.0e-10 (AF049110) prpol [Zea mays]		

Seq. No.	782	Seq. ID	OJ990503_08.9924.C97
Gene No.	1579	Strand	+
Start	1	End	1021
Name	OJ990503_08.9924.C97.o2.tw	Method	TBLASTX:Wheat
Start	435	End	729
GI	none	Score	186
Exons	435..533, 487..729		

Seq. No.	783	Seq. ID	OJ990503_08.9924.C98
Gene No.	1580	Strand	+
Start	114	End	212
Name	OJ990503_08.9924.C98.o1.gs	Method	GENSCAN
Start	114	End	212
GI	none	Score	.87
Exons	114..212		

Seq. No.	784	Seq. ID	OJ990503_08.9924.C99
Gene No.	1581	Strand	-
Start	711	End	1067
Name	OJ990503_08.9924.C99.o1.gs	Method	GENSCAN
Start	711	End	1067

GI	none	Score	.62
Exons	711..1067		

Seq. No.	785	Seq. ID	OJ990713_05.9924.C2
Gene No.	1582	Strand	+
Start	1	End	1295
Name	OJ990713_05.9924.C2.o1.np	Method	AAT/NAP
Start	1	End	498
GI	5734635	Score	605
Exons	1..498		
GI Descrip.	(AP000391) hypothetical protein [Oryza sativa]		

Seq. No.	785	Seq. ID	OJ990713_05.9924.C2
Gene No.	1582	Strand	+
Start	1	End	1295
Name	OJ990713_05.9924.C2.o1.gs	Method	GENSCAN
Start	106	End	1295
GI	none	Score	.8
Exons	106..249, 920..993, 1216..1295		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1583	Strand	+
Start	1	End	1806
Name	OJ990713_05.9924.C3.o1.np	Method	AAT/NAP
Start	1	End	1806
GI	3435279	Score	509
Exons	1..619, 1752..1806		
GI Descrip.	(AF082391) protein kinase homolog [Arabidopsis thaliana]		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1583	Strand	+
Start	1	End	1806
Name	OJ990713_05.9924.C3.o1.gs	Method	GENSCAN
Start	101	End	823
GI	none	Score	.56
Exons	101..823		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1584	Strand	+
Start	10981	End	14382
Name	OJ990713_05.9924.C3.o3.np	Method	AAT/NAP
Start	10981	End	14382
GI	6498434	Score	72
Exons	10981..11142, 12039..12126, 14330..14382		
GI Descrip.	(AP000815) hypothetical protein [Oryza sativa]		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1585	Strand	+
Start	15089	End	15249
Name	OJ990713_05.9924.C3.o5.np	Method	AAT/NAP
Start	15089	End	15249
GI	5777617	Score	92
Exons	15089..15249		
GI Descrip.	(AJ245900) CAA30375.1 protein [Oryza sativa]		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1586	Strand	-

Start	5876	End	10071
Name	OJ990713_05.9924.C3.o3.gs	Method	GENSCAN
Start	5876	End	10071
GI	none	Score	.62
Exons	5876..6259, 9619..10071		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1586	Strand	-
Start	5876	End	10071
Name	OJ990713_05.9924.C3.o2.np	Method	AAT/NAP
Start	9762	End	10071
GI	4559367	Score	95
Exons	9762..10071		
GI Descrip.	(AC006585) putative MADS-box protein [Arabidopsis thaliana]		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1587	Strand	-
Start	13662	End	15789
Name	OJ990713_05.9924.C3.o4.gs	Method	GENSCAN
Start	13662	End	15789
GI	none	Score	.62
Exons	13662..14490, 14761..14953, 15384..15789		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1587	Strand	-
Start	13662	End	15789
Name	OJ990713_05.9924.C3.o4.np	Method	AAT/NAP
Start	13665	End	14907
GI	4455245	Score	529
Exons	13665..14035, 14069..14483, 14526..14683, 14736..14907		
GI Descrip.	(AL035523) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1587	Strand	-
Start	13662	End	15789
Name	OJ990713_05.9924.C3.o2.gp	Method	AAT/GAP
Start	14114	End	14333
GI	427582	Score	432
Exons	14114..14333		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o1.tc	Method	TBLASTX:Cress
Start	4	End	705
GI	none	Score	127
Exons	4..102, 5..103, 226..414, 227..451, 482..625, 538..705		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o1.ts	Method	TBLASTX:Soybean
Start	4	End	625
GI	none	Score	131
Exons	4..102, 5..103, 226..414, 227..451, 269..433, 482..625, 485..589, 541..624		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o1.tm	Method	TBLASTX:Maize
Start	5	End	625
GI	none	Score	132
Exons	5..103, 7..102, 211..414, 227..451, 482..625, 538..624		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o1.tw	Method	TBLASTX:Wheat
Start	284	End	625
GI	none	Score	203
Exons	284..451, 334..447, 482..625, 541..624		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o3.tm	Method	TBLASTX:Maize
Start	13791	End	14213
GI	none	Score	154
Exons	13791..14021, 13800..13946, 13802..14044, 13804..13965, 13986..14066, 14039..14137, 14058..14213		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o2.tm	Method	TBLASTX:Maize
Start	14229	End	14498
GI	none	Score	143
Exons	14229..14339, 14233..14328, 14326..14400, 14327..14491, 14331..14498, 14331..14492		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o2.ts	Method	TBLASTX:Soybean
Start	14337	End	14960
GI	none	Score	63
Exons	14337..14426, 14337..14477, 14568..14609, 14736..14807, 14913..14960		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o7.tm	Method	TBLASTX:Maize
Start	14565	End	14834
GI	none	Score	93
Exons	14565..14645, 14647..14769, 14682..14768, 14751..14834, 14764..14826		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o6.tm	Method	TBLASTX:Maize
Start	19295	End	19474

GI	none	Score	164
Exons	19295..19474, 19305..19415		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o6.np	Method	AAT/NAP
Start	19313	End	20224
GI	2618696	Score	566
Exons	19313..20224		
GI Descrip.	(AC002510) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o3.gp	Method	AAT/GAP
Start	19414	End	19874
GI	LIB3433-057-P1-K1-E12	Score	793
Exons	19414..19874		
GI Descrip.	'2618696 5.0e-25 (AC002510) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o5.tm	Method	TBLASTX:Maize
Start	19538	End	19706
GI	none	Score	229
Exons	19538..19705, 19539..19706		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o3.ts	Method	TBLASTX:Soybean
Start	19541	End	19724
GI	none	Score	135
Exons	19541..19723, 19542..19724		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o4.tm	Method	TBLASTX:Maize
Start	19923	End	20412
GI	none	Score	76
Exons	19923..19970, 20024..20218, 20025..20159, 20168..20212, 20244..20264, 20261..20314, 20269..20313, 20353..20412, 20379..20396		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1588	Strand	-
Start	19313	End	20420
Name	OJ990713_05.9924.C3.o4.gp	Method	AAT/GAP
Start	19996	End	20420
GI	54717_1.R1084	Score	823
Exons	19996..20420		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1589	Strand	
Start	24480	End	24659
Name	OJ990713_05.9924.C3.o2.tc	Method	TBLASTX:Cress
Start	24480	End	24659
GI	none	Score	151
Exons	24480..24647, 24493..24648, 24540..24659		

Seq. No.	786	Seq. ID	OJ990713_05.9924.C3
Gene No.	1590	Strand	
Start	27782	End	27972
Name	OJ990713_05.9924.C3.o2.tw	Method	TBLASTX:Wheat
Start	27782	End	27972
GI	none	Score	158
Exons	27782..27970, 27782..27967, 27783..27971, 27783..27971, 27796..27972, 27796..27972		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1591	Strand	+
Start	12527	End	13483
Name	OJ990713_05.9924.C4.o4.gs	Method	GENSCAN
Start	12527	End	13483
GI	none	Score	.73
Exons	12527..12712, 12761..12910, 12943..13104, 13337..13483		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1592	Strand	+
Start	13991	End	19340
Name	OJ990713_05.9924.C4.o5.gs	Method	GENSCAN
Start	13991	End	19340
GI	none	Score	.52
Exons	13991..14381, 14909..15046, 15142..15301, 15433..15565, 15653..15799, 15912..16073, 16538..16726, 17173..17728, 18103..18216, 18238..18485, 18558..18668, 19080..19340		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1592	Strand	+
Start	13991	End	19340
Name	OJ990713_05.9924.C4.o4.gp	Method	AAT/GAP
Start	14243	End	16242
GI	91997_1.R1084	Score	1942
Exons	14243..14381, 14909..15046, 15142..15301, 15433..15565, 15653..15799, 15912..16242		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1592	Strand	+
Start	13991	End	19340
Name	OJ990713_05.9924.C4.o2.np	Method	AAT/NAP
Start	17197	End	17549
GI	2464913	Score	153
Exons	17197..17273, 17324..17549		
GI Descrip.	(Z99708) sugar transporter like protein [Arabidopsis thaliana]		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4

Gene No.	1593	Strand	-
Start	4737	End	8122
Name	OJ990713_05.9924.C4.o2.gp	Method	AAT/GAP
Start	4596	End	5031
GI	7139_1.R1084	Score	794
Exons	4596..5031		
GI Descrip.	'4726079/gb|AAD28303.1|AF143940_1 3.0e-39 (AF143940) SWI2/SNF2-like protein [Arabidopsis thaliana]'		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1593	Strand	-
Start	4737	End	8122
Name	OJ990713_05.9924.C4.o2.gs	Method	GENSCAN
Start	4737	End	8122
GI	none	Score	.97
Exons	4737..5096, 5107..6468, 7103..8122		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1594	Strand	-
Start	12136	End	12222
Name	OJ990713_05.9924.C4.o1.tc	Method	TBLASTX:Cress
Start	4785	End	7414
GI	none	Score	74
Exons	4785..4916, 6145..6312, 6197..6313, 6358..6489, 7166..7270, 7298..7414		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1594	Strand	-
Start	12136	End	12222
Name	OJ990713_05.9924.C4.o1.tm	Method	TBLASTX:Maize
Start	5170	End	6070
GI	none	Score	177
Exons	5170..5361, 5171..5362, 5309..5611, 5362..5856, 5542..5856, 5947..6069, 5990..6070		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1594	Strand	-
Start	12136	End	12222
Name	OJ990713_05.9924.C4.o2.tm	Method	TBLASTX:Maize
Start	7100	End	7519
GI	none	Score	412
Exons	7100..7519, 7101..7517		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1594	Strand	-
Start	12136	End	12222
Name	OJ990713_05.9924.C4.o3.gp	Method	AAT/GAP
Start	12136	End	12222
GI	90742_1.R1084	Score	76
Exons	12136..12222		
GI Descrip.	'5734616/dbj|AP000391.1|AP000391 4.0e-29 Oryza sativa genomic DNA, chromosome 6, clone:P0538C01'		

Seq. No.	787	Seq. ID	OJ990713_05.9924.C4
Gene No.	1595	Strand	
Start	17253	End	17535
Name	OJ990713_05.9924.C4.o1.ts	Method	TBLASTX:Soybean

Start	17253	End	17535
GI	none	Score	80
Exons	17253..17351, 17340..17456, 17341..17535, 17343..17531		

Seq. No.	788	Seq. ID	OJ990713_05.9924.C5
Gene No.	1596	Strand	-
Start	2378	End	2794
Name	OJ990713_05.9924.C5.o2.gs	Method	GENSCAN
Start	2378	End	2794
GI	none	Score	.62
Exons	2378..2541, 2675..2794		

Seq. No.	789	Seq. ID	OJ990713_05.9924.C6
Gene No.	1597	Strand	+
Start	1	End	4537
Name	OJ990713_05.9924.C6.o1.np	Method	AAT/NAP
Start	1	End	4537
GI	5042454	Score	3298
Exons	1..27, 240..341, 398..2286, 2820..3237, 4048..4233, 4484..4537		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		

Seq. No.	789	Seq. ID	OJ990713_05.9924.C6
Gene No.	1597	Strand	+
Start	1	End	4537
Name	OJ990713_05.9924.C6.o1.gs	Method	GENSCAN
Start	416	End	1968
GI	none	Score	.48
Exons	416..1264, 1331..1592, 1745..1968		

Seq. No.	789	Seq. ID	OJ990713_05.9924.C6
Gene No.	1598	Strand	-
Start	7015	End	7312
Name	OJ990713_05.9924.C6.o1.tw	Method	TBLASTX:Wheat
Start	910	End	1462
GI	none	Score	34
Exons	910..945, 1070..1117, 1124..1222, 1129..1221, 1189..1428, 1205..1462		

Seq. No.	789	Seq. ID	OJ990713_05.9924.C6
Gene No.	1598	Strand	-
Start	7015	End	7312
Name	OJ990713_05.9924.C6.o1.tm	Method	TBLASTX:Maize
Start	1075	End	1360
GI	none	Score	193
Exons	1075..1359, 1112..1360		

Seq. No.	789	Seq. ID	OJ990713_05.9924.C6
Gene No.	1598	Strand	-
Start	7015	End	7312
Name	OJ990713_05.9924.C6.o2.tm	Method	TBLASTX:Maize
Start	1965	End	2108
GI	none	Score	184
Exons	1965..2108, 1970..2104		

Seq. No.	789	Seq. ID	OJ990713_05.9924.C6
Gene No.	1598	Strand	-
Start	7015	End	7312

Name	OJ990713_05.9924.C6.o2.tw	Method	TBLASTX:Wheat
Start	3030	End	3326
GI	none	Score	273
Exons	3030..3326, 3047..3322, 3090..3323		

Seq. No.	789	Seq. ID	OJ990713_05.9924.C6
Gene No.	1598	Strand	-
Start	7015	End	7312
Name	OJ990713_05.9924.C6.o3.gs	Method	GENSCAN
Start	7015	End	7312
GI	none	Score	.63
Exons	7015..7068, 7230..7312		

Seq. No.	790	Seq. ID	OJ990713_05.9924.C7
Gene No.	1599	Strand	-
Start	1	End	3718
Name	OJ990713_05.9924.C7.o1.np	Method	AAT/NAP
Start	1	End	1085
GI	6907086	Score	649
Exons	1..245, 306..1085		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	790	Seq. ID	OJ990713_05.9924.C7
Gene No.	1599	Strand	-
Start	1	End	3718
Name	OJ990713_05.9924.C7.o1.gs	Method	GENSCAN
Start	331	End	2797
GI	none	Score	.67
Exons	331..904, 2583..2797		

Seq. No.	790	Seq. ID	OJ990713_05.9924.C7
Gene No.	1599	Strand	-
Start	1	End	3718
Name	OJ990713_05.9924.C7.o2.np	Method	AAT/NAP
Start	769	End	3718
GI	4680186	Score	144
Exons	769..810, 2006..2196, 2669..2748, 3697..3718		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1600	Strand	+
Start	3584	End	4462
Name	OJ990713_05.9924.C8.o1.gs	Method	GENSCAN
Start	3584	End	4462
GI	none	Score	.45
Exons	3584..3885, 4270..4462		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1601	Strand	+
Start	7077	End	12624
Name	OJ990713_05.9924.C8.o2.gs	Method	GENSCAN
Start	7077	End	12624
GI	none	Score	.91
Exons	7077..7128, 8356..8463, 8568..8742, 8829..8979, 9073..9214, 9500..9552, 10248..10643, 10754..10855, 11456..11683, 12066..12188, 12358..12624		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1601	Strand	+
Start	7077	End	12624
Name	OJ990713_05.9924.C8.o1.np	Method	AAT/NAP
Start	8821	End	12564
GI	5706502	Score	317
Exons	8821..8960, 9826..10027, 10266..10773, 11475..11673, 12339..12564		
GI Descrip.	(AL109739) putative phosphomevalonate kinase [Schizosaccharomyces pombe]		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1601	Strand	+
Start	7077	End	12624
Name	OJ990713_05.9924.C8.o2.gp	Method	AAT/GAP
Start	11435	End	12396
GI	none	Score	703
Exons	11435..11683, 12073..12188, 12358..12396		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1602	Strand	+
Start	18588	End	20382
Name	OJ990713_05.9924.C8.o2.np	Method	AAT/NAP
Start	18479	End	19821
GI	5091605	Score	176
Exons	18479..18777, 19757..19821		
GI Descrip.	(AC007858) 10A19I.9 [Oryza sativa]		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1602	Strand	+
Start	18588	End	20382
Name	OJ990713_05.9924.C8.o4.gs	Method	GENSCAN
Start	18588	End	20382
GI	none	Score	.68
Exons	18588..18826, 18847..18995, 19061..19173, 19667..19734, 20307..20382		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1603	Strand	+
Start	25884	End	25971
Name	OJ990713_05.9924.C8.o3.np	Method	AAT/NAP
Start	25884	End	25971
GI	6721547	Score	76
Exons	25884..25971		
GI Descrip.	(AP001073) Similar to Oryza sativa gene for Pib. (AB013448)		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1604	Strand	+
Start	27930	End	33334
Name	OJ990713_05.9924.C8.o3.gp	Method	AAT/GAP
Start	27930	End	29083
GI	700407	Score	714
Exons	27930..28074, 28769..28931, 29013..29083		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1604	Strand	+
Start	27930	End	33334

Name	OJ990713_05.9924.C8.o4.np	Method	AAT/NAP
Start	28826	End	32793
GI	4006914	Score	1351
Exons	28826..28931, 29013..29107, 29217..29308, 30298..30391, 30465..30537, 30623..30755, 31167..31341, 31486..31626, 31802..31897, 31984..32104, 32410..32537, 32623..32793		
GI Descrip.	(Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1604	Strand	+
Start	27930	End	33334
Name	OJ990713_05.9924.C8.o8.gs	Method	GENSCAN
Start	28826	End	33334
GI	none	Score	.81
Exons	28826..28931, 29013..29107, 29217..29308, 30298..30391, 30589..30755, 31167..31341, 31486..31626, 31802..31897, 31984..32125, 32410..32537, 32623..32766, 33089..33334		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1604	Strand	+
Start	27930	End	33334
Name	OJ990713_05.9924.C8.o4.gp	Method	AAT/GAP
Start	30309	End	31357
GI	43229_1.R1084	Score	816
Exons	30309..30391, 30465..30537, 30623..30756, 31167..31357		
GI Descrip.	'4006914/emb|CAB16844.1| 1.0e-61 (Z99708) serine C-palmitoyltransferase like protein [Arabidopsis thaliana]'		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1604	Strand	+
Start	27930	End	33334
Name	OJ990713_05.9924.C8.o5.gp	Method	AAT/GAP
Start	32504	End	32699
GI	701925	Score	143
Exons	32504..32537, 32623..32699		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1605	Strand	+
Start	40468	End	41044
Name	OJ990713_05.9924.C8.o10.gs	Method	GENSCAN
Start	40468	End	41044
GI	none	Score	.86
Exons	40468..40539, 40601..41044		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1606	Strand	-
Start	14855	End	18245
Name	OJ990713_05.9924.C8.o3.gs	Method	GENSCAN
Start	14855	End	18245
GI	none	Score	.65
Exons	14855..15174, 15200..15255, 15284..15415, 15584..15924, 16074..16128, 18151..18245		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1607	Strand	-
Start	24216	End	26616

Name	OJ990713_05.9924.C8.o6.gs	Method	GENSCAN
Start	24216	End	26616
GI	none	Score	.91
Exons	24216..24322, 26454..26616		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1608	Strand	-
Start	27793	End	28116
Name	OJ990713_05.9924.C8.o7.gs	Method	GENSCAN
Start	27793	End	28116
GI	none	Score	.94
Exons	27793..28116		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o2.ts	Method	TBLASTX:Soybean
Start	8829	End	9137
GI	none	Score	219
Exons	8829..8990, 8830..9003, 9072..9137, 9073..9120		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o3.tm	Method	TBLASTX:Maize
Start	8830	End	9403
GI	none	Score	229
Exons	8830..9003, 8830..8979, 9026..9175, 9051..9194, 9072..9212, 9265..9387, 9268..9390, 9272..9403, 9272..9397		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o1.tm	Method	TBLASTX:Maize
Start	9499	End	12633
GI	none	Score	98
Exons	9499..9558, 9499..9552, 10245..10508, 10246..10506, 10429..10527, 10442..10507, 10510..10557, 10512..10643, 10515..10643, 10589..10651, 10751..10858, 10756..10854, 11456..11683, 11463..11672, 12058..12189, 12063..12203, 12063..12188, 12354..12632, 12357..12623, 12358..12633		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o3.ts	Method	TBLASTX:Soybean
Start	10500	End	10676
GI	none	Score	224
Exons	10500..10676, 10500..10676		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o6.tm	Method	TBLASTX:Maize
Start	18543	End	18715
GI	none	Score	190
Exons	18543..18668, 18546..18710, 18560..18715		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o5.tm	Method	TBLASTX:Maize
Start	28815	End	29089
GI	none	Score	151
Exons	28815..28931, 28816..28932, 28817..28939, 28818..28937, 29000..29080, 29001..29081, 29003..29089		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o5.ts	Method	TBLASTX:Soybean
Start	28817	End	29273
GI	none	Score	69
Exons	28817..28933, 29003..29107, 29214..29270, 29214..29273		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o1.ts	Method	TBLASTX:Soybean
Start	30295	End	32058
GI	none	Score	129
Exons	30295..30384, 30296..30412, 30456..30545, 30464..30535, 30487..30540, 30489..30545, 30621..30755, 30622..30756, 31165..31341, 31167..31340, 31450..31644, 31479..31628, 31483..31656, 31485..31655, 31795..31872, 31796..31897, 31966..32058, 31989..32045		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o4.tm	Method	TBLASTX:Maize
Start	30295	End	30666
GI	none	Score	146
Exons	30295..30393, 30296..30424, 30439..30588, 30479..30550, 30544..30609, 30621..30665, 30622..30666		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o1.tc	Method	TBLASTX:Cress
Start	30456	End	31304
GI	none	Score	107
Exons	30456..30545, 30458..30535, 30460..30540, 30621..30755, 30622..30756, 30622..30759, 31090..31275, 31165..31302, 31167..31304		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o2.tm	Method	TBLASTX:Maize
Start	31966	End	40089
GI	none	Score	144
Exons	31966..32124, 31970..32140, 31970..32134, 31971..32141, 32385..32537, 32395..32538, 32396..32539, 32400..32540,		

32620..32814, 32621..32800, 32622..32801, 39970..40038,
39980..40072, 40005..40040, 40039..40089, 40040..40087

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o2.tc	Method	TBLASTX:Cress
Start	32412	End	32771
GI	none	Score	93
Exons	32412..32537, 32453..32533, 32620..32763, 32628..32771		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o4.ts	Method	TBLASTX:Soybean
Start	32617	End	32798
GI	none	Score	202
Exons	32617..32784, 32622..32798		

Seq. No.	791	Seq. ID	OJ990713_05.9924.C8
Gene No.	1609	Strand	-
Start	33673	End	40089
Name	OJ990713_05.9924.C8.o9.gs	Method	GENSCAN
Start	33673	End	39779
GI	none	Score	.77
Exons	33673..33749, 34515..34549, 34644..34738, 34831..34886, 34990..35062, 35145..35225, 35281..35343, 36002..36142, 36225..36335, 37141..37364, 37563..38039, 38303..38462, 38540..38592, 39065..39346, 39542..39660, 39775..39779		

Seq. No.	792	Seq. ID	OJ990713_05.9924.C9
Gene No.	1610	Strand	+
Start	1	End	1349
Name	OJ990713_05.9924.C9.o1.np	Method	AAT/NAP
Start	1	End	1349
GI	6721556	Score	80
Exons	1..180, 1297..1349		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa] gi|6815081|dbj|BAA90367.1| (AP001081) hypothetical protein [Oryza sativa]		

Seq. No.	792	Seq. ID	OJ990713_05.9924.C9
Gene No.	1610	Strand	+
Start	1	End	1349
Name	OJ990713_05.9924.C9.o1.gs	Method	GENSCAN
Start	60	End	809
GI	none	Score	.72
Exons	60..264, 725..809		

Seq. No.	793	Seq. ID	OJ990503_02.9919.C1
Gene No.	1611	Strand	+
Start	700	End	968
Name	OJ990503_02.9919.C1.o1.gp	Method	AAT/GAP
Start	700	End	968
GI	29264_1.R1084	Score	457
Exons	700..968		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450		

[Arabidopsis thaliana]'

Seq. No.	794	Seq. ID	OJ990503_02.9919.C3
Gene No.	1612	Strand	+
Start	1	End	521
Name	OJ990503_02.9919.C3.o1.gp	Method	AAT/GAP
Start	1	End	521
GI	12586_1.R1084	Score	765
Exons	1..145, 246..521		
GI Descrip.	'2494075/sp|Q43272|GAPN_MAIZE 1.0e-129 NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [NADP+]) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1084478_pir__S43833 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - maize >gi_474408_emb_CAA53075_ (X75326) glyceraldehyde-3-'		

Seq. No.	794	Seq. ID	OJ990503_02.9919.C3
Gene No.	1612	Strand	+
Start	1	End	521
Name	OJ990503_02.9919.C3.o1.np	Method	AAT/NAP
Start	1	End	356
GI	3913711	Score	346
Exons	1..145, 246..356		
GI Descrip.	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [NADP+]) (TRIOSEPHOSPHATE DEHYDROGENASE) gi|4379384|emb|CAA53076| (X75327) glyceraldehyde-3-phosphate dehydrogenase (nonphosphorylating,NADP+) [Pisum sativum]		

Seq. No.	794	Seq. ID	OJ990503_02.9919.C3
Gene No.	1612	Strand	+
Start	1	End	521
Name	OJ990503_02.9919.C3.o1.ts	Method	TBLASTX:Soybean
Start	13	End	359
GI	none	Score	211
Exons	13..141, 26..145, 234..359, 245..355		

Seq. No.	794	Seq. ID	OJ990503_02.9919.C3
Gene No.	1612	Strand	+
Start	1	End	521
Name	OJ990503_02.9919.C3.o1.tm	Method	TBLASTX:Maize
Start	27	End	472
GI	none	Score	105
Exons	27..146, 28..144, 29..151, 47..151, 108..155, 234..365, 243..365, 245..376, 245..379, 418..471, 418..471, 419..472		

Seq. No.	794	Seq. ID	OJ990503_02.9919.C3
Gene No.	1612	Strand	+
Start	1	End	521
Name	OJ990503_02.9919.C3.o1.tc	Method	TBLASTX:Cress
Start	39	End	359
GI	none	Score	87
Exons	39..146, 44..151, 85..144, 234..359, 245..355		

Seq. No.	794	Seq. ID	OJ990503_02.9919.C3

Gene No.	1612	Strand	+
Start	1	End	521
Name	OJ990503_02.9919.C3.o1.gs	Method	GENSCAN
Start	65	End	359
GI	none	Score	.79
Exons	65..145, 213..359		

Seq. No.	795	Seq. ID	OJ990503_02.9919.C4
Gene No.	1613	Strand	+
Start	517	End	668
Name	OJ990503_02.9919.C4.o1.gs	Method	GENSCAN
Start	517	End	668
GI	none	Score	.8
Exons	517..668		

Seq. No.	796	Seq. ID	OJ990503_02.9919.C5
Gene No.	1614	Strand	+
Start	1	End	530
Name	OJ990503_02.9919.C5.o1.np	Method	AAT/NAP
Start	1	End	530
GI	6623876	Score	157
Exons	1..125, 507..530		
GI Descrip.	(AC018722) unknown protein [Arabidopsis thaliana]		

Seq. No.	796	Seq. ID	OJ990503_02.9919.C5
Gene No.	1614	Strand	+
Start	1	End	530
Name	OJ990503_02.9919.C5.o1.tm	Method	TBLASTX:Maize
Start	2	End	125
GI	none	Score	202
Exons	2..124, 3..125, 15..89, 15..125		

Seq. No.	796	Seq. ID	OJ990503_02.9919.C5
Gene No.	1614	Strand	+
Start	1	End	530
Name	OJ990503_02.9919.C5.o1.ts	Method	TBLASTX:Soybean
Start	3	End	129
GI	none	Score	191
Exons	3..125, 5..124, 10..129, 10..129		

Seq. No.	797	Seq. ID	OJ990503_02.9919.C6
Gene No.	1615	Strand	+
Start	1	End	716
Name	OJ990503_02.9919.C6.o1.np	Method	AAT/NAP
Start	1	End	716
GI	1345978	Score	518
Exons	1..241, 324..467, 583..716		
GI Descrip.	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR gi|457631 (L29214) omega-6 desaturase [Brassica napus]		

Seq. No.	797	Seq. ID	OJ990503_02.9919.C6
Gene No.	1615	Strand	+
Start	1	End	716
Name	OJ990503_02.9919.C6.o1.gp	Method	AAT/GAP
Start	46	End	190
GI	29264_1.R1084	Score	244
Exons	46..190		

GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		
Seq. No.	797	Seq. ID	OJ990503_02.9919.C6
Gene No.	1615	Strand	+
Start	1	End	716
Name	OJ990503_02.9919.C6.o1.tm	Method	TBLASTX:Maize
Start	47	End	716
GI	none	Score	270
Exons	47..253, 56..244, 61..249, 321..392, 323..466, 324..467, 423..467, 571..714, 582..716, 582..716		
Seq. No.	797	Seq. ID	OJ990503_02.9919.C6
Gene No.	1615	Strand	+
Start	1	End	716
Name	OJ990503_02.9919.C6.o1.tc	Method	TBLASTX:Cress
Start	74	End	714
GI	none	Score	193
Exons	74..253, 79..249, 137..250, 323..466, 324..467, 438..467, 570..707, 571..714, 582..710, 583..714		
Seq. No.	797	Seq. ID	OJ990503_02.9919.C6
Gene No.	1615	Strand	+
Start	1	End	716
Name	OJ990503_02.9919.C6.o1.ts	Method	TBLASTX:Soybean
Start	89	End	716
GI	none	Score	180
Exons	89..253, 91..249, 323..466, 324..467, 571..714, 582..716		
Seq. No.	797	Seq. ID	OJ990503_02.9919.C6
Gene No.	1615	Strand	+
Start	1	End	716
Name	OJ990503_02.9919.C6.o1.gs	Method	GENSCAN
Start	129	End	241
GI	none	Score	.49
Exons	129..241		
Seq. No.	797	Seq. ID	OJ990503_02.9919.C6
Gene No.	1615	Strand	+
Start	1	End	716
Name	OJ990503_02.9919.C6.o2.gp	Method	AAT/GAP
Start	194	End	716
GI	LIB3434-049-P1-K1-D7	Score	472
Exons	194..241, 324..467, 583..716		
GI Descrip.	'1345978/sp|P48627|FD6C_BRANA 2.0e-83 OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_457631 (L29214) omega-6 desaturase [Brassica napus]'		
Seq. No.	798	Seq. ID	OJ990503_02.9919.C9
Gene No.	1616	Strand	+
Start	69	End	600
Name	OJ990503_02.9919.C9.o1.gp	Method	AAT/GAP
Start	69	End	600
GI	40242_1.R1084	Score	1028
Exons	69..600		
GI Descrip.	'1345978/sp|P48627|FD6C_BRANA 2.0e-42 OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_457631 (L29214) omega-6		

desaturase [Brassica napus]'

Seq. No.	798	Seq. ID	OJ990503_02.9919.C9
Gene No.	1617	Strand	-
Start	457	End	600
Name	OJ990503_02.9919.C9.o1.tm	Method	TBLASTX:Maize
Start	422	End	600
GI	none	Score	212
Exons	422..598, 445..600, 449..598, 457..600		

Seq. No.	798	Seq. ID	OJ990503_02.9919.C9
Gene No.	1617	Strand	-
Start	457	End	600
Name	OJ990503_02.9919.C9.o1.ts	Method	TBLASTX:Soybean
Start	422	End	600
GI	none	Score	212
Exons	422..598, 445..600, 449..598, 457..600		

Seq. No.	798	Seq. ID	OJ990503_02.9919.C9
Gene No.	1617	Strand	-
Start	457	End	600
Name	OJ990503_02.9919.C9.o1.tc	Method	TBLASTX:Cress
Start	454	End	600
GI	none	Score	119
Exons	454..600, 463..600		

Seq. No.	798	Seq. ID	OJ990503_02.9919.C9
Gene No.	1617	Strand	-
Start	457	End	600
Name	OJ990503_02.9919.C9.o1.np	Method	AAT/NAP
Start	457	End	600
GI	1345978	Score	215
Exons	457..600		
GI Descrip.	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR gi|457631 (L29214) omega-6 desaturase [Brassica napus]		

Seq. No.	799	Seq. ID	OJ990503_02.9919.C12
Gene No.	1618	Strand	+
Start	112	End	264
Name	OJ990503_02.9919.C12.o1.gs	Method	GENSCAN
Start	112	End	264
GI	none	Score	.67
Exons	112..264		

Seq. No.	799	Seq. ID	OJ990503_02.9919.C12
Gene No.	1619	Strand	-
Start	715	End	1346
Name	OJ990503_02.9919.C12.o2.gs	Method	GENSCAN
Start	715	End	1032
GI	none	Score	.58
Exons	715..1032		

Seq. No.	799	Seq. ID	OJ990503_02.9919.C12
Gene No.	1619	Strand	-
Start	715	End	1346
Name	OJ990503_02.9919.C12.o1.np	Method	AAT/NAP
Start	718	End	1346

GI	6498436	Score	78
Exons	718..1014, 1233..1346		
GI Descrip.	(AP000815) hypothetical protein [Oryza sativa]		

Seq. No.	800	Seq. ID	OJ990503_02.9919.C13
Gene No.	1620	Strand	+
Start	92	End	184
Name	OJ990503_02.9919.C13.o1.gs	Method	GENSCAN
Start	92	End	184
GI	none	Score	.65
Exons	92..184		

Seq. No.	801	Seq. ID	OJ990503_02.9919.C15
Gene No.	1621	Strand	-
Start	123	End	435
Name	OJ990503_02.9919.C15.o1.gs	Method	GENSCAN
Start	123	End	435
GI	none	Score	.64
Exons	123..224, 313..435		

Seq. No.	802	Seq. ID	OJ990503_02.9919.C18
Gene No.	1622	Strand	-
Start	431	End	608
Name	OJ990503_02.9919.C18.o1.gs	Method	GENSCAN
Start	431	End	608
GI	none	Score	.85
Exons	431..608		

Seq. No.	803	Seq. ID	OJ990503_02.9919.C19
Gene No.	1623	Strand	-
Start	156	End	726
Name	OJ990503_02.9919.C19.o1.gs	Method	GENSCAN
Start	156	End	726
GI	none	Score	.45
Exons	156..247, 632..726		

Seq. No.	804	Seq. ID	OJ990503_02.9919.C20
Gene No.	1624	Strand	-
Start	557	End	1444
Name	OJ990503_02.9919.C20.o1.gs	Method	GENSCAN
Start	557	End	757
GI	none	Score	.73
Exons	557..757		

Seq. No.	804	Seq. ID	OJ990503_02.9919.C20
Gene No.	1624	Strand	-
Start	557	End	1444
Name	OJ990503_02.9919.C20.o1.np	Method	AAT/NAP
Start	560	End	1444
GI	124121	Score	123
Exons	560..748, 1358..1444		
GI Descrip.	SUBTILISIN INHIBITORS I AND II (ASI-I AND ASI-II)		

Seq. No.	805	Seq. ID	OJ990503_02.9919.C21
Gene No.	1625	Strand	+
Start	210	End	332
Name	OJ990503_02.9919.C21.o1.gs	Method	GENSCAN

Start	210	End	332
GI	none	Score	.95
Exons	210..332		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24
Gene No.	1626	Strand	+
Start	1464	End	2215
Name	OJ990503_02.9919.C24.o1.gs	Method	GENSCAN
Start	1464	End	2215
GI	none	Score	.7
Exons	1464..1608, 1935..2215		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24
Gene No.	1627	Strand	-
Start	943	End	2591
Name	OJ990503_02.9919.C24.o1.np	Method	AAT/NAP
Start	943	End	2591
GI	5915816	Score	103
Exons	943..1091, 2507..2591		
GI Descrip.	CYTOCHROME P450 71A9 (P450 CP1) gi|3334659|emb|CAA71513| (Y10489) putative cytochrome P450 [Glycine max]		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24
Gene No.	1627	Strand	-
Start	943	End	2591
Name	OJ990503_02.9919.C24.o1.tm	Method	TBLASTX:Maize
Start	1424	End	1665
GI	none	Score	255
Exons	1424..1654, 1425..1655, 1426..1656, 1426..1665		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24
Gene No.	1627	Strand	-
Start	943	End	2591
Name	OJ990503_02.9919.C24.o1.ts	Method	TBLASTX:Soybean
Start	1424	End	1656
GI	none	Score	78
Exons	1424..1573, 1426..1536, 1426..1656, 1426..1647, 1597..1656		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24
Gene No.	1627	Strand	-
Start	943	End	2591
Name	OJ990503_02.9919.C24.o1.gp	Method	AAT/GAP
Start	1425	End	1882
GI	33945_1.R1084	Score	420
Exons	1425..1655, 1861..1882		
GI Descrip.	'2583133 4.0e-27 (AC002387) unknown protein [Arabidopsis thaliana]'		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24
Gene No.	1627	Strand	-
Start	943	End	2591
Name	OJ990503_02.9919.C24.o1.tw	Method	TBLASTX:Wheat
Start	1425	End	1578
GI	none	Score	177
Exons	1425..1571, 1426..1578, 1426..1572		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24

Gene No.	1627	Strand	-
Start	943	End	2591
Name	OJ990503_02.9919.C24.o1.tc	Method	TBLASTX:Cress
Start	1426	End	1656
GI	none	Score	57
Exons	1426..1470, 1480..1590, 1609..1656		

Seq. No.	806	Seq. ID	OJ990503_02.9919.C24
Gene No.	1627	Strand	-
Start	943	End	2591
Name	OJ990503_02.9919.C24.o2.np	Method	AAT/NAP
Start	1426	End	1596
GI	6850926	Score	182
Exons	1426..1596		
GI Descrip.	(AJ271662) hypothetical protein [Cicer arietinum]		

Seq. No.	807	Seq. ID	OJ990503_02.9919.C25
Gene No.	1628	Strand	+
Start	228	End	6331
Name	OJ990503_02.9919.C25.o1.gs	Method	GENSCAN
Start	228	End	5237
GI	none	Score	.61
Exons	228..348, 2673..2821, 2910..3011, 3908..4052, 4180..4217, 4583..4963, 5059..5237		

Seq. No.	807	Seq. ID	OJ990503_02.9919.C25
Gene No.	1628	Strand	+
Start	228	End	6331
Name	OJ990503_02.9919.C25.o1.np	Method	AAT/NAP
Start	4052	End	6331
GI	619383	Score	82
Exons	4052..4087, 4613..4936, 6302..6331		
GI Descrip.	apolipoprotein D, apoD [human, plasma, Peptide, 246 aa]		

Seq. No.	807	Seq. ID	OJ990503_02.9919.C25
Gene No.	1628	Strand	+
Start	228	End	6331
Name	OJ990503_02.9919.C25.o2.gp	Method	AAT/GAP
Start	4530	End	5449
GI	68464_1.R1084	Score	1563
Exons	4530..4963, 5059..5449		
GI Descrip.	'732003/sp|P39281|BLC_ECOLI 1.0e-15 OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR >gi_2125977_pir__I84534 outer membrane lipoprotein - Escherichia coli >gi_536993 (U14003) ORF_f177 [Escherichia coli] >gi_717134 (U21726) lipocalin precursor [Escherichia coli] >gi_1790592 (AE000487) outer membrane lipoprotein (lipocalin) [Escherichia coli]'		

Seq. No.	807	Seq. ID	OJ990503_02.9919.C25
Gene No.	1629	Strand	-
Start	189	End	359
Name	OJ990503_02.9919.C25.o1.gp	Method	AAT/GAP
Start	189	End	359
GI	33945_1.R1084	Score	290
Exons	189..359		
GI Descrip.	'2583133 4.0e-27 (AC002387) unknown protein [Arabidopsis thaliana]'		

Seq. No.	807	Seq. ID	OJ990503_02.9919.C25
Gene No.	1630	Strand	
Start	4511	End	5253
Name	OJ990503_02.9919.C25.o1.tm	Method	TBLASTX:Maize
Start	4511	End	5253
GI	none	Score	38
Exons	4511..4570, 4512..4565, 4607..4966, 4612..4797, 4835..4879, 4940..4963, 5058..5138, 5059..5250, 5206..5253		

Seq. No.	807	Seq. ID	OJ990503_02.9919.C25
Gene No.	1630	Strand	
Start	4511	End	5253
Name	OJ990503_02.9919.C25.o1.tc	Method	TBLASTX:Cress
Start	4606	End	5244
GI	none	Score	496
Exons	4606..4797, 4607..4966, 4835..4879, 4936..4971, 5058..5144, 5059..5217, 5170..5244, 5205..5240		

Seq. No.	807	Seq. ID	OJ990503_02.9919.C25
Gene No.	1630	Strand	
Start	4511	End	5253
Name	OJ990503_02.9919.C25.o1.ts	Method	TBLASTX:Soybean
Start	4606	End	5142
GI	none	Score	496
Exons	4606..4797, 4607..4966, 5059..5142		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1631	Strand	+
Start	529	End	15775
Name	OJ990503_02.9919.C26.o1.gs	Method	GENSCAN
Start	529	End	15775
GI	none	Score	.48
Exons	529..1052, 1974..2286, 2350..2668, 4787..4841, 6076..6268, 6355..6570, 6737..7226, 7696..7945, 8061..8134, 10215..10287, 10294..11094, 11577..11600, 11874..12086, 12131..12244, 12433..12557, 15433..15775		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1631	Strand	+
Start	529	End	15775
Name	OJ990503_02.9919.C26.o1.np	Method	AAT/NAP
Start	3968	End	4272
GI	6069646	Score	67
Exons	3968..4163, 4245..4272		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1631	Strand	+
Start	529	End	15775
Name	OJ990503_02.9919.C26.o2.np	Method	AAT/NAP
Start	10282	End	11106
GI	6503290	Score	831

Exons	10282..11106		
GI Descrip.	(AC011713) Similar to gb|U21855 CCR4-associated factor 1 (CAF1) from Mus musculus. ESTs gb|AAA394972, gb|AA585812 and gb|H77015 come from this gene. [Arabidopsis thaliana]		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1632	Strand	-
Start	10192	End	11190
Name	OJ990503_02.9919.C26.o4.tm	Method	TBLASTX:Maize
Start	2417	End	2560
GI	none	Score	193
Exons	2417..2560, 2427..2558, 2501..2560		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1632	Strand	-
Start	10192	End	11190
Name	OJ990503_02.9919.C26.o2.tm	Method	TBLASTX:Maize
Start	5934	End	6507
GI	none	Score	60
Exons	5934..5981, 5937..5981, 5941..5982, 5979..6068, 5981..6067, 6141..6266, 6142..6279, 6180..6266, 6354..6506, 6354..6506, 6361..6507, 6373..6507		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1632	Strand	-
Start	10192	End	11190
Name	OJ990503_02.9919.C26.o1.gp	Method	AAT/GAP
Start	10192	End	11190
GI	32278_1.R1084	Score	1951
Exons	10192..11190		
GI Descrip.	'4263711/gb|AAD15397| 7.0e-90 (AC006223) putative CCR4-associated transcription factor [Arabidopsis thaliana]'		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1632	Strand	-
Start	10192	End	11190
Name	OJ990503_02.9919.C26.o1.tc	Method	TBLASTX:Cress
Start	10300	End	11094
GI	none	Score	255
Exons	10300..10560, 10392..10487, 10572..10904, 10573..11094, 10636..11073, 10977..11093		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1632	Strand	-
Start	10192	End	11190
Name	OJ990503_02.9919.C26.o1.ts	Method	TBLASTX:Soybean
Start	10303	End	11102
GI	none	Score	293
Exons	10303..10560, 10308..10508, 10572..10904, 10573..11094, 10636..11088, 10968..11102		

Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1632	Strand	-
Start	10192	End	11190
Name	OJ990503_02.9919.C26.o3.tm	Method	TBLASTX:Maize
Start	10303	End	10578
GI	none	Score	327

Exons	10303..10578, 10308..10505		
Seq. No.	808	Seq. ID	OJ990503_02.9919.C26
Gene No.	1632	Strand	-
Start	10192	End	11190
Name	OJ990503_02.9919.C26.o1.tm	Method	TBLASTX:Maize
Start	10581	End	11105
GI	none	Score	432
Exons	10581..10904, 10582..10905, 10912..11082, 10939..11082, 10955..11086, 10955..11098, 10965..11105, 11064..11105		
Seq. No.	809	Seq. ID	OJ990503_02.9919.C27
Gene No.	1633	Strand	+
Start	901	End	1181
Name	OJ990503_02.9919.C27.o1.gs	Method	GENSCAN
Start	901	End	1181
GI	none	Score	.51
Exons	901..978, 1068..1181		
Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1634	Strand	+
Start	172	End	1985
Name	OJ990503_02.9919.C28.o1.gs	Method	GENSCAN
Start	172	End	1985
GI	none	Score	.58
Exons	172..249, 339..452, 746..809, 1467..1704, 1724..1985		
Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1635	Strand	+
Start	2476	End	3259
Name	OJ990503_02.9919.C28.o2.gs	Method	GENSCAN
Start	2476	End	3259
GI	none	Score	.76
Exons	2476..2536, 3186..3259		
Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1636	Strand	+
Start	4003	End	6661
Name	OJ990503_02.9919.C28.o3.gs	Method	GENSCAN
Start	4003	End	4287
GI	none	Score	.7
Exons	4003..4095, 4201..4287		
Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1636	Strand	+
Start	4003	End	6661
Name	OJ990503_02.9919.C28.o1.np	Method	AAT/NAP
Start	4162	End	6661
GI	5915816	Score	102
Exons	4162..4227, 5609..5677, 6513..6661		
GI Descrip.	CYTOCHROME P450 71A9 (P450 CP1) gi|3334659|emb|CAA71513| (Y10489) putative cytochrome P450 [Glycine max]		
Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o4.gs	Method	GENSCAN

Start	5861	End	16220
GI	none	Score	.48
Exons	5861..5936, 8215..8294, 8729..8858, 8944..8993, 9750..9890, 10448..10588, 10685..10911, 11209..11334, 13238..13523, 13588..13707, 14511..14651, 15400..15449, 16030..16093, 16167..16220		

Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o2.gp	Method	AAT/GAP
Start	7922	End	8797
GI	77202_1.R1084	Score	776
Exons	7922..8294, 8729..8797		
GI Descrip.	'3482971/emb|CAA20527.1| 1.0e-13 (AL031369) putative protein [Arabidopsis thaliana]'		

Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o1.tc	Method	TBLASTX:Cress
Start	8211	End	10594
GI	none	Score	93
Exons	8211..8297, 8217..8297, 8726..8860, 8799..8882, 8943..8999, 8944..9003, 9750..9803, 9783..9878, 9792..9833, 9825..9890, 10445..10594, 10449..10583		

Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o1.ts	Method	TBLASTX:Soybean
Start	8211	End	10601
GI	none	Score	89
Exons	8211..8297, 8212..8295, 8217..8297, 8564..8605, 8701..8874, 8726..8860, 8778..8870, 8938..9003, 8943..8999, 9743..9862, 9747..9890, 9748..9891, 10445..10591, 10445..10600, 10449..10601		

Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o2.np	Method	AAT/NAP
Start	8211	End	10561
GI	6623876	Score	640
Exons	8211..8294, 8729..8858, 8944..8993, 9750..9890, 10448..10561		
GI Descrip.	(AC018722) unknown protein [Arabidopsis thaliana]		

Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o1.tm	Method	TBLASTX:Maize
Start	8211	End	10627
GI	none	Score	100
Exons	8211..8297, 8212..8295, 8726..8860, 8728..8850, 8777..8860, 8778..8873, 8943..8999, 8944..9003, 9747..9890, 9748..9882, 9748..9891, 10445..10627, 10448..10594, 10449..10604		

Seq. No.	810	Seq. ID	OJ990503_02.9919.C28

Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o3.np	Method	AAT/NAP
Start	11822	End	12231
GI	6539570	Score	182
Exons	11822..11888, 12038..12231		
GI Descrip.	(AP000836) hypothetical protein [Oryza sativa]		

Seq. No.	810	Seq. ID	OJ990503_02.9919.C28
Gene No.	1637	Strand	-
Start	5861	End	16220
Name	OJ990503_02.9919.C28.o4.np	Method	AAT/NAP
Start	12368	End	13860
GI	6630699	Score	91
Exons	12368..12454, 13800..13860		
GI Descrip.	(AP000969) hypothetical protein [Oryza sativa] gi|6721536|dbj|BAA89566.1| (AP001073) hypothetical protein [Oryza sativa]		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1638	Strand	+
Start	1001	End	1114
Name	OJ990503_02.9919.C29.o1.gs	Method	GENSCAN
Start	1001	End	1114
GI	none	Score	.98
Exons	1001..1114		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1639	Strand	+
Start	2366	End	7080
Name	OJ990503_02.9919.C29.o1.np	Method	AAT/NAP
Start	2366	End	6883
GI	2494075	Score	2217
Exons	2366..2516, 2984..3177, 3284..3412, 5067..5186, 5266..5402, 5484..5639, 6080..6458, 6556..6672, 6773..6883		
GI Descrip.	NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [NADP+]) (TRIOSEPHOSPHATE DEHYDROGENASE) gi|1084478|pir||S43833 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - maize gi|474408|emb|CAA53075| (X75326) glyceraldehyde-3-phosphate dehydrogenas		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1639	Strand	+
Start	2366	End	7080
Name	OJ990503_02.9919.C29.o3.gs	Method	GENSCAN
Start	5061	End	6886
GI	none	Score	.86
Exons	5061..5186, 5266..5402, 5484..5639, 6080..6458, 6556..6672, 6740..6886		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1639	Strand	+
Start	2366	End	7080
Name	OJ990503_02.9919.C29.o1.gp	Method	AAT/GAP
Start	5499	End	7080

GI	12586_1.R1084	Score	1771
Exons	5499..5639, 6080..6458, 6556..6672, 6773..7080		
GI Descrip.	'2494075/sp|Q43272|GAPN_MAIZE 1.0e-129 NADP-DEPENDENT GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (NON-PHOSPHORYLATING GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE) (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [NADP+]) (TRIOSEPHOSPHATE DEHYDROGENASE) >gi_1084478_pir__S43833 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (EC 1.2.1.9) - maize >gi_474408_emb_CAA53075_ (X75326) glyceraldehyde-3-'		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1640	Strand	-
Start	2319	End	3465
Name	OJ990503_02.9919.C29.o2.gs	Method	GENSCAN
Start	2319	End	3465
GI	none	Score	.59
Exons	2319..2424, 2500..2610, 2771..3465		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o4.tm	Method	TBLASTX:Maize
Start	2368	End	3036
GI	none	Score	231
Exons	2368..2514, 2369..2515, 2982..3035, 2983..3036		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o1.tc	Method	TBLASTX:Cress
Start	2369	End	6452
GI	none	Score	207
Exons	2369..2515, 2374..2511, 2982..3179, 2983..3180, 3281..3415, 3283..3411, 5055..5186, 5069..5185, 5263..5400, 5265..5402, 5454..5639, 5482..5637, 6077..6451, 6078..6452		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o1.ts	Method	TBLASTX:Soybean
Start	2374	End	6886
GI	none	Score	210
Exons	2374..2511, 2375..2515, 2983..3180, 2994..3179, 3281..3430, 3283..3411, 5055..5186, 5069..5188, 5069..5185, 5073..5198, 5202..5402, 5263..5400, 5264..5404, 5265..5405, 5454..5633, 5482..5637, 5485..5667, 5487..5639, 6067..6198, 6077..6454, 6078..6458, 6080..6472, 6259..6459, 6520..6672, 6540..6668, 6555..6674, 6761..6886, 6772..6882		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o2.tm	Method	TBLASTX:Maize
Start	5055	End	6293
GI	none	Score	203
Exons	5055..5186, 5069..5188, 5069..5185, 5263..5400, 5263..5400, 5265..5438, 5265..5402, 5454..5633, 5482..5637, 5482..5646,		

5484..5639, 6073..6198, 6077..6286, 6078..6293

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o3.tm	Method	TBLASTX:Maize
Start	6555	End	6999
GI	none	Score	201
Exons	6555..6671, 6556..6678, 6574..6678, 6761..6892, 6770..6892, 6771..6893, 6772..6903, 6772..6906, 6945..6998, 6945..6998, 6946..6999		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o3.tc	Method	TBLASTX:Cress
Start	6566	End	6886
GI	none	Score	87
Exons	6566..6673, 6571..6678, 6612..6671, 6761..6886, 6772..6882		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o2.gp	Method	AAT/GAP
Start	7239	End	7998
GI	40242_1.R1084	Score	1248
Exons	7239..7788, 7889..7998		
GI Descrip.	'1345978/sp|P48627|FD6C_BRANA 2.0e-42 OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_457631 (L29214) omega-6 desaturase [Brassica napus]'		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o1.tm	Method	TBLASTX:Maize
Start	7575	End	11847
GI	none	Score	239
Exons	7575..7622, 7592..7789, 7615..7791, 7619..7789, 7627..7791, 7889..8014, 7889..8002, 7891..8013, 8883..9002, 8884..9003, 8888..9013, 9801..9992, 9803..9994, 9812..9991, 10095..10226, 10096..10227, 10103..10234, 10104..10238, 10575..10760, 10590..10748, 10597..10749, 10864..10908, 10864..11007, 10865..11008, 10871..11008, 10939..11010, 11078..11329, 11082..11270, 11087..11275, 11778..11846, 11782..11847		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o2.ts	Method	TBLASTX:Soybean
Start	7627	End	11242
GI	none	Score	74
Exons	7627..7713, 7631..7708, 7711..7791, 7715..7792, 7883..8002, 7893..7982, 8883..9002, 8883..9002, 8884..9003, 9801..9992, 9810..9992, 9812..10015, 9817..9993, 10099..10218, 10101..10163, 10102..10218, 10103..10219, 10103..10234, 10572..10760, 10596..10748, 10597..10749, 10864..11007, 10865..11008, 11078..11242, 11082..11240		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o4.gs	Method	GENSCAN
Start	7627	End	12009
GI	none	Score	.55
Exons	7627..7788, 7889..7946, 8887..9002, 10104..10226, 11090..11202, 11780..11831, 11923..12009		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o2.np	Method	AAT/NAP
Start	7627	End	12096
GI	1345978	Score	1490
Exons	7627..7788, 7889..8003, 8884..9002, 9815..9992, 10104..10226, 10597..10748, 10864..11007, 11090..11303, 11978..12096		
GI Descrip.	OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR gi|457631 (L29214) omega-6 desaturase [Brassica napus]		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o2.tc	Method	TBLASTX:Cress
Start	7633	End	11257
GI	none	Score	131
Exons	7633..7791, 7640..7789, 7889..8002, 7893..7982, 8883..9002, 8883..9002, 8890..9003, 9810..9986, 9812..9985, 10103..10234, 10104..10238, 10575..10760, 10591..10749, 10864..11007, 10865..11008, 11078..11257, 11081..11194, 11082..11252		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o3.gp	Method	AAT/GAP
Start	9878	End	10762
GI	uC-osflcyp028a03b1	Score	933
Exons	9878..10226, 10597..10762		
GI Descrip.	'1345978/sp|P48627|FD6C_BRANA 2.0e-55 OMEGA-6 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR >gi_457631 (L29214) omega-6 desaturase [Brassica napus]'		

Seq. No.	811	Seq. ID	OJ990503_02.9919.C29
Gene No.	1641	Strand	-
Start	7239	End	12214
Name	OJ990503_02.9919.C29.o4.gp	Method	AAT/GAP
Start	11141	End	12214
GI	29264_1.R1084	Score	963
Exons	11141..11322, 11780..11831, 11923..12214		
GI Descrip.	'4176420/dbj|BAA37167| 2.0e-11 (AB008097) cytochrome P450 [Arabidopsis thaliana]'		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1642	Strand	-
Start	1	End	1982
Name	OJ990503_02.9919.C30.o1.np	Method	AAT/NAP

Start	1	End	1982
GI	6705984	Score	1346
Exons	1..24, 179..1982		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1643	Strand	-
Start	4043	End	6054
Name	OJ990503_02.9919.C30.o1.tm	Method	TBLASTX:Maize
Start	497	End	733
GI	none	Score	94
Exons	497..733, 503..703, 606..728		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1643	Strand	-
Start	4043	End	6054
Name	OJ990503_02.9919.C30.o2.ts	Method	TBLASTX:Soybean
Start	497	End	733
GI	none	Score	94
Exons	497..733, 503..703, 606..728		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1643	Strand	-
Start	4043	End	6054
Name	OJ990503_02.9919.C30.o2.tw	Method	TBLASTX:Wheat
Start	501	End	970
GI	none	Score	97
Exons	501..683, 512..682, 541..684, 689..970, 701..970		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1643	Strand	-
Start	4043	End	6054
Name	OJ990503_02.9919.C30.o1.tw	Method	TBLASTX:Wheat
Start	1376	End	1888
GI	none	Score	177
Exons	1376..1888, 1382..1849, 1479..1874		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1643	Strand	-
Start	4043	End	6054
Name	OJ990503_02.9919.C30.o1.ts	Method	TBLASTX:Soybean
Start	1487	End	1870
GI	none	Score	152
Exons	1487..1675, 1700..1870		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1643	Strand	-
Start	4043	End	6054
Name	OJ990503_02.9919.C30.o2.tm	Method	TBLASTX:Maize
Start	1703	End	1888
GI	none	Score	150
Exons	1703..1888, 1704..1877		

Seq. No.	812	Seq. ID	OJ990503_02.9919.C30
Gene No.	1643	Strand	-
Start	4043	End	6054
Name	OJ990503_02.9919.C30.o2.np	Method	AAT/NAP

Start	4043	End	6054
GI	6498436	Score	50
Exons	4043..4203, 6028..6054		
GI Descrip.	(AP000815) hypothetical protein [Oryza sativa]		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1644	Strand	+
Start	1	End	955
Name	OJ990503_02.9919.C31.o1.np	Method	AAT/NAP
Start	1	End	931
GI	2980770	Score	913
Exons	1..931		
GI Descrip.	(AL022198) putative protein kinase [Arabidopsis thaliana]		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1644	Strand	+
Start	1	End	955
Name	OJ990503_02.9919.C31.o1.gs	Method	GENSCAN
Start	44	End	955
GI	none	Score	.82
Exons	44..955		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1645	Strand	+
Start	2209	End	2686
Name	OJ990503_02.9919.C31.o2.gs	Method	GENSCAN
Start	2209	End	2686
GI	none	Score	.82
Exons	2209..2323, 2496..2686		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1646	Strand	+
Start	6077	End	7347
Name	OJ990503_02.9919.C31.o2.np	Method	AAT/NAP
Start	6077	End	7347
GI	124121	Score	131
Exons	6077..6163, 7159..7347		
GI Descrip.	SUBTILISIN INHIBITORS I AND II (ASI-I AND ASI-II)		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1647	Strand	+
Start	10887	End	11245
Name	OJ990503_02.9919.C31.o1.gp	Method	AAT/GAP
Start	10887	End	11245
GI	700142	Score	718
Exons	10887..11245		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1648	Strand	-
Start	4040	End	11940
Name	OJ990503_02.9919.C31.o1.tc	Method	TBLASTX:Cress
Start	1	End	439
GI	none	Score	615
Exons	1..93, 2..439, 148..438		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1648	Strand	-

Start	4040	End	11940
Name	OJ990503_02.9919.C31.o1.tm	Method	TBLASTX:Maize
Start	1	End	916
GI	none	Score	611
Exons	1..438, 2..439, 536..595, 538..594, 619..669, 623..916, 796..915		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1648	Strand	-
Start	4040	End	11940
Name	OJ990503_02.9919.C31.o1.ts	Method	TBLASTX:Soybean
Start	1	End	948
GI	none	Score	596
Exons	1..93, 2..439, 151..438, 533..595, 538..594, 608..679, 634..669, 719..763, 764..916, 805..948		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1648	Strand	-
Start	4040	End	11940
Name	OJ990503_02.9919.C31.o1.tw	Method	TBLASTX:Wheat
Start	236	End	436
GI	none	Score	189
Exons	236..436, 244..432		

Seq. No.	813	Seq. ID	OJ990503_02.9919.C31
Gene No.	1648	Strand	-
Start	4040	End	11940
Name	OJ990503_02.9919.C31.o3.gs	Method	GENSCAN
Start	4040	End	11940
GI	none	Score	.46
Exons	4040..4156, 6078..6280, 7272..7405, 8060..8094, 10985..11131, 11214..11377, 11802..11940		

Seq. No.	814	Seq. ID	OJ990503_02.9919.C33
Gene No.	1649	Strand	+
Start	1	End	2380
Name	OJ990503_02.9919.C33.o1.np	Method	AAT/NAP
Start	1	End	2380
GI	6523547	Score	134
Exons	1..253, 913..1385, 1498..1546, 2310..2380		
GI Descrip.	(AJ242540) hydroxyproline-rich glycoprotein DZ-HRGP [Volvox carteri f. nagariensis]		

Seq. No.	814	Seq. ID	OJ990503_02.9919.C33
Gene No.	1649	Strand	+
Start	1	End	2380
Name	OJ990503_02.9919.C33.o1.gs	Method	GENSCAN
Start	89	End	1561
GI	none	Score	.81
Exons	89..205, 509..662, 966..1123, 1223..1360, 1445..1561		

Seq. No.	814	Seq. ID	OJ990503_02.9919.C33
Gene No.	1649	Strand	+
Start	1	End	2380
Name	OJ990503_02.9919.C33.o1.gp	Method	AAT/GAP
Start	1011	End	1813
GI	none	Score	1156
Exons	1011..1123, 1223..1360, 1445..1813		

Seq. No.	814	Seq. ID	OJ990503_02.9919.C33
Gene No.	1650	Strand	-
Start	2255	End	2605
Name	OJ990503_02.9919.C33.o1.tm	Method	TBLASTX:Maize
Start	1073	End	1542
GI	none	Score	68
Exons	1073..1132, 1082..1123, 1222..1365, 1223..1366, 1444..1542, 1445..1540		

Seq. No.	814	Seq. ID	OJ990503_02.9919.C33
Gene No.	1650	Strand	-
Start	2255	End	2605
Name	OJ990503_02.9919.C33.o1.ts	Method	TBLASTX:Soybean
Start	1079	End	1555
GI	none	Score	55
Exons	1079..1132, 1222..1362, 1223..1366, 1444..1554, 1445..1555		

Seq. No.	814	Seq. ID	OJ990503_02.9919.C33
Gene No.	1650	Strand	-
Start	2255	End	2605
Name	OJ990503_02.9919.C33.o2.gs	Method	GENSCAN
Start	2255	End	2605
GI	none	Score	.65
Exons	2255..2347, 2519..2605		

Seq. No.	815	Seq. ID	OJ990503_02.9919.C39
Gene No.	1651	Strand	+
Start	537	End	623
Name	OJ990503_02.9919.C39.o1.gs	Method	GENSCAN
Start	537	End	623
GI	none	Score	.6
Exons	537..623		

Seq. No.	816	Seq. ID	OJ990503_02.9919.C41
Gene No.	1652	Strand	-
Start	1	End	394
Name	OJ990503_02.9919.C41.o1.np	Method	AAT/NAP
Start	1	End	394
GI	2980770	Score	530
Exons	1..394		
GI Descrip.	(AL022198) putative protein kinase [Arabidopsis thaliana]		

Seq. No.	816	Seq. ID	OJ990503_02.9919.C41
Gene No.	1652	Strand	-
Start	1	End	394
Name	OJ990503_02.9919.C41.o1.ts	Method	TBLASTX:Soybean
Start	1	End	391
GI	none	Score	72
Exons	1..390, 5..151, 209..391		

Seq. No.	816	Seq. ID	OJ990503_02.9919.C41
Gene No.	1652	Strand	-
Start	1	End	394
Name	OJ990503_02.9919.C41.o1.tm	Method	TBLASTX:Maize
Start	1	End	394
GI	none	Score	284

Exons	1..393, 2..394		
Seq. No.	816	Seq. ID	OJ990503_02.9919.C41
Gene No.	1652	Strand	-
Start	1	End	394
Name	OJ990503_02.9919.C41.o1.tc	Method	TBLASTX:Cress
Start	13	End	391
GI	none	Score	58
Exons	13..390, 20..151, 209..391		
Seq. No.	816	Seq. ID	OJ990503_02.9919.C41
Gene No.	1652	Strand	-
Start	1	End	394
Name	OJ990503_02.9919.C41.o1.gs	Method	GENSCAN
Start	44	End	346
GI	none	Score	.68
Exons	44..346		
Seq. No.	816	Seq. ID	OJ990503_02.9919.C41
Gene No.	1652	Strand	-
Start	1	End	394
Name	OJ990503_02.9919.C41.o1.tw	Method	TBLASTX:Wheat
Start	52	End	391
GI	none	Score	57
Exons	52..150, 56..151, 238..390, 287..391		
Seq. No.	817	Seq. ID	OJ990503_02.9919.C43
Gene No.	1653	Strand	-
Start	296	End	434
Name	OJ990503_02.9919.C43.o1.gs	Method	GENSCAN
Start	296	End	434
GI	none	Score	.92
Exons	296..434		
Seq. No.	818	Seq. ID	OJ990503_02.9919.C45
Gene No.	1654	Strand	-
Start	489	End	604
Name	OJ990503_02.9919.C45.o1.gs	Method	GENSCAN
Start	489	End	604
GI	none	Score	.81
Exons	489..604		
Seq. No.	819	Seq. ID	OJ990423_04.9919.C2
Gene No.	1655	Strand	+
Start	108	End	173
Name	OJ990423_04.9919.C2.o1.tc	Method	TBLASTX:Cress
Start	1	End	148
GI	none	Score	224
Exons	1..147, 2..148		
Seq. No.	819	Seq. ID	OJ990423_04.9919.C2
Gene No.	1655	Strand	+
Start	108	End	173
Name	OJ990423_04.9919.C2.o1.np	Method	AAT/NAP
Start	108	End	173
GI	6685159	Score	124
Exons	108..173		

GI Descrip. (AF219140) gastric cancer-related protein GCYS-20 [Homo sapiens]

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1656	Strand	+
Start	8011	End	10987
Name	OJ990423_04.9919.C6.o1.np	Method	AAT/NAP
Start	8011	End	10987
GI	2583130	Score	1160
Exons	8011..10136, 10188..10605, 10908..10987		
GI Descrip.	(AC002387) putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1657	Strand	+
Start	13497	End	18399
Name	OJ990423_04.9919.C6.o3.np	Method	AAT/NAP
Start	13497	End	17936
GI	3426051	Score	1129
Exons	13497..13679, 13940..14053, 14161..14223, 15059..15186, 16516..16597, 16690..16741, 16833..16930, 17163..17324, 17802..17936		
GI Descrip.	(AC005168) putative Na+ dependent ileal bile acid transporter [Arabidopsis thaliana]		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1657	Strand	+
Start	13497	End	18399
Name	OJ990423_04.9919.C6.o1.gp	Method	AAT/GAP
Start	13995	End	14223
GI	9200_1.R1084	Score	144
Exons	13995..14053, 14161..14223		
GI Descrip.	'3426051 9.0e-41 (AC005168) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1657	Strand	+
Start	13497	End	18399
Name	OJ990423_04.9919.C6.o2.gp	Method	AAT/GAP
Start	16516	End	16986
GI	9200_1.R1084	Score	349
Exons	16516..16597, 16690..16741, 16833..16986		
GI Descrip.	'3426051 9.0e-41 (AC005168) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1657	Strand	+
Start	13497	End	18399
Name	OJ990423_04.9919.C6.o3.gp	Method	AAT/GAP
Start	17172	End	18399
GI	2342_1.R1084	Score	1182
Exons	17172..17324, 17802..17891, 18018..18399		
GI Descrip.	'3426051 4.0e-25 (AC005168) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1658	Strand	+
Start	29046	End	30199

Name	OJ990423_04.9919.C6.o4.np	Method	AAT/NAP
Start	29046	End	30199
GI	5852181	Score	127
Exons	29046..29365, 30023..30199		
GI Descrip.	(AL117265) zhb0011.1 [Oryza sativa]		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1659	Strand	+
Start	32757	End	34797
Name	OJ990423_04.9919.C6.o4.gp	Method	AAT/GAP
Start	32729	End	33047
GI	71335_1.R1084	Score	613
Exons	32729..33047		
GI Descrip.	'4914451/emb|CAB43691.1| 9.0e-11 (AL050398) dimethylaniline monooxygenase-like protein [Arabidopsis thaliana]'		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1659	Strand	+
Start	32757	End	34797
Name	OJ990423_04.9919.C6.o5.np	Method	AAT/NAP
Start	32745	End	34797
GI	4914451	Score	1183
Exons	32745..33386, 33763..34015, 34274..34392, 34567..34797		
GI Descrip.	(AL050398) dimethylaniline monooxygenase-like protein [Arabidopsis thaliana]		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1659	Strand	+
Start	32757	End	34797
Name	OJ990423_04.9919.C6.o6.gs	Method	GENSCAN
Start	32757	End	34782
GI	none	Score	.96
Exons	32757..33386, 33763..34011, 34270..34392, 34564..34782		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1660	Strand	+
Start	44287	End	48852
Name	OJ990423_04.9919.C6.o8.gs	Method	GENSCAN
Start	44287	End	47903
GI	none	Score	.63
Exons	44287..44304, 47256..47506, 47673..47882, 47900..47903		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1660	Strand	+
Start	44287	End	48852
Name	OJ990423_04.9919.C6.o6.np	Method	AAT/NAP
Start	47234	End	48852
GI	6539588	Score	129
Exons	47234..47498, 48779..48852		
GI Descrip.	(AP000837) hypothetical protein [Oryza sativa]		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1661	Strand	+
Start	54859	End	58082
Name	OJ990423_04.9919.C6.o7.np	Method	AAT/NAP
Start	54859	End	58079
GI	6907089	Score	4237

Exons	54859..56120, 56219..58079		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		
Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1661	Strand	+
Start	54859	End	58082
Name	OJ990423_04.9919.C6.o10.gs	Method	GENSCAN
Start	54859	End	58082
GI	none	Score	.98
Exons	54859..56120, 56219..58082		
Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1662	Strand	-
Start	4800	End	7434
Name	OJ990423_04.9919.C6.o2.gs	Method	GENSCAN
Start	4800	End	7434
GI	none	Score	.94
Exons	4800..4931, 6431..6949, 7357..7434		
Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1663	Strand	-
Start	48567	End	53727
Name	OJ990423_04.9919.C6.o9.gs	Method	GENSCAN
Start	48567	End	53727
GI	none	Score	.55
Exons	48567..48859, 51689..51801, 52344..52432, 53232..53405, 53604..53647, 53703..53727		
Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o3.tm	Method	TBLASTX:Maize
Start	8084	End	8873
GI	none	Score	99
Exons	8084..8248, 8231..8320, 8328..8510, 8568..8708, 8790..8873		
Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o1.tw	Method	TBLASTX:Wheat
Start	8128	End	8498
GI	none	Score	226
Exons	8128..8319, 8129..8320, 8327..8497, 8334..8498		
Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o2.tw	Method	TBLASTX:Wheat
Start	8672	End	9089
GI	none	Score	378
Exons	8672..9055, 8673..9056, 8760..9074, 9027..9089		
Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o1.ts	Method	TBLASTX:Soybean
Start	8793	End	9212

GI	none	Score	103
Exons	8793..8996, 8876..8992, 8994..9212, 9011..9211		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o1.tm	Method	TBLASTX:Maize
Start	8880	End	9229
GI	none	Score	312
Exons	8880..9221, 8894..9229		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o5.tw	Method	TBLASTX:Wheat
Start	9090	End	9278
GI	none	Score	215
Exons	9090..9278, 9131..9271		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o4.tw	Method	TBLASTX:Wheat
Start	9669	End	10076
GI	none	Score	166
Exons	9669..9872, 9921..10076		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o1.tc	Method	TBLASTX:Cress
Start	13557	End	14056
GI	none	Score	149
Exons	13557..13682, 13565..13687, 13798..13857, 13939..14055, 13940..14056		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o3.tc	Method	TBLASTX:Cress
Start	14161	End	15189
GI	none	Score	95
Exons	14161..14229, 15035..15187, 15058..15189, 15076..15189		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o2.tc	Method	TBLASTX:Cress
Start	16513	End	18095
GI	none	Score	131
Exons	16513..16605, 16514..16597, 16690..16740, 16831..16929, 16832..16933, 17162..17275, 17163..17273, 17273..17323, 17274..17324, 17799..17852, 17801..17890, 17801..17893, 18023..18094, 18036..18095		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-

Start	58717	End	59675
Name	OJ990423_04.9919.C6.o11.gs	Method	GENSCAN
Start	58717	End	59610
GI	none	Score	.56
Exons	58717..59610		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o8.np	Method	AAT/NAP
Start	58720	End	59675
GI	6498441	Score	1429
Exons	58720..59001, 59095..59675		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o3.tw	Method	TBLASTX:Wheat
Start	59227	End	59625
GI	none	Score	129
Exons	59227..59625, 59230..59586, 59534..59617		

Seq. No.	820	Seq. ID	OJ990423_04.9919.C6
Gene No.	1664	Strand	-
Start	58717	End	59675
Name	OJ990423_04.9919.C6.o2.tm	Method	TBLASTX:Maize
Start	59314	End	59658
GI	none	Score	166
Exons	59314..59427, 59425..59658		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1665	Strand	+
Start	5294	End	5614
Name	OJ990423_04.9919.C7.o2.np	Method	AAT/NAP
Start	5294	End	5614
GI	5922623	Score	87
Exons	5294..5389, 5576..5614		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016856|dbj|BAA85199.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o1.np	Method	AAT/NAP
Start	1	End	4711
GI	6498441	Score	5389
Exons	1..836, 1008..1487, 1680..1923, 2098..2232, 2416..2791, 2856..3317, 3648..4711		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7

Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o6.tw	Method	TBLASTX:Wheat
Start	3	End	296
GI	none	Score	97
Exons	3..296, 4..138		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o3.tm	Method	TBLASTX:Maize
Start	21	End	296
GI	none	Score	193
Exons	21..296		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o1.gs	Method	GENSCAN
Start	66	End	5500
GI	none	Score	.68
Exons	66..2789, 2869..5235, 5291..5500		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o7.tw	Method	TBLASTX:Wheat
Start	387	End	699
GI	none	Score	80
Exons	387..647, 498..686, 523..699		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o2.ts	Method	TBLASTX:Soybean
Start	447	End	1013
GI	5666795	Score	68
Exons	447..647, 702..839, 915..1013		
GI Descrip.	4206306 2.0e-10 (AF049110) prpol [Zea mays]		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o4.tw	Method	TBLASTX:Wheat
Start	702	End	4163
GI	none	Score	95
Exons	702..851, 703..840, 898..1071, 912..1160, 912..1136, 4110..4163		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o1.tw	Method	TBLASTX:Wheat
Start	1537	End	2781
GI	none	Score	399
Exons	1537..1662, 2319..2780, 2320..2781		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7

Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o1.ts	Method	TBLASTX:Soybean
Start	1761	End	2132
GI	none	Score	90
Exons	1761..2132, 1972..2115		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o2.tw	Method	TBLASTX:Wheat
Start	1786	End	2211
GI	none	Score	315
Exons	1786..2211, 1791..2210		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o2.tm	Method	TBLASTX:Maize
Start	1884	End	2268
GI	none	Score	226
Exons	1884..2267, 1903..2268		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o1.tm	Method	TBLASTX:Maize
Start	2295	End	2651
GI	none	Score	121
Exons	2295..2600, 2295..2651, 2305..2616		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o3.ts	Method	TBLASTX:Soybean
Start	2376	End	2741
GI	none	Score	117
Exons	2376..2510, 2517..2741		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o3.tw	Method	TBLASTX:Wheat
Start	2947	End	3433
GI	none	Score	168
Exons	2947..3432, 2978..3238, 3271..3420, 3296..3433		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-
Start	1	End	5500
Name	OJ990423_04.9919.C7.o5.tw	Method	TBLASTX:Wheat
Start	4171	End	4563
GI	none	Score	91
Exons	4171..4428, 4205..4444, 4403..4492, 4411..4509, 4516..4563		

Seq. No.	821	Seq. ID	OJ990423_04.9919.C7
Gene No.	1666	Strand	-

Start	1	End	5500
Name	OJ990423_04.9919.C7.o4.tm	Method	TBLASTX:Maize
Start	4273	End	4521
GI	none	Score	189
Exons	4273..4521		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1667	Strand	+
Start	6	End	4361
Name	OJ990423_04.9919.C8.o1.gs	Method	GENSCAN
Start	6	End	4361
GI	none	Score	.44
Exons	6..60, 73..154, 243..319, 1004..1132, 3637..3836, 3969..4361		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1668	Strand	+
Start	5658	End	6131
Name	OJ990423_04.9919.C8.o1.gp	Method	AAT/GAP
Start	5658	End	6131
GI	56198_1.R1084	Score	896
Exons	5658..6131		
GI Descrip.	'4874306/gb|AAD31368.1|AC006053_10 1.0e-19 (AC006053) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o2.gs	Method	GENSCAN
Start	5766	End	7157
GI	none	Score	.75
Exons	5766..7157		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o1.np	Method	AAT/NAP
Start	5781	End	7154
GI	6751706	Score	1347
Exons	5781..7154		
GI Descrip.	(AC018848) putative sulfate transporter [Arabidopsis thaliana]		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o1.tm	Method	TBLASTX:Maize
Start	5854	End	6408
GI	none	Score	468
Exons	5854..6108, 5856..6200, 5857..6408, 5889..6407		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o1.tc	Method	TBLASTX:Cress
Start	5875	End	6524
GI	none	Score	373
Exons	5875..6267, 5889..6266, 6294..6524, 6304..6498		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o1.ts	Method	TBLASTX:Soybean
Start	5991	End	6557
GI	none	Score	321
Exons	5991..6266, 5995..6291, 6265..6498, 6270..6557		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o3.tm	Method	TBLASTX:Maize
Start	6672	End	6824
GI	none	Score	73
Exons	6672..6731, 6673..6732, 6720..6824, 6744..6770		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o2.ts	Method	TBLASTX:Soybean
Start	6687	End	7107
GI	none	Score	72
Exons	6687..6857, 6688..6735, 6814..6858, 6861..7106, 6862..7107		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o2.gp	Method	AAT/GAP
Start	6767	End	7220
GI	53456_1.R1084	Score	904
Exons	6767..7220		
GI Descrip.	'4874306/gb|AAD31368.1|AC006053_10 2.0e-29 (AC006053) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o2.tc	Method	TBLASTX:Cress
Start	6798	End	7082
GI	none	Score	218
Exons	6798..7082, 6868..7080		

Seq. No.	822	Seq. ID	OJ990423_04.9919.C8
Gene No.	1669	Strand	-
Start	5766	End	7220
Name	OJ990423_04.9919.C8.o2.tm	Method	TBLASTX:Maize
Start	6825	End	7091
GI	none	Score	189
Exons	6825..7067, 6838..7083, 6999..7091		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1670	Strand	+
Start	1	End	3086
Name	OJ990423_04.9919.C9.o1.np	Method	AAT/NAP
Start	1	End	3086
GI	4539394	Score	961
Exons	1..1703, 3060..3086		

GI Descrip. (AL035526) putative protein [Arabidopsis thaliana]

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1670	Strand	+
Start	1	End	3086
Name	OJ990423_04.9919.C9.o1.gs	Method	GENSCAN
Start	60	End	1709
GI	none	Score	.51
Exons	60..1709		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1671	Strand	+
Start	11381	End	13738
Name	OJ990423_04.9919.C9.o4.gs	Method	GENSCAN
Start	11381	End	13738
GI	none	Score	.44
Exons	11381..11497, 11559..11757, 13632..13738		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o2.tc	Method	TBLASTX:Cress
Start	111	End	1355
GI	none	Score	118
Exons	111..356, 117..356, 213..641, 335..538, 360..656, 429..647, 516..887, 639..965, 653..709, 654..728, 825..1355, 987..1247, 1070..1354, 1092..1355, 1122..1247		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o2.tm	Method	TBLASTX:Maize
Start	114	End	1688
GI	none	Score	137
Exons	114..449, 117..371, 207..653, 225..362, 345..719, 357..725, 567..737, 633..1037, 653..895, 654..947, 783..950, 789..977, 867..1334, 936..1253, 987..1247, 1096..1137, 1269..1346, 1350..1688, 1364..1507		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o1.tw	Method	TBLASTX:Wheat
Start	117	End	1396
GI	none	Score	159
Exons	117..425, 312..701, 332..430, 503..589, 612..1031, 873..911, 921..1253, 938..1042, 1079..1216, 1092..1253, 1266..1358, 1268..1345, 1364..1396		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o2.ts	Method	TBLASTX:Soybean
Start	243	End	1490
GI	none	Score	138
Exons	243..449, 423..551, 849..1058, 1089..1166, 1152..1250, 1266..1364, 1284..1355, 1341..1490, 1364..1489		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o3.ts	Method	TBLASTX:Soybean
Start	567	End	842
GI	none	Score	183
Exons	567..842, 653..733, 782..841		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o3.tc	Method	TBLASTX:Cress
Start	1361	End	1700
GI	none	Score	233
Exons	1361..1699, 1368..1700		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o3.gs	Method	GENSCAN
Start	7079	End	9147
GI	none	Score	.65
Exons	7079..8150, 8253..8539, 8595..8674, 9141..9147		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o2.np	Method	AAT/NAP
Start	7208	End	8436
GI	6970472	Score	856
Exons	7208..8436		
GI Descrip.	(AB030956) OsGAI [Oryza sativa]		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o1.tc	Method	TBLASTX:Cress
Start	7220	End	8162
GI	none	Score	83
Exons	7220..7306, 7224..7307, 7304..7477, 7305..7469, 7532..7669, 7566..7670, 7685..7738, 7736..8143, 7950..8162		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o1.ts	Method	TBLASTX:Soybean
Start	7220	End	8098
GI	none	Score	81
Exons	7220..7306, 7224..7307, 7304..7477, 7305..7478, 7532..7684, 7535..7588, 7566..7667, 7694..7786, 7694..8098, 7910..8002, 7950..8087, 8041..8088		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o1.tm	Method	TBLASTX:Maize

Start	7223	End	7972
GI	none	Score	96
Exons	7223..7306, 7227..7307, 7304..7474, 7304..7477, 7305..7478, 7532..7684, 7535..7582, 7566..7667, 7685..7738, 7751..7969, 7904..7972		

Seq. No.	823	Seq. ID	OJ990423_04.9919.C9
Gene No.	1672	Strand	-
Start	7079	End	9147
Name	OJ990423_04.9919.C9.o1.gp	Method	AAT/GAP
Start	7242	End	7622
GI	1632595	Score	626
Exons	7242..7622		
GI Descrip.	5640157/emb|CAB51555.1| 2.0e-14 (AJ242531) gibberellin response modulator [Triticum aestivum]		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1673	Strand	+
Start	844	End	3250
Name	OJ990423_04.9919.C10.o1.gs	Method	GENSCAN
Start	844	End	3250
GI	none	Score	.43
Exons	844..853, 1142..1265, 2291..2547, 2705..2850, 3140..3250		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1674	Strand	+
Start	14029	End	15159
Name	OJ990423_04.9919.C10.o3.gs	Method	GENSCAN
Start	14029	End	15159
GI	none	Score	.86
Exons	14029..14202, 15108..15159		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o1.np	Method	AAT/NAP
Start	4531	End	9238
GI	4585985	Score	1688
Exons	4531..4613, 4689..5890, 6068..7840, 8189..8680, 8771..8808, 9173..9238		
GI Descrip.	(AC005287) Hypothetical protein [Arabidopsis thaliana]		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o1.tm	Method	TBLASTX:Maize
Start	4804	End	5170
GI	none	Score	249
Exons	4804..5025, 4806..5024, 5026..5160, 5030..5170		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o2.tw	Method	TBLASTX:Wheat
Start	5001	End	5394
GI	none	Score	174
Exons	5001..5024, 5026..5232, 5027..5233, 5236..5394, 5237..5392		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o2.gs	Method	GENSCAN
Start	5161	End	11243
GI	none	Score	.49
Exons	5161..6192, 6267..6445, 6575..6609, 6841..7529, 7758..7915, 8004..8906, 8990..9052, 9559..9852, 10038..10118, 10451..10540, 10628..10783, 11198..11243		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o4.tm	Method	TBLASTX:Maize
Start	5464	End	5737
GI	none	Score	83
Exons	5464..5619, 5504..5620, 5632..5736, 5632..5736, 5633..5737		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o2.tm	Method	TBLASTX:Maize
Start	6109	End	6479
GI	none	Score	66
Exons	6109..6201, 6113..6202, 6223..6477, 6225..6479		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o3.tm	Method	TBLASTX:Maize
Start	7326	End	7787
GI	none	Score	137
Exons	7326..7508, 7509..7787		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o1.tw	Method	TBLASTX:Wheat
Start	7369	End	7793
GI	none	Score	212
Exons	7369..7791, 7371..7793, 7371..7793		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243
Name	OJ990423_04.9919.C10.o1.gp	Method	AAT/GAP
Start	9236	End	9711
GI	uC-osflcyp125b08b1	Score	944
Exons	9236..9711		
GI Descrip.	'5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]'		

Seq. No.	824	Seq. ID	OJ990423_04.9919.C10
Gene No.	1675	Strand	-
Start	5161	End	11243

Name	OJ990423_04.9919.C10.o2.gp	Method	AAT/GAP
Start	10320	End	10806
GI	2427925	Score	576
Exons	10320..10367, 10451..10540, 10628..10806		

Seq. No.	825	Seq. ID	OJ990203_01.9922.C1
Gene No.	1676	Strand	+
Start	563	End	3382
Name	OJ990203_01.9922.C1.o1.gs	Method	GENSCAN
Start	563	End	3382
GI	none	Score	.87
Exons	563..649, 914..976, 2390..2467, 2554..2652, 3047..3191, 3363..3382		

Seq. No.	825	Seq. ID	OJ990203_01.9922.C1
Gene No.	1677	Strand	-
Start	4020	End	4452
Name	OJ990203_01.9922.C1.o2.gs	Method	GENSCAN
Start	4020	End	4452
GI	none	Score	.75
Exons	4020..4085, 4303..4452		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1678	Strand	+
Start	86	End	1721
Name	OJ990203_01.9922.C2.o1.gs	Method	GENSCAN
Start	86	End	1721
GI	none	Score	.42
Exons	86..460, 523..643, 1131..1529, 1600..1641, 1702..1721		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1678	Strand	+
Start	86	End	1721
Name	OJ990203_01.9922.C2.o1.np	Method	AAT/NAP
Start	375	End	1299
GI	4455356	Score	149
Exons	375..683, 1149..1299		
GI Descrip.	(AL035524) putative protein [Arabidopsis thaliana]		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1679	Strand	+
Start	1973	End	5180
Name	OJ990203_01.9922.C2.o3.np	Method	AAT/NAP
Start	1973	End	5180
GI	4680203	Score	2157
Exons	1973..2007, 3279..4951, 5105..5180		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1679	Strand	+
Start	1973	End	5180
Name	OJ990203_01.9922.C2.o1.gp	Method	AAT/GAP
Start	2829	End	4355
GI	2310235	Score	300
Exons	2829..2866, 3279..3418, 4294..4355		
GI Descrip.	5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1679	Strand	+
Start	1973	End	5180
Name	OJ990203_01.9922.C2.o2.gs	Method	GENSCAN
Start	3279	End	5165
GI	none	Score	.76
Exons	3279..4218, 4227..5165		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1679	Strand	+
Start	1973	End	5180
Name	OJ990203_01.9922.C2.o2.gp	Method	AAT/GAP
Start	3283	End	5180
GI	342_1.R1084	Score	3190
Exons	3283..5180		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1680	Strand	-
Start	1863	End	3171
Name	OJ990203_01.9922.C2.o2.np	Method	AAT/NAP
Start	1863	End	3171
GI	5777617	Score	66
Exons	1863..1973, 3124..3171		
GI Descrip.	(AJ245900) CAA30375.1 protein [Oryza sativa]		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1681	Strand	
Start	3630	End	3981
Name	OJ990203_01.9922.C2.o3.tw	Method	TBLASTX:Wheat
Start	3630	End	3981
GI	none	Score	103
Exons	3630..3737, 3720..3971, 3728..3970, 3730..3981		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1682	Strand	
Start	3902	End	4774
Name	OJ990203_01.9922.C2.o1.ts	Method	TBLASTX:Soybean
Start	3902	End	4330
GI	none	Score	102
Exons	3902..3985, 3903..3977, 3978..4040, 4035..4241, 4067..4243, 4247..4330, 4250..4312		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1682	Strand	
Start	3902	End	4774
Name	OJ990203_01.9922.C2.o1.tc	Method	TBLASTX:Cress
Start	4101	End	4447
GI	none	Score	111
Exons	4101..4241, 4103..4216, 4282..4446, 4286..4447		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1682	Strand	
Start	3902	End	4774
Name	OJ990203_01.9922.C2.o1.tw	Method	TBLASTX:Wheat

Start	4200	End	4668
GI	none	Score	69
Exons	4200..4256, 4208..4279, 4238..4357, 4264..4353, 4361..4459, 4366..4458, 4439..4663, 4459..4668, 4460..4663, 4462..4668		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1682	Strand	
Start	3902	End	4774
Name	OJ990203_01.9922.C2.o1.tm	Method	TBLASTX:Maize
Start	4244	End	4702
GI	none	Score	247
Exons	4244..4498, 4256..4498, 4508..4702		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1682	Strand	
Start	3902	End	4774
Name	OJ990203_01.9922.C2.o2.ts	Method	TBLASTX:Soybean
Start	4532	End	4774
GI	none	Score	216
Exons	4532..4774		

Seq. No.	826	Seq. ID	OJ990203_01.9922.C2
Gene No.	1683	Strand	
Start	4763	End	5180
Name	OJ990203_01.9922.C2.o2.tw	Method	TBLASTX:Wheat
Start	4763	End	5180
GI	none	Score	103
Exons	4763..4885, 4765..4908, 4882..5061, 4883..5122, 4895..5065, 5048..5179, 5087..5179, 5127..5180		

Seq. No.	827	Seq. ID	OJ990203_01.9922.C4
Gene No.	1684	Strand	+
Start	1	End	933
Name	OJ990203_01.9922.C4.o1.np	Method	AAT/NAP
Start	1	End	933
GI	5091513	Score	1149
Exons	1..933		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	827	Seq. ID	OJ990203_01.9922.C4
Gene No.	1684	Strand	+
Start	1	End	933
Name	OJ990203_01.9922.C4.o1.gs	Method	GENSCAN
Start	57	End	892
GI	none	Score	.85
Exons	57..892		

Seq. No.	828	Seq. ID	OJ990203_01.9922.C5
Gene No.	1685	Strand	+
Start	182	End	809
Name	OJ990203_01.9922.C5.o1.gs	Method	GENSCAN
Start	182	End	809
GI	none	Score	.63
Exons	182..232, 660..809		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1686	Strand	+

Start	1	End	9740
Name	OJ990203_01.9922.C6.o1.np	Method	AAT/NAP
Start	1	End	3676
GI	4680179	Score	1125
Exons	1..38, 1756..1965, 2533..3676		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1686	Strand	+
Start	1	End	9740
Name	OJ990203_01.9922.C6.o1.gs	Method	GENSCAN
Start	1030	End	9740
GI	none	Score	.53
Exons	1030..1060, 1774..1965, 2585..2622, 2714..2788, 2862..3040, 3755..4465, 5253..5398, 5704..5879, 5892..5939, 6598..6747, 7029..7211, 7386..8441, 9366..9740		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1686	Strand	+
Start	1	End	9740
Name	OJ990203_01.9922.C6.o2.np	Method	AAT/NAP
Start	3662	End	4466
GI	6539553	Score	1283
Exons	3662..4466		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1686	Strand	+
Start	1	End	9740
Name	OJ990203_01.9922.C6.o3.np	Method	AAT/NAP
Start	6724	End	9593
GI	4467097	Score	738
Exons	6724..7211, 7303..8450, 9474..9593		
GI Descrip.	(AL035538) heat shock protein 70 like protein [Arabidopsis thaliana]		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1687	Strand	+
Start	21407	End	21654
Name	OJ990203_01.9922.C6.o1.gp	Method	AAT/GAP
Start	21407	End	21654
GI	3761181	Score	438
Exons	21407..21654		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1688	Strand	+
Start	22108	End	24395
Name	OJ990203_01.9922.C6.o4.np	Method	AAT/NAP
Start	22108	End	24395
GI	5091513	Score	1745
Exons	22108..22521, 22566..23122, 23776..24395		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o2.ts	Method	TBLASTX:Soybean
Start	2822	End	3169
GI	none	Score	249
Exons	2822..3169, 2925..3143		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o4.tw	Method	TBLASTX:Wheat
Start	2888	End	3180
GI	none	Score	69
Exons	2888..2995, 2890..2991, 2891..3178, 2902..3006, 2925..3179, 3097..3180		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o4.tm	Method	TBLASTX:Maize
Start	2937	End	3251
GI	none	Score	225
Exons	2937..3251, 2972..3250		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o2.tw	Method	TBLASTX:Wheat
Start	3189	End	3609
GI	none	Score	319
Exons	3189..3485, 3194..3484, 3457..3609, 3459..3602, 3463..3609		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o1.tm	Method	TBLASTX:Maize
Start	3258	End	3609
GI	none	Score	235
Exons	3258..3461, 3260..3442, 3457..3609, 3459..3602		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o3.tm	Method	TBLASTX:Maize
Start	3675	End	3998
GI	none	Score	300
Exons	3675..3983, 3680..3997, 3684..3998		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o3.ts	Method	TBLASTX:Soybean
Start	3843	End	4220
GI	none	Score	114
Exons	3843..3974, 3843..3974, 3992..4123, 3993..4220		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o1.tw	Method	TBLASTX:Wheat
Start	3854	End	4330
GI	none	Score	101
Exons	3854..3925, 3855..3929, 3944..4330, 3945..4292, 3946..4329		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o1.ts	Method	TBLASTX:Soybean
Start	6722	End	7927
GI	none	Score	255
Exons	6722..6958, 6729..7115, 6983..7114, 7318..7374, 7365..7574, 7464..7790, 7535..7789, 7835..7927, 7836..7925		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o1.tc	Method	TBLASTX:Cress
Start	6729	End	8219
GI	none	Score	95
Exons	6729..6863, 6996..7136, 7548..7733, 7836..8219		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o2.tm	Method	TBLASTX:Maize
Start	6990	End	8147
GI	none	Score	37
Exons	6990..7025, 7032..7115, 7318..7374, 7359..7574, 7464..7829, 7535..7792, 7835..7927, 7836..7925, 7971..8147		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o2.gs	Method	GENSCAN
Start	11287	End	18962
GI	none	Score	.65
Exons	11287..11510, 12183..12486, 16256..16361, 18655..18962		

Seq. No.	829	Seq. ID	OJ990203_01.9922.C6
Gene No.	1689	Strand	-
Start	11287	End	18962
Name	OJ990203_01.9922.C6.o3.tw	Method	TBLASTX:Wheat
Start	11743	End	12144
GI	none	Score	55
Exons	11743..12144, 11794..11967		

Seq. No.	830	Seq. ID	OJ990203_01.9922.C7
Gene No.	1690	Strand	+
Start	3	End	1018
Name	OJ990203_01.9922.C7.o1.gs	Method	GENSCAN
Start	3	End	1018
GI	none	Score	.8

Exons	3..357, 615..1018		
Seq. No.	830	Seq. ID	OJ990203_01.9922.C7
Gene No.	1691	Strand	-
Start	1	End	511
Name	OJ990203_01.9922.C7.o1.np	Method	AAT/NAP
Start	1	End	511
GI	5091512	Score	634
Exons	1..511		
GI Descrip.	(AB023482) Similar to Plasmodium vivax circumsporozoite protein gene, complete cds.(M11926) [Oryza sativa]		
Seq. No.	830	Seq. ID	OJ990203_01.9922.C7
Gene No.	1692	Strand	-
Start	3114	End	3721
Name	OJ990203_01.9922.C7.o2.gp	Method	AAT/GAP
Start	3114	End	3721
GI	21474_1.R1084	Score	132
Exons	3114..3143, 3534..3630, 3700..3721		
GI Descrip.	'3894159 2.0e-10 (AC005312) hypothetical protein [Arabidopsis thaliana]'		
Seq. No.	830	Seq. ID	OJ990203_01.9922.C7
Gene No.	1692	Strand	-
Start	3114	End	3721
Name	OJ990203_01.9922.C7.o1.gp	Method	AAT/GAP
Start	3208	End	3455
GI	3761181	Score	441
Exons	3208..3455		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene		
Seq. No.	831	Seq. ID	OJ990203_01.9922.C8
Gene No.	1693	Strand	+
Start	3694	End	5643
Name	OJ990203_01.9922.C8.o1.np	Method	AAT/NAP
Start	3694	End	5643
GI	4680186	Score	251
Exons	3694..3713, 5438..5643		
GI Descrip.	(AF111709) unknown [Oryza sativa subsp. indica]		
Seq. No.	831	Seq. ID	OJ990203_01.9922.C8
Gene No.	1694	Strand	+
Start	6995	End	9618
Name	OJ990203_01.9922.C8.o2.np	Method	AAT/NAP
Start	6995	End	9618
GI	4539658	Score	106
Exons	6995..7156, 9573..9618		
GI Descrip.	(AF061282) serine carboxypeptidase-like protein [Sorghum bicolor]		
Seq. No.	831	Seq. ID	OJ990203_01.9922.C8
Gene No.	1695	Strand	-
Start	2555	End	10915
Name	OJ990203_01.9922.C8.o1.gs	Method	GENSCAN
Start	2555	End	10625
GI	none	Score	.49

Exons	2555..3931, 5403..5498, 6938..7085, 7686..7867, 7947..8045, 8140..8212, 8297..8407, 8504..8677, 8787..9618, 9744..9885, 9960..10079, 10125..10625		
Seq. No.	831	Seq. ID	OJ990203_01.9922.C8
Gene No.	1695	Strand	-
Start	2555	End	10915
Name	OJ990203_01.9922.C8.o1.gp	Method	AAT/GAP
Start	5189	End	5571
GI	uC-osflcyp033a04b1	Score	668
Exons	5189..5571		
GI Descrip.	'6016845/dbj|AP000570.1|AP000570 3.0e-59 Oryza sativa genomic DNA, chromosome 1, clone:P0711E10'		

Seq. No.	831	Seq. ID	OJ990203_01.9922.C8
Gene No.	1695	Strand	-
Start	2555	End	10915
Name	OJ990203_01.9922.C8.o3.np	Method	AAT/NAP
Start	7700	End	10915
GI	4680204	Score	887
Exons	7700..7837, 8188..8407, 8504..8677, 8787..9885, 9960..10915		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	831	Seq. ID	OJ990203_01.9922.C8
Gene No.	1695	Strand	-
Start	2555	End	10915
Name	OJ990203_01.9922.C8.o2.tw	Method	TBLASTX:Wheat
Start	8338	End	8860
GI	none	Score	68
Exons	8338..8409, 8509..8691, 8516..8641, 8780..8860		

Seq. No.	831	Seq. ID	OJ990203_01.9922.C8
Gene No.	1695	Strand	-
Start	2555	End	10915
Name	OJ990203_01.9922.C8.o1.tw	Method	TBLASTX:Wheat
Start	10350	End	10753
GI	none	Score	84
Exons	10350..10520, 10483..10650, 10515..10751, 10602..10751, 10613..10753, 10643..10753		

Seq. No.	832	Seq. ID	OJ990203_01.9922.C10
Gene No.	1696	Strand	+
Start	1	End	1051
Name	OJ990203_01.9922.C10.o1.np	Method	AAT/NAP
Start	1	End	1048
GI	5103193	Score	1830
Exons	1..1048		
GI Descrip.	(AP000342) transposase of Tn10 [Plasmid R100] gi|5738084|gb|AAD50242.1|AF162223_1 (AF162223) IS10-left transposase [Shigella flexneri]		

Seq. No.	832	Seq. ID	OJ990203_01.9922.C10
Gene No.	1696	Strand	+
Start	1	End	1051
Name	OJ990203_01.9922.C10.o1.gs	Method	GENSCAN
Start	113	End	1051
GI	none	Score	.78

Exons	113..1051		
Seq. No.	833	Seq. ID	OJ990203_01.9922.C12
Gene No.	1697	Strand	-
Start	319	End	412
Name	OJ990203_01.9922.C12.o1.gs	Method	GENSCAN
Start	319	End	412
GI	none	Score	.86
Exons	319..412		
Seq. No.	834	Seq. ID	OJ990203_01.9922.C13
Gene No.	1698	Strand	-
Start	1	End	124
Name	OJ990203_01.9922.C13.o1.gp	Method	AAT/GAP
Start	1	End	124
GI	LIB3477-003-P1-K1-E9	Score	188
Exons	1..124		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		
Seq. No.	835	Seq. ID	OJ990203_01.9922.C15
Gene No.	1699	Strand	-
Start	762	End	1412
Name	OJ990203_01.9922.C15.o1.np	Method	AAT/NAP
Start	762	End	1270
GI	3810596	Score	102
Exons	762..1270		
GI Descrip.	(AC005398) putative retroelement pol polyprotein [Arabidopsis thaliana]		
Seq. No.	835	Seq. ID	OJ990203_01.9922.C15
Gene No.	1699	Strand	-
Start	762	End	1412
Name	OJ990203_01.9922.C15.o1.gs	Method	GENSCAN
Start	797	End	1412
GI	none	Score	.46
Exons	797..986, 1071..1412		
Seq. No.	836	Seq. ID	OJ990203_01.9922.C16
Gene No.	1700	Strand	-
Start	10	End	652
Name	OJ990203_01.9922.C16.o1.gs	Method	GENSCAN
Start	10	End	652
GI	none	Score	.72
Exons	10..195, 287..652		
Seq. No.	837	Seq. ID	OJ990203_01.9922.C17
Gene No.	1701	Strand	+
Start	2042	End	2652
Name	OJ990203_01.9922.C17.o2.gs	Method	GENSCAN
Start	2042	End	2652
GI	none	Score	.87
Exons	2042..2190, 2432..2621, 2626..2652		
Seq. No.	837	Seq. ID	OJ990203_01.9922.C17
Gene No.	1702	Strand	-

Start	1	End	2198
Name	OJ990203_01.9922.C17.o1.np	Method	AAT/NAP
Start	1	End	2198
GI	5922634	Score	82
Exons	1..42, 1451..1525, 2097..2198		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6016867|dbj|BAA85210.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	837	Seq. ID	OJ990203_01.9922.C17
Gene No.	1702	Strand	-
Start	1	End	2198
Name	OJ990203_01.9922.C17.o1.gs	Method	GENSCAN
Start	608	End	1894
GI	none	Score	.79
Exons	608..1894		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1703	Strand	+
Start	327	End	527
Name	OJ990203_01.9922.C18.o1.gs	Method	GENSCAN
Start	327	End	527
GI	none	Score	.95
Exons	327..527		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1704	Strand	+
Start	8033	End	19140
Name	OJ990203_01.9922.C18.o1.np	Method	AAT/NAP
Start	7901	End	18827
GI	2853076	Score	1394
Exons	7901..8035, 8124..8803, 10383..10445, 11044..11123, 11476..11624, 12399..12475, 12888..13071, 13143..13231, 14043..14273, 14953..15150, 15252..15335, 16057..16440, 16573..16758, 18699..18827		
GI Descrip.	(AL021768) putative protein [Arabidopsis thaliana]		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1704	Strand	+
Start	8033	End	19140
Name	OJ990203_01.9922.C18.o4.gs	Method	GENSCAN
Start	8033	End	18785
GI	none	Score	.95
Exons	8033..8803, 10353..10445, 11044..11123, 11506..11623, 12401..12475, 12888..13044, 13143..13231, 14043..14296, 14979..15150, 15252..15335, 16057..16373, 16605..16758, 18238..18319, 18425..18504, 18624..18785		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1704	Strand	+
Start	8033	End	19140
Name	OJ990203_01.9922.C18.o1.gp	Method	AAT/GAP
Start	8481	End	11569
GI	uC-osroM202040f02b1	Score	996
Exons	8481..8803, 10383..10445, 11044..11123, 11506..11569		
GI Descrip.	'2853076/emb|CAA16926.1| 5.0e-39 (AL021768) putative protein [Arabidopsis thaliana]'		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1704	Strand	+
Start	8033	End	19140
Name	OJ990203_01.9922.C18.o3.gp	Method	AAT/GAP
Start	18454	End	19140
GI	none	Score	483
Exons	18454..18504, 18624..18785, 19073..19140		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1705	Strand	-
Start	6065	End	6959
Name	OJ990203_01.9922.C18.o3.gs	Method	GENSCAN
Start	6065	End	6959
GI	none	Score	.78
Exons	6065..6232, 6437..6553, 6681..6959		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1706	Strand	
Start	8408	End	8719
Name	OJ990203_01.9922.C18.o1.tc	Method	TBLASTX:Cress
Start	8408	End	8719
GI	none	Score	116
Exons	8408..8485, 8498..8719		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1707	Strand	
Start	14979	End	15297
Name	OJ990203_01.9922.C18.o2.tm	Method	TBLASTX:Maize
Start	14979	End	15297
GI	none	Score	272
Exons	14979..15149, 14980..15153, 14982..15155, 15200..15295, 15250..15297, 15250..15297		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1708	Strand	
Start	16173	End	19162
Name	OJ990203_01.9922.C18.o1.tm	Method	TBLASTX:Maize
Start	16173	End	19162
GI	none	Score	81
Exons	16173..16280, 16174..16281, 16175..16279, 16252..16443, 16259..16372, 16499..16543, 16604..16759, 16604..16759, 16605..16760, 16605..16760, 16606..16761, 18214..18318, 18235..18318, 18236..18322, 18237..18341, 18417..18506, 18424..18504, 18621..18845, 18623..18787, 19058..19135, 19071..19151, 19072..19161, 19082..19162		

Seq. No.	838	Seq. ID	OJ990203_01.9922.C18
Gene No.	1708	Strand	
Start	16173	End	19162
Name	OJ990203_01.9922.C18.o2.tc	Method	TBLASTX:Cress
Start	18424	End	19123
GI	none	Score	83
Exons	18424..18504, 18621..18785, 18621..18767, 18629..18769, 19064..19123		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19

Gene No.	1709	Strand	+
Start	396	End	9629
Name	OJ990203_01.9922.C19.o1.gs	Method	GENSCAN
Start	396	End	6565
GI	none	Score	.72
Exons	396..410, 1026..1106, 1393..1483, 3412..3645, 4416..4515, 4896..4935, 6018..6239, 6380..6565		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1709	Strand	+
Start	396	End	9629
Name	OJ990203_01.9922.C19.o3.np	Method	AAT/NAP
Start	5579	End	9629
GI	4680183	Score	136
Exons	5579..5606, 9510..9629		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1709	Strand	+
Start	396	End	9629
Name	OJ990203_01.9922.C19.o1.gp	Method	AAT/GAP
Start	6434	End	6622
GI	2796895	Score	341
Exons	6434..6622		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1710	Strand	-
Start	7445	End	9507
Name	OJ990203_01.9922.C19.o2.np	Method	AAT/NAP
Start	7445	End	9507
GI	6721561	Score	84
Exons	7445..7511, 9421..9507		
GI Descrip.	(AP001073) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6815086|dbj|BAA90372.1| (AP001081) EST AU082058(C12976) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1710	Strand	-
Start	7445	End	9507
Name	OJ990203_01.9922.C19.o1.np	Method	AAT/NAP
Start	7664	End	7919
GI	6850344	Score	165
Exons	7664..7919		
GI Descrip.	(AC022354) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1711	Strand	-
Start	10387	End	11866
Name	OJ990203_01.9922.C19.o1.tm	Method	TBLASTX:Maize
Start	1017	End	2172
GI	none	Score	95
Exons	1017..1100, 1020..1106, 1022..1102, 1024..1107, 1229..1417, 1230..1424, 1242..1427, 1423..1476, 1437..1475, 2061..2117, 2062..2100, 2079..2171, 2098..2172, 2110..2172		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1711	Strand	-
Start	10387	End	11866
Name	OJ990203_01.9922.C19.o2.tm	Method	TBLASTX:Maize
Start	7650	End	7907
GI	none	Score	117
Exons	7650..7700, 7705..7896, 7716..7907		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1711	Strand	-
Start	10387	End	11866
Name	OJ990203_01.9922.C19.o2.gs	Method	GENSCAN
Start	10387	End	11698
GI	none	Score	.87
Exons	10387..10599, 10738..10831, 10925..11107, 11622..11698		

Seq. No.	839	Seq. ID	OJ990203_01.9922.C19
Gene No.	1711	Strand	-
Start	10387	End	11866
Name	OJ990203_01.9922.C19.o4.np	Method	AAT/NAP
Start	11009	End	11866
GI	1184100	Score	138
Exons	11009..11166, 11323..11866		
GI Descrip.	(U45958) pistil extensin-like protein [Nicotiana alata]		

Seq. No.	840	Seq. ID	OJ990203_01.9922.C20
Gene No.	1712	Strand	+
Start	1902	End	2978
Name	OJ990203_01.9922.C20.o2.gs	Method	GENSCAN
Start	1902	End	2978
GI	none	Score	.83
Exons	1902..2067, 2196..2446, 2556..2738, 2811..2978		

Seq. No.	840	Seq. ID	OJ990203_01.9922.C20
Gene No.	1713	Strand	+
Start	3269	End	3534
Name	OJ990203_01.9922.C20.o1.gp	Method	AAT/GAP
Start	3269	End	3534
GI	4968598	Score	484
Exons	3269..3534		

Seq. No.	840	Seq. ID	OJ990203_01.9922.C20
Gene No.	1714	Strand	-
Start	159	End	2460
Name	OJ990203_01.9922.C20.o1.gs	Method	GENSCAN
Start	159	End	1105
GI	none	Score	.65
Exons	159..542, 550..613, 666..1105		

Seq. No.	840	Seq. ID	OJ990203_01.9922.C20
Gene No.	1714	Strand	-
Start	159	End	2460
Name	OJ990203_01.9922.C20.o1.np	Method	AAT/NAP
Start	206	End	2460
GI	6721562	Score	395
Exons	206..938, 2335..2460		

GI Descrip. (AP001073) Similar to Zea mays 22-kDa alpha zein gene cluster; hypothetical protein. (AF031569) [Oryza sativa] gi|6815087|dbj|BAA90373.1| (AP001081) Similar to Zea mays 22-kDa alpha zein gene cluster; hypothetical protein. (AF031569) [Oryza sativa]

Seq. No.	840	Seq. ID	OJ990203_01.9922.C20
Gene No.	1714	Strand	-
Start	159	End	2460
Name	OJ990203_01.9922.C20.o1.tw	Method	TBLASTX:Wheat
Start	408	End	800
GI	none	Score	100
Exons	408..683, 523..669, 642..755, 652..753, 756..800		

Seq. No.	840	Seq. ID	OJ990203_01.9922.C20
Gene No.	1714	Strand	-
Start	159	End	2460
Name	OJ990203_01.9922.C20.o1.tm	Method	TBLASTX:Maize
Start	522	End	782
GI	none	Score	189
Exons	522..782		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o1.np	Method	AAT/NAP
Start	1	End	2333
GI	4416302	Score	692
Exons	1..1003, 2311..2333		

GI Descrip. (AF105716) copia-type pol polyprotein [Zea mays]

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o1.gs	Method	GENSCAN
Start	8	End	5402
GI	none	Score	.42
Exons	8..923, 1045..1734, 1850..2325, 2902..4814, 4982..5402		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o1.tm	Method	TBLASTX:Maize
Start	107	End	742
GI	none	Score	283
Exons	107..259, 254..598, 255..614, 675..740, 677..742		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o1.ts	Method	TBLASTX:Soybean
Start	107	End	568
GI	none	Score	157
Exons	107..235, 257..568, 264..551		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-

Start	1	End	5402
Name	OJ990203_01.9922.C21.o1.tc	Method	TBLASTX:Cress
Start	108	End	551
GI	none	Score	71
Exons	108..245, 113..244, 260..550, 465..551		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o2.tw	Method	TBLASTX:Wheat
Start	410	End	967
GI	none	Score	137
Exons	410..598, 411..584, 656..697, 737..967, 835..948		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o2.tm	Method	TBLASTX:Maize
Start	1019	End	1268
GI	none	Score	81
Exons	1019..1135, 1026..1259, 1026..1268, 1030..1263		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o1.tw	Method	TBLASTX:Wheat
Start	1023	End	1322
GI	none	Score	149
Exons	1023..1262, 1026..1271, 1030..1263, 1040..1273, 1266..1322, 1276..1317		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o2.np	Method	AAT/NAP
Start	1074	End	4755
GI	4544372	Score	310
Exons	1074..1549, 4705..4755		
GI Descrip.	(AC006920) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o2.ts	Method	TBLASTX:Soybean
Start	1119	End	1484
GI	none	Score	134
Exons	1119..1253, 1260..1484		

Seq. No.	841	Seq. ID	OJ990203_01.9922.C21
Gene No.	1715	Strand	-
Start	1	End	5402
Name	OJ990203_01.9922.C21.o3.ts	Method	TBLASTX:Soybean
Start	1894	End	2232
GI	none	Score	197
Exons	1894..2232		

Seq. No.	842	Seq. ID	OJ990203_01.9922.C24
Gene No.	1716	Strand	+
Start	38	End	197
Name	OJ990203_01.9922.C24.o1.gs	Method	GENSCAN
Start	38	End	197
GI	none	Score	.84
Exons	38..197		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1717	Strand	+
Start	897	End	1314
Name	OJ990203_01.9922.C26.o4.gp	Method	AAT/GAP
Start	897	End	1314
GI	LIB3431-028-P1-N1-A10	Score	836
Exons	897..1314		
GI Descrip.	'4680203/gb|AAD27566.1|AF114171_7 3.0e-33 (AF114171) TNP2-like protein [Sorghum bicolor]'		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1718	Strand	-
Start	37	End	2133
Name	OJ990203_01.9922.C26.o1.gp	Method	AAT/GAP
Start	37	End	2133
GI	342_1.R1084	Score	3262
Exons	37..543, 653..750, 833..852, 888..2133		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1718	Strand	-
Start	37	End	2133
Name	OJ990203_01.9922.C26.o5.gp	Method	AAT/GAP
Start	173	End	2133
GI	342_1.R1084	Score	3025
Exons	173..543, 653..750, 833..852, 888..2133		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1718	Strand	-
Start	37	End	2133
Name	OJ990203_01.9922.C26.o1.np	Method	AAT/NAP
Start	954	End	2133
GI	4680203	Score	973
Exons	954..1936, 2100..2133		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1718	Strand	-
Start	37	End	2133
Name	OJ990203_01.9922.C26.o1.gs	Method	GENSCAN
Start	960	End	1991
GI	none	Score	.53
Exons	960..1991		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1718	Strand	-

Start	37	End	2133
Name	OJ990203_01.9922.C26.o1.tw	Method	TBLASTX:Wheat
Start	1008	End	2131
GI	none	Score	52
Exons	1008..1100, 1009..1074, 1089..1169, 1174..1254, 1182..1322, 1183..1323, 1270..1365, 1302..1361, 1368..1412, 1373..1408, 1407..2126, 1422..1739, 1696..2118, 1880..2131		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1718	Strand	-
Start	37	End	2133
Name	OJ990203_01.9922.C26.o1.tc	Method	TBLASTX:Cress
Start	1590	End	2041
GI	none	Score	88
Exons	1590..1739, 1590..2033, 1696..2037, 1882..2037, 1886..2041		

Seq. No.	843	Seq. ID	OJ990203_01.9922.C26
Gene No.	1718	Strand	-
Start	37	End	2133
Name	OJ990203_01.9922.C26.o2.np	Method	AAT/NAP
Start	1974	End	2133
GI	4558686	Score	124
Exons	1974..2133		
GI Descrip.	(AC006586) putative TNP2-like transposon protein [Arabidopsis thaliana]		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1719	Strand	-
Start	1	End	2489
Name	OJ990703_46.9A03.C1.o1.np	Method	AAT/NAP
Start	1	End	2489
GI	4680204	Score	831
Exons	1..997, 1089..2489		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1719	Strand	-
Start	1	End	2489
Name	OJ990703_46.9A03.C1.o2.np	Method	AAT/NAP
Start	147	End	2489
GI	4680204	Score	827
Exons	147..331, 502..997, 1089..2489		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1720	Strand	-
Start	5568	End	7085
Name	OJ990703_46.9A03.C1.o3.tw	Method	TBLASTX:Wheat
Start	1479	End	1880
GI	none	Score	66
Exons	1479..1649, 1480..1554, 1639..1824, 1644..1880, 1686..1880		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1720	Strand	-
Start	5568	End	7085
Name	OJ990703_46.9A03.C1.o1.tw	Method	TBLASTX:Wheat
Start	5084	End	6401

GI	none	Score	52
Exons	5084..5176, 5085..5150, 5165..5233, 5181..5240, 5193..5246, 5241..5399, 5250..5330, 5276..5398, 5346..5441, 5378..5437, 5443..5490, 5444..5488, 5483..6400, 5499..6401		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1720	Strand	-
Start	5568	End	7085
Name	OJ990703_46.9A03.C1.o3.np	Method	AAT/NAP
Start	5568	End	7085
GI	6742729	Score	2206
Exons	5568..7085		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1720	Strand	-
Start	5568	End	7085
Name	OJ990703_46.9A03.C1.o1.tc	Method	TBLASTX:Cress
Start	5666	End	6113
GI	none	Score	95
Exons	5666..5815, 5666..6109, 5670..6113, 5778..6113		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1720	Strand	-
Start	5568	End	7085
Name	OJ990703_46.9A03.C1.o1.tm	Method	TBLASTX:Maize
Start	6044	End	6358
GI	none	Score	133
Exons	6044..6283, 6072..6347, 6326..6358		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1720	Strand	-
Start	5568	End	7085
Name	OJ990703_46.9A03.C1.o2.tw	Method	TBLASTX:Wheat
Start	6402	End	6811
GI	none	Score	59
Exons	6402..6488, 6404..6487, 6497..6736, 6561..6737, 6749..6811		

Seq. No.	844	Seq. ID	OJ990703_46.9A03.C1
Gene No.	1720	Strand	-
Start	5568	End	7085
Name	OJ990703_46.9A03.C1.o1.ts	Method	TBLASTX:Soybean
Start	6864	End	7082
GI	none	Score	189
Exons	6864..7082		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1721	Strand	+
Start	60	End	181
Name	OJ990703_46.9A03.C2.o1.gs	Method	GENSCAN
Start	60	End	181
GI	none	Score	.77
Exons	60..181		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1722	Strand	+
Start	2216	End	2560

Name	OJ990703_46.9A03.C2.o3.gs	Method	GENSCAN
Start	2216	End	2560
GI	none	Score	.79
Exons	2216..2560		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1723	Strand	+
Start	9669	End	10004
Name	OJ990703_46.9A03.C2.o5.gs	Method	GENSCAN
Start	9669	End	10004
GI	none	Score	.81
Exons	9669..10004		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1724	Strand	+
Start	15277	End	17460
Name	OJ990703_46.9A03.C2.o7.gs	Method	GENSCAN
Start	15277	End	17460
GI	none	Score	.9
Exons	15277..17460		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1725	Strand	+
Start	18265	End	20345
Name	OJ990703_46.9A03.C2.o4.np	Method	AAT/NAP
Start	18265	End	20345
GI	6815052	Score	195
Exons	18265..18294, 19274..19426, 19495..19582, 20250..20345		
GI Descrip.	(AP001080) hypothetical protein [Oryza sativa]		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1726	Strand	+
Start	21799	End	22410
Name	OJ990703_46.9A03.C2.o5.np	Method	AAT/NAP
Start	21799	End	22410
GI	1076211	Score	195
Exons	21799..22410		
GI Descrip.	hypothetical protein VSP-3 - Chlamydomonas reinhardtii gi|530876 (L29029) amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265 [Chlamydomonas reinhardtii]		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o1.np	Method	AAT/NAP
Start	1	End	797
GI	4680203	Score	814
Exons	1..797		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o2.np	Method	AAT/NAP
Start	1	End	11906
GI	6069667	Score	865

Exons	1..62, 3114..3319, 3351..3370, 3430..3484, 9638..9763, 10693..10801, 11156..11263, 11759..11906		
GI Descrip.	(AP000616) similar to UMP/CMP kinase (AF000147) [Oryza sativa]		
Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o1.ts	Method	TBLASTX:Soybean
Start	33	End	323
GI	none	Score	100
Exons	33..98, 105..323, 109..315		
Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o1.tw	Method	TBLASTX:Wheat
Start	90	End	491
GI	none	Score	158
Exons	90..347, 95..337, 103..345, 105..356, 106..348, 339..491, 356..472		
Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o2.gs	Method	GENSCAN
Start	396	End	797
GI	none	Score	.81
Exons	396..797		
Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o1.gp	Method	AAT/GAP
Start	659	End	1278
GI	2310235	Score	289
Exons	659..797, 1241..1278		
GI Descrip.	5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]		
Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o2.tw	Method	TBLASTX:Wheat
Start	5470	End	5769
GI	none	Score	183
Exons	5470..5769, 5472..5687		
Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1727	Strand	-
Start	1	End	14650
Name	OJ990703_46.9A03.C2.o6.gs	Method	GENSCAN
Start	11365	End	14650
GI	none	Score	.7
Exons	11365..11468, 11759..11914, 12001..12038, 13013..13107, 13571..13665, 14044..14345, 14475..14650		
Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2

Gene No.	1728	Strand	
Start	15310	End	15611
Name	OJ990703_46.9A03.C2.o1.tc	Method	TBLASTX:Cress
Start	15310	End	15611
GI	none	Score	116
Exons	15310..15453, 15523..15609, 15525..15611		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1729	Strand	
Start	15525	End	15792
Name	OJ990703_46.9A03.C2.o1.tm	Method	TBLASTX:Maize
Start	15525	End	15792
GI	none	Score	157
Exons	15525..15620, 15526..15621, 15697..15792, 15717..15791		

Seq. No.	845	Seq. ID	OJ990703_46.9A03.C2
Gene No.	1730	Strand	
Start	17247	End	17445
Name	OJ990703_46.9A03.C2.o2.ts	Method	TBLASTX:Soybean
Start	17247	End	17445
GI	none	Score	197
Exons	17247..17441, 17257..17445		

Seq. No.	846	Seq. ID	OJ990703_46.9A03.C3
Gene No.	1731	Strand	+
Start	109	End	421
Name	OJ990703_46.9A03.C3.o1.gs	Method	GENSCAN
Start	109	End	421
GI	none	Score	.45
Exons	109..421		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1732	Strand	+
Start	1	End	7834
Name	OJ990703_46.9A03.C5.o1.np	Method	AAT/NAP
Start	1	End	2289
GI	4680203	Score	925
Exons	1..493, 558..683, 840..1046, 1323..2289		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1732	Strand	+
Start	1	End	7834
Name	OJ990703_46.9A03.C5.o1.gs	Method	GENSCAN
Start	273	End	7834
GI	none	Score	.72
Exons	273..469, 486..1732, 1766..1876, 2171..2266, 2929..3529, 4335..4586, 4645..4770, 5163..5538, 5755..5928, 6122..6435, 6450..6784, 6868..7119, 7200..7310, 7398..7458, 7608..7700, 7778..7834		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1733	Strand	+
Start	13318	End	14970
Name	OJ990703_46.9A03.C5.o3.np	Method	AAT/NAP
Start	13318	End	14970
GI	3461840	Score	467

Exons	13318..14001, 14338..14970		
GI Descrip.	(AC005315) putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o3.tw	Method	TBLASTX:Wheat
Start	1	End	166
GI	none	Score	194
Exons	1..165, 2..166		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o1.tw	Method	TBLASTX:Wheat
Start	930	End	2132
GI	none	Score	556
Exons	930..1685, 1175..1459, 1664..1837, 1698..1853, 1841..1945, 1842..1946, 1959..2063, 1964..2062, 2070..2132		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o2.tm	Method	TBLASTX:Maize
Start	974	End	1289
GI	none	Score	398
Exons	974..1285, 975..1289		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o2.tc	Method	TBLASTX:Cress
Start	1220	End	1643
GI	none	Score	325
Exons	1220..1459, 1221..1643		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o3.tm	Method	TBLASTX:Maize
Start	1539	End	1834
GI	none	Score	159
Exons	1539..1709, 1713..1832, 1731..1820, 1742..1834		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o4.tm	Method	TBLASTX:Maize
Start	8484	End	10103
GI	none	Score	90
Exons	8484..8771, 8632..8766, 9829..9954, 9972..10103, 9974..10000, 10017..10103		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518

Name	OJ990703_46.9A03.C5.o2.ts	Method	TBLASTX:Soybean
Start	8523	End	10103
GI	none	Score	67
Exons	8523..8771, 9829..9954, 9972..10103, 10017..10103		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o3.tc	Method	TBLASTX:Cress
Start	8523	End	10103
GI	none	Score	90
Exons	8523..8771, 9829..9954, 10017..10103		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o2.np	Method	AAT/NAP
Start	10557	End	12102
GI	6716785	Score	388
Exons	10557..10587, 11734..11860, 11942..12102		
GI Descrip.	(AF220539) 40s ribosomal protein S23 [Euphorbia esula]		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o3.gs	Method	GENSCAN
Start	10755	End	12518
GI	none	Score	.6
Exons	10755..11159, 11734..11860, 11942..12096, 12300..12518		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o1.tc	Method	TBLASTX:Cress
Start	11723	End	12096
GI	none	Score	169
Exons	11723..11863, 11734..11859, 11736..11861, 11941..12096, 11942..12094		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o1.ts	Method	TBLASTX:Soybean
Start	11723	End	12097
GI	none	Score	166
Exons	11723..11863, 11733..11858, 11734..11871, 11734..11859, 11941..12096, 11942..12097, 11942..12097		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o1.tm	Method	TBLASTX:Maize
Start	11726	End	12097
GI	none	Score	200
Exons	11726..11863, 11734..11859, 11792..11860, 11941..12093, 11941..12096, 11942..12097, 11942..12097		

Seq. No.	847	Seq. ID	OJ990703_46.9A03.C5
Gene No.	1734	Strand	-
Start	10755	End	12518
Name	OJ990703_46.9A03.C5.o2.tw	Method	TBLASTX:Wheat
Start	11732	End	12096
GI	none	Score	188
Exons	11732..11863, 11734..11871, 11734..11859, 11941..12096, 11942..12094		

Seq. No.	848	Seq. ID	OJ990703_46.9A03.C6
Gene No.	1735	Strand	+
Start	473	End	1103
Name	OJ990703_46.9A03.C6.o1.np	Method	AAT/NAP
Start	473	End	1103
GI	2498930	Score	736
Exons	473..536, 703..1103		
GI Descrip.	DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]		

Seq. No.	848	Seq. ID	OJ990703_46.9A03.C6
Gene No.	1735	Strand	+
Start	473	End	1103
Name	OJ990703_46.9A03.C6.o1.gs	Method	GENSCAN
Start	477	End	1097
GI	none	Score	1
Exons	477..536, 703..1097		

Seq. No.	849	Seq. ID	OJ990703_46.9A03.C8
Gene No.	1736	Strand	-
Start	11	End	760
Name	OJ990703_46.9A03.C8.o1.np	Method	AAT/NAP
Start	11	End	760
GI	5902447	Score	488
Exons	11..760		
GI Descrip.	(AB030283) orf4 [Oryza sativa]		

Seq. No.	850	Seq. ID	OJ990703_46.9A03.C9
Gene No.	1737	Strand	+
Start	1	End	310
Name	OJ990703_46.9A03.C9.o1.np	Method	AAT/NAP
Start	1	End	293
GI	1084462	Score	341
Exons	1..293		
GI Descrip.	RCg2 protein - rice gi|786130 (L27209) RCc2 [Oryza sativa] gi|786134 (L27210) root-specific protein [Oryza sativa]		

Seq. No.	850	Seq. ID	OJ990703_46.9A03.C9
Gene No.	1737	Strand	+
Start	1	End	310
Name	OJ990703_46.9A03.C9.o1.tm	Method	TBLASTX:Maize
Start	6	End	293
GI	none	Score	111
Exons	6..92, 7..93, 96..149, 128..292, 129..293		

Seq. No.	850	Seq. ID	OJ990703_46.9A03.C9
Gene No.	1737	Strand	+
Start	1	End	310

Name	OJ990703_46.9A03.C9.o1.ts	Method	TBLASTX:Soybean
Start	7	End	293
GI	none	Score	68
Exons	7..93, 42..95, 134..286, 135..293		

Seq. No.	850	Seq. ID	OJ990703_46.9A03.C9
Gene No.	1737	Strand	+
Start	1	End	310
Name	OJ990703_46.9A03.C9.o1.tc	Method	TBLASTX:Cress
Start	22	End	310
GI	none	Score	74
Exons	22..132, 128..310, 129..296		

Seq. No.	850	Seq. ID	OJ990703_46.9A03.C9
Gene No.	1737	Strand	+
Start	1	End	310
Name	OJ990703_46.9A03.C9.o1.tw	Method	TBLASTX:Wheat
Start	52	End	293
GI	none	Score	56
Exons	52..93, 135..293, 137..286		

Seq. No.	850	Seq. ID	OJ990703_46.9A03.C9
Gene No.	1737	Strand	+
Start	1	End	310
Name	OJ990703_46.9A03.C9.o1.gs	Method	GENSCAN
Start	70	End	296
GI	none	Score	.72
Exons	70..296		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1738	Strand	+
Start	370	End	427
Name	OJ990703_46.9A03.C10.o1.gs	Method	GENSCAN
Start	370	End	427
GI	none	Score	.65
Exons	370..427		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1739	Strand	+
Start	2349	End	2759
Name	OJ990703_46.9A03.C10.o1.np	Method	AAT/NAP
Start	2349	End	2759
GI	1084462	Score	474
Exons	2349..2759		
GI Descrip.	RCg2 protein - rice gi|786130 (L27209) RCc2 [Oryza sativa] gi|786134 (L27210) root-specific protein [Oryza sativa]		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1740	Strand	+
Start	5490	End	5903
Name	OJ990703_46.9A03.C10.o2.np	Method	AAT/NAP
Start	5490	End	5900
GI	1084462	Score	468
Exons	5490..5900		
GI Descrip.	RCg2 protein - rice gi|786130 (L27209) RCc2 [Oryza sativa] gi|786134 (L27210) root-specific protein [Oryza sativa]		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1740	Strand	+
Start	5490	End	5903
Name	OJ990703_46.9A03.C10.o3.gs	Method	GENSCAN
Start	5490	End	5903
GI	none	Score	.71
Exons	5490..5903		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1741	Strand	+
Start	8545	End	9985
Name	OJ990703_46.9A03.C10.o3.np	Method	AAT/NAP
Start	8545	End	9985
GI	3551960	Score	111
Exons	8545..9012, 9961..9985		
GI Descrip.	(AF082033) senescence-associated protein 15 [Hemerocallis hybrid cultivar]		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1742	Strand	-
Start	2325	End	4401
Name	OJ990703_46.9A03.C10.o2.gs	Method	GENSCAN
Start	2325	End	4401
GI	none	Score	.51
Exons	2325..2711, 4000..4401		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1743	Strand	-
Start	7439	End	8998
Name	OJ990703_46.9A03.C10.o1.tc	Method	TBLASTX:Cress
Start	2348	End	5903
GI	none	Score	47
Exons	2348..2407, 2349..2408, 2511..2615, 2514..2573, 2595..2762, 2618..2752, 5652..5756, 5736..5903, 5759..5893		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1743	Strand	-
Start	7439	End	8998
Name	OJ990703_46.9A03.C10.o1.tm	Method	TBLASTX:Maize
Start	2490	End	5900
GI	none	Score	94
Exons	2490..2558, 2490..2558, 2594..2758, 2595..2759, 2601..2759, 2602..2760, 5630..5698, 5631..5699, 5735..5899, 5736..5900, 5742..5900		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1743	Strand	-
Start	7439	End	8998
Name	OJ990703_46.9A03.C10.o1.ts	Method	TBLASTX:Soybean
Start	2514	End	5900
GI	none	Score	84
Exons	2514..2606, 2601..2759, 2603..2752, 2628..2774, 5654..5725, 5655..5747, 5742..5900, 5744..5893, 5760..5900		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1743	Strand	-
Start	7439	End	8998

Name	OJ990703_46.9A03.C10.o1.tw	Method	TBLASTX:Wheat
Start	2517	End	5900
GI	none	Score	58
Exons	2517..2567, 2517..2567, 2601..2759, 2603..2752, 5658..5699, 5742..5900, 5744..5893		

Seq. No.	851	Seq. ID	OJ990703_46.9A03.C10
Gene No.	1743	Strand	-
Start	7439	End	8998
Name	OJ990703_46.9A03.C10.o4.gs	Method	GENSCAN
Start	7439	End	8998
GI	none	Score	.95
Exons	7439..7825, 8391..8531, 8578..8707, 8874..8998		

Seq. No.	852	Seq. ID	OJ990703_46.9A03.C11
Gene No.	1744	Strand	-
Start	726	End	863
Name	OJ990703_46.9A03.C11.o1.gs	Method	GENSCAN
Start	726	End	863
GI	none	Score	.68
Exons	726..863		

Seq. No.	853	Seq. ID	OJ990703_46.9A03.C12
Gene No.	1745	Strand	-
Start	1	End	1393
Name	OJ990703_46.9A03.C12.o1.np	Method	AAT/NAP
Start	1	End	1393
GI	6705984	Score	2140
Exons	1..1393		
GI Descrip.	(AB033235) gag-pol polyprotein [Oryza sativa]		

Seq. No.	853	Seq. ID	OJ990703_46.9A03.C12
Gene No.	1745	Strand	-
Start	1	End	1393
Name	OJ990703_46.9A03.C12.o1.gs	Method	GENSCAN
Start	66	End	1282
GI	none	Score	.55
Exons	66..529, 685..1282		

Seq. No.	853	Seq. ID	OJ990703_46.9A03.C12
Gene No.	1745	Strand	-
Start	1	End	1393
Name	OJ990703_46.9A03.C12.o1.tw	Method	TBLASTX:Wheat
Start	510	End	1084
GI	none	Score	45
Exons	510..584, 513..596, 536..865, 557..856, 585..869, 878..1084, 896..1042, 903..1058		

Seq. No.	853	Seq. ID	OJ990703_46.9A03.C12
Gene No.	1745	Strand	-
Start	1	End	1393
Name	OJ990703_46.9A03.C12.o1.ts	Method	TBLASTX:Soybean
Start	638	End	1037
GI	none	Score	50
Exons	638..859, 651..860, 896..1036, 903..1037		

Seq. No.	853	Seq. ID	OJ990703_46.9A03.C12

Gene No.	1745	Strand	-
Start	1	End	1393
Name	OJ990703_46.9A03.C12.o1.tm	Method	TBLASTX:Maize
Start	869	End	1081
GI	none	Score	171
Exons	869..1081, 870..1079		

Seq. No.	854	Seq. ID	OJ990703_46.9A03.C13
Gene No.	1746	Strand	+
Start	827	End	1216
Name	OJ990703_46.9A03.C13.o1.gs	Method	GENSCAN
Start	827	End	1216
GI	none	Score	.6
Exons	827..1216		

Seq. No.	854	Seq. ID	OJ990703_46.9A03.C13
Gene No.	1747	Strand	+
Start	3106	End	5146
Name	OJ990703_46.9A03.C13.o2.np	Method	AAT/NAP
Start	3106	End	5146
GI	6721171	Score	106
Exons	3106..3292, 5094..5146		
GI Descrip.	(AC016829) unknown protein [Arabidopsis thaliana]		

Seq. No.	854	Seq. ID	OJ990703_46.9A03.C13
Gene No.	1748	Strand	-
Start	2034	End	3496
Name	OJ990703_46.9A03.C13.o2.gs	Method	GENSCAN
Start	2034	End	3496
GI	none	Score	.83
Exons	2034..2146, 2417..2466, 2973..3185, 3240..3496		

Seq. No.	854	Seq. ID	OJ990703_46.9A03.C13
Gene No.	1749	Strand	-
Start	4876	End	5146
Name	OJ990703_46.9A03.C13.o1.tm	Method	TBLASTX:Maize
Start	3105	End	3318
GI	none	Score	89
Exons	3105..3194, 3118..3195, 3185..3235, 3195..3317, 3232..3318		

Seq. No.	854	Seq. ID	OJ990703_46.9A03.C13
Gene No.	1749	Strand	-
Start	4876	End	5146
Name	OJ990703_46.9A03.C13.o1.gp	Method	AAT/GAP
Start	4876	End	5146
GI	LIB3434-015-P1-K1-E7	Score	534
Exons	4876..5146		
GI Descrip.	'5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]'		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1750	Strand	+
Start	2794	End	2928
Name	OJ990703_46.9A03.C15.o2.np	Method	AAT/NAP
Start	2794	End	2928
GI	6716785	Score	140
Exons	2794..2928		

GI Descrip. (AF220539) 40s ribosomal protein S23 [Euphorbia esula]

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1751	Strand	+
Start	3593	End	6554
Name	OJ990703_46.9A03.C15.o3.np	Method	AAT/NAP
Start	3593	End	6554
GI	1084462	Score	350
Exons	3593..3728, 5583..5618, 6292..6554		
GI Descrip.	RCg2 protein - rice gi|786130 (L27209) RCc2 [Oryza sativa] gi|786134 (L27210) root-specific protein [Oryza sativa]		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1752	Strand	-
Start	1	End	11534
Name	OJ990703_46.9A03.C15.o1.np	Method	AAT/NAP
Start	1	End	1049
GI	5902448	Score	427
Exons	1..23, 769..1049		
GI Descrip.	(AB030283) orf3 [Oryza sativa]		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1752	Strand	-
Start	1	End	11534
Name	OJ990703_46.9A03.C15.o1.gs	Method	GENSCAN
Start	333	End	11534
GI	none	Score	.6
Exons	333..545, 600..769, 882..1130, 3711..3798, 5445..5649, 6215..6550, 8169..8231, 8738..8790, 10051..10121, 10297..10500, 11490..11534		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1752	Strand	-
Start	1	End	11534
Name	OJ990703_46.9A03.C15.o2.tm	Method	TBLASTX:Maize
Start	465	End	678
GI	none	Score	91
Exons	465..554, 478..555, 545..595, 592..678, 598..657		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1752	Strand	-
Start	1	End	11534
Name	OJ990703_46.9A03.C15.o1.tc	Method	TBLASTX:Cress
Start	3436	End	6557
GI	none	Score	61
Exons	3436..3522, 3511..3573, 6273..6398, 6387..6476, 6410..6472, 6477..6557		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1752	Strand	-
Start	1	End	11534
Name	OJ990703_46.9A03.C15.o1.tw	Method	TBLASTX:Wheat
Start	6282	End	6557
GI	none	Score	68
Exons	6282..6353, 6299..6550, 6376..6408, 6393..6557, 6393..6557		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15

Gene No.	1752	Strand	-
Start	1	End	11534
Name	OJ990703_46.9A03.C15.o1.tm	Method	TBLASTX:Maize
Start	6299	End	6554
GI	none	Score	116
Exons	6299..6385, 6300..6398, 6393..6476, 6395..6478, 6477..6554, 6477..6527		

Seq. No.	855	Seq. ID	OJ990703_46.9A03.C15
Gene No.	1752	Strand	-
Start	1	End	11534
Name	OJ990703_46.9A03.C15.o1.ts	Method	TBLASTX:Soybean
Start	6305	End	6554
GI	none	Score	102
Exons	6305..6388, 6306..6398, 6393..6476, 6395..6478, 6477..6554		

Seq. No.	856	Seq. ID	OJ990703_46.9A03.C16
Gene No.	1753	Strand	+
Start	113	End	161
Name	OJ990703_46.9A03.C16.o1.gs	Method	GENSCAN
Start	113	End	161
GI	none	Score	.45
Exons	113..161		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1754	Strand	+
Start	429	End	9764
Name	OJ990703_46.9A03.C17.o1.gs	Method	GENSCAN
Start	429	End	4949
GI	none	Score	.75
Exons	429..478, 2201..2406, 3235..3941, 4026..4949		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1754	Strand	+
Start	429	End	9764
Name	OJ990703_46.9A03.C17.o1.np	Method	AAT/NAP
Start	910	End	9764
GI	5922631	Score	3969
Exons	910..934, 3045..3695, 3735..3885, 4012..4307, 4335..4864, 7847..7947, 8554..9764		
GI Descrip.	(AP000492) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] gi|6016864|dbj|BAA85207.1| (AP000570) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativ		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1755	Strand	-
Start	1	End	404
Name	OJ990703_46.9A03.C17.o1.gp	Method	AAT/GAP
Start	1	End	404
GI	25792_1.R1084	Score	733
Exons	1..404		
GI Descrip.	'4512233/dbj|AB014743.1|AB014743 0.0e+00 Oryza sativa copia-type retrotransposon RIRE7 DNA, partial sequence'		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1756	Strand	
Start	3306	End	3701
Name	OJ990703_46.9A03.C17.o6.tw	Method	TBLASTX:Wheat
Start	3306	End	3701
GI	none	Score	254
Exons	3306..3701		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1757	Strand	
Start	4356	End	4739
Name	OJ990703_46.9A03.C17.o4.tw	Method	TBLASTX:Wheat
Start	4356	End	4739
GI	none	Score	317
Exons	4356..4739, 4481..4723		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1758	Strand	
Start	7964	End	8450
Name	OJ990703_46.9A03.C17.o1.tw	Method	TBLASTX:Wheat
Start	7964	End	8420
GI	none	Score	487
Exons	7964..8419, 7965..8420		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1758	Strand	
Start	7964	End	8450
Name	OJ990703_46.9A03.C17.o3.ts	Method	TBLASTX:Soybean
Start	8004	End	8369
GI	none	Score	121
Exons	8004..8225, 8235..8369		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1758	Strand	
Start	7964	End	8450
Name	OJ990703_46.9A03.C17.o1.tm	Method	TBLASTX:Maize
Start	8094	End	8450
GI	none	Score	355
Exons	8094..8450, 8135..8428		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1759	Strand	
Start	8535	End	9248
Name	OJ990703_46.9A03.C17.o2.tw	Method	TBLASTX:Wheat
Start	8535	End	8959
GI	none	Score	391
Exons	8535..8921, 8535..8942, 8579..8959, 8654..8941		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1759	Strand	
Start	8535	End	9248
Name	OJ990703_46.9A03.C17.o1.ts	Method	TBLASTX:Soybean
Start	8583	End	8980
GI	none	Score	243
Exons	8583..8921, 8630..8773, 8810..8980		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1759	Strand	
Start	8535	End	9248
Name	OJ990703_46.9A03.C17.o2.tm	Method	TBLASTX:Maize
Start	8682	End	9125
GI	none	Score	253
Exons	8682..8921, 8723..8935, 8958..9101, 8970..9086, 9099..9125		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1759	Strand	
Start	8535	End	9248
Name	OJ990703_46.9A03.C17.o5.tw	Method	TBLASTX:Wheat
Start	8964	End	9248
GI	none	Score	269
Exons	8964..9245, 8967..9071, 9153..9248		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1760	Strand	
Start	9240	End	9671
Name	OJ990703_46.9A03.C17.o2.ts	Method	TBLASTX:Soybean
Start	9240	End	9628
GI	none	Score	238
Exons	9240..9626, 9248..9628		

Seq. No.	857	Seq. ID	OJ990703_46.9A03.C17
Gene No.	1760	Strand	
Start	9240	End	9671
Name	OJ990703_46.9A03.C17.o3.tw	Method	TBLASTX:Wheat
Start	9249	End	9671
GI	none	Score	380
Exons	9249..9671, 9254..9595		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1761	Strand	+
Start	1	End	1107
Name	OJ990703_46.9A03.C18.o1.np	Method	AAT/NAP
Start	1	End	1107
GI	5902445	Score	1660
Exons	1..1107		
GI Descrip.	(AB030283) GAG-POL precursor [Oryza sativa]		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1762	Strand	-
Start	363	End	671
Name	OJ990703_46.9A03.C18.o1.gs	Method	GENSCAN
Start	363	End	671
GI	none	Score	.75
Exons	363..671		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1763	Strand	-
Start	701	End	1652
Name	OJ990703_46.9A03.C18.o1.tm	Method	TBLASTX:Maize
Start	23	End	302
GI	none	Score	369
Exons	23..301, 24..302		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1763	Strand	-
Start	701	End	1652
Name	OJ990703_46.9A03.C18.o1.tw	Method	TBLASTX:Wheat
Start	114	End	508
GI	none	Score	385
Exons	114..494, 119..496, 419..508		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1763	Strand	-
Start	701	End	1652
Name	OJ990703_46.9A03.C18.o3.tm	Method	TBLASTX:Maize
Start	440	End	713
GI	none	Score	99
Exons	440..538, 441..539, 530..604, 534..614, 627..713		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1763	Strand	-
Start	701	End	1652
Name	OJ990703_46.9A03.C18.o2.tw	Method	TBLASTX:Wheat
Start	509	End	1052
GI	none	Score	294
Exons	509..592, 510..974, 644..775, 960..1052		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1763	Strand	-
Start	701	End	1652
Name	OJ990703_46.9A03.C18.o2.np	Method	AAT/NAP
Start	701	End	1652
GI	6691716	Score	366
Exons	701..824, 1215..1525, 1598..1652		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	858	Seq. ID	OJ990703_46.9A03.C18
Gene No.	1763	Strand	-
Start	701	End	1652
Name	OJ990703_46.9A03.C18.o2.tm	Method	TBLASTX:Maize
Start	804	End	1061
GI	none	Score	139
Exons	804..977, 917..976, 956..1057, 957..1061		

Seq. No.	859	Seq. ID	OJ990703_46.9A03.C19
Gene No.	1764	Strand	-
Start	172	End	278
Name	OJ990703_46.9A03.C19.o1.np	Method	AAT/NAP
Start	172	End	278
GI	5852093	Score	66
Exons	172..278		
GI Descrip.	(AL117264) zwh16.1 [Oryza sativa]		

Seq. No.	860	Seq. ID	OJ990323_31.9A15.C1
Gene No.	1765	Strand	-
Start	241	End	537
Name	OJ990323_31.9A15.C1.o1.gs	Method	GENSCAN
Start	241	End	537

GI	none	Score	.73
Exons	241..537		

Seq. No.	861	Seq. ID	OJ990323_31.9A15.C2
Gene No.	1766	Strand	+
Start	3115	End	5728
Name	OJ990323_31.9A15.C2.o1.gs	Method	GENSCAN
Start	3115	End	5728
GI	none	Score	.48
Exons	3115..3401, 4062..4111, 5649..5728		

Seq. No.	861	Seq. ID	OJ990323_31.9A15.C2
Gene No.	1767	Strand	+
Start	7562	End	15106
Name	OJ990323_31.9A15.C2.o3.gs	Method	GENSCAN
Start	7562	End	15106
GI	none	Score	.48
Exons	7562..7737, 8306..8402, 8467..8568, 12030..12053, 12727..12762, 14364..14410, 14935..15106		

Seq. No.	862	Seq. ID	OJ990323_31.9A15.C3
Gene No.	1768	Strand	-
Start	1	End	1368
Name	OJ990323_31.9A15.C3.o1.np	Method	AAT/NAP
Start	1	End	1368
GI	6587849	Score	121
Exons	1..26, 967..1368		
GI Descrip.	(AC006551) Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	862	Seq. ID	OJ990323_31.9A15.C3
Gene No.	1768	Strand	-
Start	1	End	1368
Name	OJ990323_31.9A15.C3.o1.gs	Method	GENSCAN
Start	127	End	360
GI	none	Score	.43
Exons	127..360		

Seq. No.	863	Seq. ID	OJ990323_31.9A15.C4
Gene No.	1769	Strand	-
Start	1	End	183
Name	OJ990323_31.9A15.C4.o1.np	Method	AAT/NAP
Start	1	End	183
GI	2583130	Score	87
Exons	1..183		
GI Descrip.	(AC002387) putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]		

Seq. No.	863	Seq. ID	OJ990323_31.9A15.C4
Gene No.	1770	Strand	-
Start	915	End	2875
Name	OJ990323_31.9A15.C4.o1.gs	Method	GENSCAN
Start	915	End	2875
GI	none	Score	.84
Exons	915..980, 1644..1725, 2363..2502, 2532..2629, 2656..2875		

Seq. No.	863	Seq. ID	OJ990323_31.9A15.C4

Gene No.	1771	Strand	-
Start	5651	End	6393
Name	OJ990323_31.9A15.C4.o1.gp	Method	AAT/GAP
Start	5651	End	6290
GI	none	Score	847
Exons	5651..5870, 6021..6290		

Seq. No.	863	Seq. ID	OJ990323_31.9A15.C4
Gene No.	1771	Strand	-
Start	5651	End	6393
Name	OJ990323_31.9A15.C4.o2.gp	Method	AAT/GAP
Start	5754	End	6393
GI	none	Score	851
Exons	5754..5870, 6021..6393		

Seq. No.	863	Seq. ID	OJ990323_31.9A15.C4
Gene No.	1772	Strand	-
Start	7296	End	7485
Name	OJ990323_31.9A15.C4.o2.np	Method	AAT/NAP
Start	7296	End	7485
GI	6728874	Score	154
Exons	7296..7485		
GI Descrip.	(AC008113) F12A21.16 [Arabidopsis thaliana]		

Seq. No.	863	Seq. ID	OJ990323_31.9A15.C4
Gene No.	1772	Strand	-
Start	7296	End	7485
Name	OJ990323_31.9A15.C4.o3.gp	Method	AAT/GAP
Start	7383	End	7485
GI	427011	Score	183
Exons	7383..7485		

Seq. No.	864	Seq. ID	OJ990323_31.9A15.C5
Gene No.	1773	Strand	-
Start	1	End	1061
Name	OJ990323_31.9A15.C5.o1.np	Method	AAT/NAP
Start	1	End	1061
GI	6728874	Score	213
Exons	1..257, 883..1061		
GI Descrip.	(AC008113) F12A21.16 [Arabidopsis thaliana]		

Seq. No.	864	Seq. ID	OJ990323_31.9A15.C5
Gene No.	1773	Strand	-
Start	1	End	1061
Name	OJ990323_31.9A15.C5.o1.tc	Method	TBLASTX:Cress
Start	29	End	166
GI	none	Score	64
Exons	29..166, 50..166		

Seq. No.	864	Seq. ID	OJ990323_31.9A15.C5
Gene No.	1773	Strand	-
Start	1	End	1061
Name	OJ990323_31.9A15.C5.o1.tm	Method	TBLASTX:Maize
Start	96	End	378
GI	none	Score	88
Exons	96..146, 97..147, 98..169, 135..170, 159..377, 175..378, 175..378		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1774	Strand	+
Start	2510	End	2616
Name	OJ990323_31.9A15.C6.o1.gs	Method	GENSCAN
Start	2510	End	2616
GI	none	Score	.96
Exons	2510..2616		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1775	Strand	+
Start	3692	End	9377
Name	OJ990323_31.9A15.C6.o2.gs	Method	GENSCAN
Start	3692	End	9377
GI	none	Score	.53
Exons	3692..3786, 5697..6158, 7500..7670, 8328..8674, 8945..9129, 9306..9377		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1776	Strand	+
Start	11041	End	13413
Name	OJ990323_31.9A15.C6.o4.gs	Method	GENSCAN
Start	11041	End	13413
GI	none	Score	.99
Exons	11041..13413		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1777	Strand	+
Start	14040	End	20456
Name	OJ990323_31.9A15.C6.o1.np	Method	AAT/NAP
Start	14040	End	19746
GI	3935164	Score	1969
Exons	14040..14099, 16369..18060, 18109..19746		
GI Descrip.	(AC004557) F17L21.7 [Arabidopsis thaliana]		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1777	Strand	+
Start	14040	End	20456
Name	OJ990323_31.9A15.C6.o6.gs	Method	GENSCAN
Start	15413	End	20456
GI	none	Score	.65
Exons	15413..15417, 16095..16977, 17211..18409, 18540..19626, 19660..19749, 20316..20456		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1778	Strand	-
Start	5508	End	5762
Name	OJ990323_31.9A15.C6.o1.gp	Method	AAT/GAP
Start	5508	End	5762
GI	454466	Score	403
Exons	5508..5762		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1779	Strand	-
Start	9831	End	10321
Name	OJ990323_31.9A15.C6.o3.gs	Method	GENSCAN
Start	9831	End	10321

GI	none	Score	.87
Exons	9831..10007, 10265..10321		
Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1780	Strand	-
Start	13944	End	14482
Name	OJ990323_31.9A15.C6.o1.tc	Method	TBLASTX:Cress
Start	11422	End	13386
GI	none	Score	93
Exons	11422..11604, 12499..12612, 12564..12596, 12625..12648, 12661..13152, 12661..12795, 12873..12995, 13053..13160, 13261..13386, 13261..13380		
Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1780	Strand	-
Start	13944	End	14482
Name	OJ990323_31.9A15.C6.o5.ts	Method	TBLASTX:Soybean
Start	12606	End	12753
GI	none	Score	184
Exons	12606..12749, 12607..12753, 12625..12753		
Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1780	Strand	-
Start	13944	End	14482
Name	OJ990323_31.9A15.C6.o3.tm	Method	TBLASTX:Maize
Start	12618	End	13371
GI	none	Score	442
Exons	12618..12782, 12619..13197, 12873..13127, 13240..13371		
Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1780	Strand	-
Start	13944	End	14482
Name	OJ990323_31.9A15.C6.o1.tw	Method	TBLASTX:Wheat
Start	12672	End	13077
GI	none	Score	197
Exons	12672..12824, 12673..12825, 12805..13077, 12829..13065		
Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1780	Strand	-
Start	13944	End	14482
Name	OJ990323_31.9A15.C6.o2.ts	Method	TBLASTX:Soybean
Start	12754	End	13437
GI	none	Score	81
Exons	12754..12843, 12756..12806, 12832..12999, 12873..13001, 13015..13233, 13213..13437		
Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1780	Strand	-
Start	13944	End	14482
Name	OJ990323_31.9A15.C6.o5.gs	Method	GENSCAN
Start	13944	End	14482
GI	none	Score	.41
Exons	13944..14083, 14245..14482		
Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1781	Strand	
Start	16474	End	17073

Name	OJ990323_31.9A15.C6.o6.tw	Method	TBLASTX:Wheat
Start	16474	End	16728
GI	none	Score	195
Exons	16474..16728, 16476..16721		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1781	Strand	
Start	16474	End	17073
Name	OJ990323_31.9A15.C6.o7.tm	Method	TBLASTX:Maize
Start	16552	End	16883
GI	none	Score	205
Exons	16552..16734, 16554..16718, 16567..16719, 16771..16869, 16788..16883		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1781	Strand	
Start	16474	End	17073
Name	OJ990323_31.9A15.C6.o5.tc	Method	TBLASTX:Cress
Start	16780	End	17073
GI	none	Score	153
Exons	16780..16983, 16791..16982, 16984..17070, 16987..17073		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1782	Strand	
Start	17167	End	17653
Name	OJ990323_31.9A15.C6.o4.tm	Method	TBLASTX:Maize
Start	17167	End	17623
GI	none	Score	80
Exons	17167..17238, 17225..17623, 17244..17621		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1782	Strand	
Start	17167	End	17653
Name	OJ990323_31.9A15.C6.o4.ts	Method	TBLASTX:Soybean
Start	17229	End	17618
GI	none	Score	265
Exons	17229..17618		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1782	Strand	
Start	17167	End	17653
Name	OJ990323_31.9A15.C6.o2.tc	Method	TBLASTX:Cress
Start	17244	End	17653
GI	none	Score	325
Exons	17244..17648, 17411..17479, 17507..17653		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1782	Strand	
Start	17167	End	17653
Name	OJ990323_31.9A15.C6.o3.tw	Method	TBLASTX:Wheat
Start	17298	End	17644
GI	none	Score	353
Exons	17298..17642, 17300..17413, 17438..17644		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755

Name	OJ990323_31.9A15.C6.o3.ts	Method	TBLASTX:Soybean
Start	18219	End	18711
GI	5509260	Score	258
Exons	18219..18557, 18236..18490, 18529..18711, 18535..18564, 18549..18695		
GI Descrip.	-		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o6.tm	Method	TBLASTX:Maize
Start	18263	End	18509
GI	none	Score	275
Exons	18263..18415, 18264..18509, 18267..18455, 18301..18465		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o3.tc	Method	TBLASTX:Cress
Start	18327	End	18580
GI	none	Score	207
Exons	18327..18557, 18353..18580		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o4.tw	Method	TBLASTX:Wheat
Start	18383	End	18894
GI	none	Score	142
Exons	18383..18580, 18384..18557, 18555..18773, 18559..18726, 18712..18894		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o2.tm	Method	TBLASTX:Maize
Start	18515	End	18960
GI	none	Score	57
Exons	18515..18559, 18516..18557, 18558..18701, 18559..18960, 18720..18947		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o4.tc	Method	TBLASTX:Cress
Start	18772	End	19023
GI	none	Score	197
Exons	18772..19023		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o2.tw	Method	TBLASTX:Wheat
Start	18895	End	19326
GI	none	Score	155
Exons	18895..19068, 18903..19067, 19060..19221, 19066..19326, 19269..19325		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o1.tm	Method	TBLASTX:Maize
Start	19003	End	19395
GI	none	Score	508
Exons	19003..19395, 19012..19395		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o1.ts	Method	TBLASTX:Soybean
Start	19090	End	19686
GI	none	Score	515
Exons	19090..19686, 19284..19613		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o5.tm	Method	TBLASTX:Maize
Start	19396	End	19689
GI	none	Score	303
Exons	19396..19689, 19401..19688		

Seq. No.	865	Seq. ID	OJ990323_31.9A15.C6
Gene No.	1783	Strand	
Start	18219	End	19755
Name	OJ990323_31.9A15.C6.o5.tw	Method	TBLASTX:Wheat
Start	19548	End	19755
GI	none	Score	199
Exons	19548..19727, 19552..19755		

Seq. No.	866	Seq. ID	OJ990323_31.9A15.C7
Gene No.	1784	Strand	-
Start	147	End	803
Name	OJ990323_31.9A15.C7.o1.gs	Method	GENSCAN
Start	147	End	803
GI	none	Score	.46
Exons	147..166, 704..803		

Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1785	Strand	+
Start	392	End	943
Name	OJ990323_31.9A15.C8.o1.gs	Method	GENSCAN
Start	392	End	943
GI	none	Score	.46
Exons	392..943		

Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1786	Strand	+
Start	917	End	9151
Name	OJ990323_31.9A15.C8.o1.np	Method	AAT/NAP
Start	917	End	7257
GI	5441880	Score	1315
Exons	917..1925, 2367..2416, 2678..2974, 3542..3715, 3822..4127, 4646..4910, 5008..5272, 7209..7257		

GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		
Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1786	Strand	+
Start	917	End	9151
Name	OJ990323_31.9A15.C8.o2.gs	Method	GENSCAN
Start	1610	End	9151
GI	none	Score	.63
Exons	1610..2762, 2880..2993, 3546..3696, 3779..4547, 4640..4840, 4864..4937, 5030..5297, 5552..5783, 5849..5929, 5966..6086, 6807..7071, 7232..7313, 8396..8487, 8539..8667, 8809..8868, 8873..9151		
Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1787	Strand	-
Start	5933	End	9092
Name	OJ990323_31.9A15.C8.o1.tm	Method	TBLASTX:Maize
Start	1486	End	2068
GI	none	Score	126
Exons	1486..1608, 1487..1639, 1639..1944, 1640..1948, 1988..2068, 1990..2016		
Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1787	Strand	-
Start	5933	End	9092
Name	OJ990323_31.9A15.C8.o1.tw	Method	TBLASTX:Wheat
Start	1777	End	2164
GI	none	Score	192
Exons	1777..1926, 1778..1954, 1778..1927, 1967..2164, 1975..2022, 1979..2068, 2001..2087		
Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1787	Strand	-
Start	5933	End	9092
Name	OJ990323_31.9A15.C8.o2.tw	Method	TBLASTX:Wheat
Start	3861	End	6903
GI	none	Score	92
Exons	3861..3914, 3864..3917, 3923..4051, 3924..4052, 4086..4121, 4158..4190, 6802..6903		
Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1787	Strand	-
Start	5933	End	9092
Name	OJ990323_31.9A15.C8.o3.np	Method	AAT/NAP
Start	5933	End	9092
GI	6815109	Score	140
Exons	5933..5972, 8197..8391, 8900..9092		
GI Descrip.	(AP001081) hypothetical protein [Oryza sativa]		
Seq. No.	867	Seq. ID	OJ990323_31.9A15.C8
Gene No.	1787	Strand	-
Start	5933	End	9092
Name	OJ990323_31.9A15.C8.o2.np	Method	AAT/NAP
Start	6888	End	9075
GI	5042454	Score	302

Exons	6888..7254, 8109..8574, 8975..9075		
GI Descrip.	(AC007789) putative polyprotein [Oryza sativa]		
Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o4.tw	Method	TBLASTX:Wheat
Start	1098	End	1485
GI	none	Score	323
Exons	1098..1484, 1109..1483, 1333..1485		
Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o1.np	Method	AAT/NAP
Start	1104	End	4988
GI	6539553	Score	6085
Exons	1104..4988		
GI Descrip.	(AP000836) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa] gi|6539590|dbj|BAA88206.1| (AP000837) Similar to Oryza australiensis retrotransposon RIRE1 (D85597) [Oryza sativa]		
Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o3.tm	Method	TBLASTX:Maize
Start	1233	End	1538
GI	none	Score	320
Exons	1233..1538, 1247..1516, 1251..1538		
Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o1.tm	Method	TBLASTX:Maize
Start	2041	End	2363
GI	none	Score	212
Exons	2041..2295, 2048..2362, 2068..2361, 2181..2363		
Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o4.tm	Method	TBLASTX:Maize
Start	2564	End	2998
GI	none	Score	300
Exons	2564..2998, 2773..2973		
Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o5.tw	Method	TBLASTX:Wheat
Start	2638	End	2833
GI	none	Score	71
Exons	2638..2730, 2639..2833, 2642..2833		
Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+

Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o3.ts	Method	TBLASTX:Soybean
Start	2786	End	3184
GI	none	Score	197
Exons	2786..3010, 2794..2964, 3011..3184		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o1.tw	Method	TBLASTX:Wheat
Start	2834	End	3588
GI	none	Score	764
Exons	2834..3520, 2842..3288, 2891..3310, 3375..3515, 3430..3516, 3517..3588, 3517..3570, 3519..3578		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o1.ts	Method	TBLASTX:Soybean
Start	3523	End	3972
GI	5509260	Score	345
Exons	3523..3972, 3726..3821, 3894..3953		
GI Descrip.	-		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o1.tc	Method	TBLASTX:Cress
Start	3579	End	3861
GI	none	Score	273
Exons	3579..3773, 3604..3861		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o2.tm	Method	TBLASTX:Maize
Start	3642	End	4083
GI	none	Score	331
Exons	3642..3824, 3643..4083, 3778..3960, 3894..4004		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o3.tw	Method	TBLASTX:Wheat
Start	3643	End	4194
GI	none	Score	307
Exons	3643..3987, 4027..4194, 4044..4190		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o2.ts	Method	TBLASTX:Soybean
Start	4038	End	4383
GI	none	Score	294
Exons	4038..4238, 4039..4383		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9

Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o5.tm	Method	TBLASTX:Maize
Start	4201	End	4533
GI	none	Score	290
Exons	4201..4533, 4201..4491		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o4.ts	Method	TBLASTX:Soybean
Start	4384	End	4742
GI	none	Score	93
Exons	4384..4482, 4563..4742		

Seq. No.	868	Seq. ID	OJ990323_31.9A15.C9
Gene No.	1788	Strand	+
Start	1104	End	4988
Name	OJ990323_31.9A15.C9.o2.tw	Method	TBLASTX:Wheat
Start	4389	End	4851
GI	none	Score	96
Exons	4389..4460, 4390..4464, 4391..4462, 4478..4555, 4479..4556, 4480..4557, 4480..4557, 4548..4817, 4554..4850, 4597..4851, 4745..4846		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1789	Strand	+
Start	3217	End	3563
Name	OJ990323_31.9A15.C10.o1.gp	Method	AAT/GAP
Start	3217	End	3563
GI	61605_3.R1084	Score	345
Exons	3217..3563		
GI Descrip.	'1402920/emb|CAA66965| 2.0e-20 (X98321) peroxidase [Arabidopsis thaliana]'		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1790	Strand	+
Start	9566	End	11336
Name	OJ990323_31.9A15.C10.o2.np	Method	AAT/NAP
Start	9566	End	11336
GI	5922620	Score	93
Exons	9566..9629, 11213..11336		
GI Descrip.	(AP000492) EST D15357(C0514) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa] gi|6016853|dbj|BAA85196.1| (AP000570) EST D15357(C0514) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1791	Strand	+
Start	11386	End	17011
Name	OJ990323_31.9A15.C10.o4.np	Method	AAT/NAP
Start	11386	End	17011
GI	6063554	Score	201
Exons	11386..11408, 14018..14297, 14333..14453, 14698..14886, 16182..16214, 16841..17011		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464)		

correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1791	Strand	+
Start	11386	End	17011
Name	OJ990323_31.9A15.C10.o5.gp	Method	AAT/GAP
Start	16396	End	16770
GI	2427387	Score	614
Exons	16396..16770		
GI Descrip.	5852170/emb|AL117265.1|OST17804 3.0e-94 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1792	Strand	+
Start	18776	End	22742
Name	OJ990323_31.9A15.C10.o4.gs	Method	GENSCAN
Start	18776	End	22742
GI	none	Score	.48
Exons	18776..18998, 19019..19122, 19817..19888, 20725..20846, 21159..21324, 21705..21775, 22451..22614, 22654..22742		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1792	Strand	+
Start	18776	End	22742
Name	OJ990323_31.9A15.C10.o6.gp	Method	AAT/GAP
Start	21000	End	22560
GI	26282_1.R1084	Score	814
Exons	21000..21324, 22451..22560		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 3.0e-94 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1793	Strand	-
Start	2468	End	8657
Name	OJ990323_31.9A15.C10.o1.np	Method	AAT/NAP
Start	2468	End	8657
GI	4680203	Score	2738
Exons	2468..3278, 6195..6360, 6644..6875, 7019..8657		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1793	Strand	-
Start	2468	End	8657
Name	OJ990323_31.9A15.C10.o3.gp	Method	AAT/GAP
Start	4539	End	5275
GI	101153_1.R1084	Score	654
Exons	4539..4769, 5092..5275		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-115 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o1.tw	Method	TBLASTX:Wheat
Start	2510	End	6763
GI	none	Score	34

Exons	2510..2614, 2522..2614, 2600..2683, 2615..2683, 2721..2810, 2724..2816, 2734..2838, 2794..2880, 2817..2876, 2882..2905, 2883..2924, 2886..2927, 2893..2928, 2907..3044, 2937..3044, 2938..3054, 2953..3051, 3096..3260, 3108..3281, 3133..3261, 6181..6273, 6211..6441, 6272..6442, 6285..6461, 6447..6551, 6447..6623, 6448..6603, 6576..6611, 6603..6725, 6614..6757, 6668..6763		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o2.tc	Method	TBLASTX:Cress
Start	3098	End	6452
GI	none	Score	99
Exons	3098..3274, 3120..3281, 3123..3260, 3133..3261, 6181..6273, 6211..6441, 6272..6442, 6285..6452, 6320..6442		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o2.tm	Method	TBLASTX:Maize
Start	6394	End	6775
GI	none	Score	69
Exons	6394..6444, 6447..6611, 6481..6612, 6614..6715, 6731..6775		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o4.tw	Method	TBLASTX:Wheat
Start	6778	End	7193
GI	none	Score	62
Exons	6778..6918, 6778..6849, 6844..7023, 6926..7006, 7016..7069, 7018..7071, 7020..7073, 7036..7191, 7047..7193, 7048..7191		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o2.tw	Method	TBLASTX:Wheat
Start	7287	End	7753
GI	none	Score	147
Exons	7287..7490, 7288..7314, 7322..7513, 7336..7491, 7491..7583, 7493..7591, 7494..7586, 7595..7699, 7599..7700, 7697..7753, 7701..7745		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o1.tm	Method	TBLASTX:Maize
Start	7328	End	7706
GI	none	Score	100
Exons	7328..7444, 7454..7696, 7455..7706		

Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o1.tc	Method	TBLASTX:Cress
Start	7541	End	7904

GI	none	Score	53
Exons	7541..7882, 7560..7688, 7737..7904		
Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o1.ts	Method	TBLASTX:Soybean
Start	7622	End	8050
GI	none	Score	98
Exons	7622..7891, 7635..7868, 7976..8050		
Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o3.tw	Method	TBLASTX:Wheat
Start	7968	End	8323
GI	none	Score	250
Exons	7968..8225, 7982..8233, 8231..8323		
Seq. No.	869	Seq. ID	OJ990323_31.9A15.C10
Gene No.	1794	Strand	-
Start	11476	End	12820
Name	OJ990323_31.9A15.C10.o3.np	Method	AAT/NAP
Start	11476	End	12820
GI	6630699	Score	92
Exons	11476..11559, 12801..12820		
GI Descrip.	(AP000969) hypothetical protein [Oryza sativa] gi|6721536|dbj|BAA89566.1| (AP001073) hypothetical protein [Oryza sativa]		
Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1795	Strand	+
Start	1	End	1903
Name	OJ990323_31.9A15.C11.o1.gp	Method	AAT/GAP
Start	1	End	1903
GI	19519_1.R1084	Score	2254
Exons	1..102, 583..645, 737..976, 1052..1903		
GI Descrip.	'4103324 1.0e-166 (AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]'		
Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1795	Strand	+
Start	1	End	1903
Name	OJ990323_31.9A15.C11.o1.np	Method	AAT/NAP
Start	1	End	1720
GI	4103324	Score	1540
Exons	1..102, 583..645, 737..976, 1052..1720		
GI Descrip.	(AF022716) GDP-mannose pyrophosphorylase [Solanum tuberosum]		
Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1795	Strand	+
Start	1	End	1903
Name	OJ990323_31.9A15.C11.o1.gs	Method	GENSCAN
Start	547	End	1723
GI	none	Score	.98
Exons	547..645, 737..976, 1052..1723		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1796	Strand	+
Start	3894	End	8125
Name	OJ990323_31.9A15.C11.o2.gs	Method	GENSCAN
Start	3894	End	8125
GI	none	Score	.74
Exons	3894..3920, 4703..4973, 4979..5085, 7415..7470, 8104..8125		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1797	Strand	+
Start	9819	End	9981
Name	OJ990323_31.9A15.C11.o2.gp	Method	AAT/GAP
Start	9819	End	9981
GI	LIB3432-008-P1-K1-F11	Score	123
Exons	9819..9908, 9961..9981		
GI Descrip.	'5852170/emb|AL117265.1|OST17804 1.0e-151 Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804'		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1798	Strand	-
Start	9503	End	11805
Name	OJ990323_31.9A15.C11.o3.gs	Method	GENSCAN
Start	9503	End	11805
GI	none	Score	.5
Exons	9503..9728, 9933..9998, 10171..10508, 11161..11413, 11504..11805		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o1.tc	Method	TBLASTX:Cress
Start	1	End	1724
GI	none	Score	179
Exons	1..105, 3..95, 580..648, 582..647, 736..912, 736..981, 740..982, 1036..1617, 1052..1723, 1497..1724		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o1.tm	Method	TBLASTX:Maize
Start	1	End	1429
GI	none	Score	179
Exons	1..105, 3..98, 580..648, 582..656, 736..978, 736..981, 740..982, 1005..1403, 1030..1428, 1052..1429		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o1.ts	Method	TBLASTX:Soybean
Start	1	End	1462
GI	none	Score	179
Exons	1..105, 1..105, 3..152, 580..648, 582..647, 603..662, 734..910, 736..909, 736..981, 740..982, 1003..1461, 1050..1190, 1052..1462		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o1.tw	Method	TBLASTX:Wheat

Start	769	End	1102
GI	none	Score	62
Exons	769..981, 774..977, 776..982, 961..1101, 1052..1102		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o3.tm	Method	TBLASTX:Maize
Start	1429	End	1761
GI	none	Score	503
Exons	1429..1761, 1430..1723, 1476..1736		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o3.ts	Method	TBLASTX:Soybean
Start	1463	End	1728
GI	none	Score	410
Exons	1463..1723, 1463..1549, 1504..1617, 1598..1723, 1669..1728		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o2.tw	Method	TBLASTX:Wheat
Start	4542	End	15994
GI	none	Score	55
Exons	4542..4583, 13417..13521, 15730..15993, 15785..15994		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o3.gp	Method	AAT/GAP
Start	14732	End	16142
GI	16043_1.R1084	Score	2574
Exons	14732..15491, 15590..16142		
GI Descrip.	'1890573/emb|CAA63661| 1.0e-126 (X93173) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]'		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o2.tm	Method	TBLASTX:Maize
Start	15087	End	15922
GI	none	Score	153
Exons	15087..15284, 15098..15283, 15293..15490, 15315..15485, 15369..15491, 15584..15742, 15586..15921, 15590..15922		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o3.tw	Method	TBLASTX:Wheat
Start	15093	End	15337
GI	none	Score	119
Exons	15093..15254, 15107..15256, 15287..15337		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-

Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o2.np	Method	AAT/NAP
Start	15101	End	16068
GI	1890573	Score	1098
Exons	15101..15491, 15590..16068		
GI Descrip.	(X93173) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o2.tc	Method	TBLASTX:Cress
Start	15113	End	15921
GI	none	Score	73
Exons	15113..15241, 15284..15436, 15324..15434, 15440..15484, 15441..15515, 15587..15679, 15589..15774, 15590..15733, 15778..15921, 15785..15892		

Seq. No.	870	Seq. ID	OJ990323_31.9A15.C11
Gene No.	1799	Strand	-
Start	14732	End	16142
Name	OJ990323_31.9A15.C11.o2.ts	Method	TBLASTX:Soybean
Start	15122	End	15918
GI	none	Score	68
Exons	15122..15226, 15296..15436, 15440..15490, 15586..15780, 15632..15727, 15778..15918, 15779..15889		

Seq. No.	871	Seq. ID	OJ990503_30.9A20.C1
Gene No.	1800	Strand	-
Start	31	End	283
Name	OJ990503_30.9A20.C1.o1.gs	Method	GENSCAN
Start	31	End	283
GI	none	Score	.58
Exons	31..171, 280..283		

Seq. No.	872	Seq. ID	OJ990503_30.9A20.C2
Gene No.	1801	Strand	+
Start	2026	End	2908
Name	OJ990503_30.9A20.C2.o1.gp	Method	AAT/GAP
Start	2026	End	2908
GI	48723_1.R1084	Score	936
Exons	2026..2105, 2198..2279, 2428..2570, 2678..2908		
GI Descrip.	'4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene'		

Seq. No.	872	Seq. ID	OJ990503_30.9A20.C2
Gene No.	1802	Strand	-
Start	3933	End	4839
Name	OJ990503_30.9A20.C2.o1.np	Method	AAT/NAP
Start	3933	End	4839
GI	6006381	Score	221
Exons	3933..4141, 4606..4839		
GI Descrip.	(AP000559) hypothetical protein [Oryza sativa]		

Seq. No.	873	Seq. ID	OJ990503_30.9A20.C4
Gene No.	1803	Strand	-
Start	1	End	487
Name	OJ990503_30.9A20.C4.o1.np	Method	AAT/NAP

Start	1	End	487
GI	5091513	Score	795
Exons	1..487		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	873	Seq. ID	OJ990503_30.9A20.C4
Gene No.	1803	Strand	-
Start	1	End	487
Name	OJ990503_30.9A20.C4.o1.gs	Method	GENSCAN
Start	48	End	462
GI	none	Score	.92
Exons	48..462		

Seq. No.	874	Seq. ID	OJ990503_30.9A20.C5
Gene No.	1804	Strand	+
Start	1	End	1070
Name	OJ990503_30.9A20.C5.o1.np	Method	AAT/NAP
Start	1	End	1070
GI	5091513	Score	712
Exons	1..100, 519..1070		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	874	Seq. ID	OJ990503_30.9A20.C5
Gene No.	1804	Strand	+
Start	1	End	1070
Name	OJ990503_30.9A20.C5.o1.gs	Method	GENSCAN
Start	494	End	1028
GI	none	Score	.54
Exons	494..1028		

Seq. No.	875	Seq. ID	OJ990503_30.9A20.C6
Gene No.	1805	Strand	+
Start	480	End	709
Name	OJ990503_30.9A20.C6.o2.gp	Method	AAT/GAP
Start	480	End	709
GI	3761181	Score	320
Exons	480..709		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene		

Seq. No.	875	Seq. ID	OJ990503_30.9A20.C6
Gene No.	1806	Strand	-
Start	206	End	930
Name	OJ990503_30.9A20.C6.o1.gs	Method	GENSCAN
Start	206	End	930
GI	none	Score	.46
Exons	206..315, 679..930		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1807	Strand	+
Start	1	End	1858
Name	OJ990503_30.9A20.C7.o1.np	Method	AAT/NAP
Start	1	End	1858
GI	4680179	Score	1581
Exons	1..68, 277..1639, 1678..1858		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o2.tw	Method	TBLASTX:Wheat
Start	276	End	815
GI	none	Score	548
Exons	276..815, 351..809, 440..811		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o2.tm	Method	TBLASTX:Maize
Start	465	End	869
GI	none	Score	337
Exons	465..869, 519..764, 578..853		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o1.ts	Method	TBLASTX:Soybean
Start	615	End	863
GI	none	Score	272
Exons	615..863, 672..857		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o1.tw	Method	TBLASTX:Wheat
Start	822	End	1436
GI	none	Score	383
Exons	822..1169, 824..1171, 1149..1436, 1178..1417		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o3.tm	Method	TBLASTX:Maize
Start	870	End	1004
GI	none	Score	182
Exons	870..998, 872..1000, 873..1004		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o1.tm	Method	TBLASTX:Maize
Start	1005	End	1596
GI	none	Score	211
Exons	1005..1184, 1007..1156, 1010..1267, 1072..1158, 1172..1450, 1173..1451, 1414..1596		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o3.tw	Method	TBLASTX:Wheat
Start	1440	End	1736
GI	none	Score	183
Exons	1440..1646, 1441..1647, 1653..1736		

Seq. No.	876	Seq. ID	OJ990503_30.9A20.C7
Gene No.	1808	Strand	+
Start	5727	End	8007
Name	OJ990503_30.9A20.C7.o2.gs	Method	GENSCAN
Start	5727	End	8007
GI	none	Score	.84
Exons	5727..7352, 7426..8007		

Seq. No.	877	Seq. ID	OJ990503_30.9A20.C8
Gene No.	1809	Strand	+
Start	1629	End	2021
Name	OJ990503_30.9A20.C8.o2.gs	Method	GENSCAN
Start	1629	End	2021
GI	none	Score	.97
Exons	1629..2021		

Seq. No.	877	Seq. ID	OJ990503_30.9A20.C8
Gene No.	1810	Strand	+
Start	10737	End	10961
Name	OJ990503_30.9A20.C8.o4.gs	Method	GENSCAN
Start	10737	End	10961
GI	none	Score	.98
Exons	10737..10961		

Seq. No.	877	Seq. ID	OJ990503_30.9A20.C8
Gene No.	1811	Strand	-
Start	138	End	285
Name	OJ990503_30.9A20.C8.o1.gs	Method	GENSCAN
Start	138	End	285
GI	none	Score	.49
Exons	138..285		

Seq. No.	878	Seq. ID	OJ990503_30.9A20.C9
Gene No.	1812	Strand	+
Start	1177	End	2735
Name	OJ990503_30.9A20.C9.o1.np	Method	AAT/NAP
Start	1177	End	2735
GI	283045	Score	92
Exons	1177..1248, 1743..1818, 1949..2735		
GI Descrip.	hydroxyproline-rich glycoprotein - maize gi|22333|emb|CAA44844| (X63134) hydroxyproline-rich glycoprotein [Zea mays] gi|228936|prf||1814452A Hyp-rich glycoprotein [Zea mays]		

Seq. No.	878	Seq. ID	OJ990503_30.9A20.C9
Gene No.	1813	Strand	+
Start	4762	End	5504
Name	OJ990503_30.9A20.C9.o2.np	Method	AAT/NAP
Start	3543	End	5504
GI	4417306	Score	226
Exons	3543..3574, 4734..5155, 5225..5319, 5483..5504		
GI Descrip.	(AC006446) putative Athila retroelement ORF1 protein [Arabidopsis thaliana]		

Seq. No.	878	Seq. ID	OJ990503_30.9A20.C9
Gene No.	1813	Strand	+
Start	4762	End	5504
Name	OJ990503_30.9A20.C9.o2.gs	Method	GENSCAN

Start	4762	End	5390
GI	none	Score	.76
Exons	4762..4875, 5007..5390		

Seq. No.	878	Seq. ID	OJ990503_30.9A20.C9
Gene No.	1814	Strand	-
Start	1047	End	2867
Name	OJ990503_30.9A20.C9.o1.gs	Method	GENSCAN
Start	1047	End	2867
GI	none	Score	.54
Exons	1047..1115, 2202..2290, 2759..2867		

Seq. No.	878	Seq. ID	OJ990503_30.9A20.C9
Gene No.	1815	Strand	
Start	4813	End	5162
Name	OJ990503_30.9A20.C9.o1.tw	Method	TBLASTX:Wheat
Start	4813	End	5162
GI	none	Score	113
Exons	4813..4929, 4945..5124, 5127..5162		

Seq. No.	879	Seq. ID	OJ990503_30.9A20.C10
Gene No.	1816	Strand	+
Start	1	End	3955
Name	OJ990503_30.9A20.C10.o1.np	Method	AAT/NAP
Start	1	End	980
GI	6691193	Score	249
Exons	1..37, 308..980		
GI Descrip.	(AC007534) F7F22.17 [Arabidopsis thaliana]		

Seq. No.	879	Seq. ID	OJ990503_30.9A20.C10
Gene No.	1816	Strand	+
Start	1	End	3955
Name	OJ990503_30.9A20.C10.o1.gs	Method	GENSCAN
Start	285	End	2853
GI	none	Score	.6
Exons	285..421, 493..697, 870..1024, 2372..2421, 2459..2543, 2569..2711, 2757..2853		

Seq. No.	879	Seq. ID	OJ990503_30.9A20.C10
Gene No.	1816	Strand	+
Start	1	End	3955
Name	OJ990503_30.9A20.C10.o2.np	Method	AAT/NAP
Start	540	End	3955
GI	5852181	Score	70
Exons	540..591, 3640..3955		
GI Descrip.	(AL117265) zhb0011.1 [Oryza sativa]		

Seq. No.	880	Seq. ID	OJ990503_30.9A20.C11
Gene No.	1817	Strand	-
Start	172	End	720
Name	OJ990503_30.9A20.C11.o1.np	Method	AAT/NAP
Start	172	End	720
GI	6063554	Score	93
Exons	172..344, 671..720		
GI Descrip.	(AP000615) ESTs AU075609(C63344),C71850(E0464),C98611(E0464) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1818	Strand	+
Start	1	End	4628
Name	OJ990503_30.9A20.C12.o1.np	Method	AAT/NAP
Start	1	End	4628
GI	5257279	Score	1730
Exons	1..143, 3127..3664, 3729..4628		
GI Descrip.	(AP000364) Similar to Transposon MAGGY gag and pol gene homologues. (L35053) [Oryza sativa]		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1819	Strand	+
Start	4790	End	5093
Name	OJ990503_30.9A20.C12.o2.gp	Method	AAT/GAP
Start	4790	End	5093
GI	72524_1.R1084	Score	407
Exons	4790..5093		
GI Descrip.	'5091496/dbj|AB023482.2|AB023482 3.0e-84 Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence'		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1820	Strand	+
Start	7407	End	7970
Name	OJ990503_30.9A20.C12.o2.np	Method	AAT/NAP
Start	7407	End	7970
GI	5091512	Score	763
Exons	7407..7970		
GI Descrip.	(AB023482) Similar to Plasmodium vivax circumsporozoite protein gene, complete cds.(M11926) [Oryza sativa]		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1821	Strand	-
Start	99	End	794
Name	OJ990503_30.9A20.C12.o1.gs	Method	GENSCAN
Start	99	End	794
GI	none	Score	.75
Exons	99..302, 308..468, 473..794		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1822	Strand	-
Start	4734	End	4979
Name	OJ990503_30.9A20.C12.o2.tw	Method	TBLASTX:Wheat
Start	3236	End	3673
GI	none	Score	490
Exons	3236..3673, 3247..3660, 3341..3667		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1822	Strand	-
Start	4734	End	4979
Name	OJ990503_30.9A20.C12.o2.tm	Method	TBLASTX:Maize
Start	3245	End	3537
GI	none	Score	343
Exons	3245..3535, 3295..3537		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1822	Strand	-

Start	4734	End	4979
Name	OJ990503_30.9A20.C12.o1.ts	Method	TBLASTX:Soybean
Start	3729	End	4116
GI	none	Score	40
Exons	3729..3755, 3729..3782, 3759..3929, 3761..3931, 3928..4116, 3933..4115		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1822	Strand	-
Start	4734	End	4979
Name	OJ990503_30.9A20.C12.o3.tw	Method	TBLASTX:Wheat
Start	3831	End	4098
GI	none	Score	110
Exons	3831..3929, 3833..3928, 3841..3933, 3928..4098, 3942..4097		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1822	Strand	-
Start	4734	End	4979
Name	OJ990503_30.9A20.C12.o1.tm	Method	TBLASTX:Maize
Start	4014	End	4443
GI	none	Score	435
Exons	4014..4430, 4018..4443, 4174..4431		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1822	Strand	-
Start	4734	End	4979
Name	OJ990503_30.9A20.C12.o1.tw	Method	TBLASTX:Wheat
Start	4101	End	4515
GI	none	Score	127
Exons	4101..4499, 4101..4493, 4102..4515, 4177..4497		

Seq. No.	881	Seq. ID	OJ990503_30.9A20.C12
Gene No.	1822	Strand	-
Start	4734	End	4979
Name	OJ990503_30.9A20.C12.o1.gp	Method	AAT/GAP
Start	4734	End	4979
GI	3761181	Score	397
Exons	4734..4979		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene		

Seq. No.	882	Seq. ID	OJ990503_30.9A20.C13
Gene No.	1823	Strand	-
Start	48	End	1409
Name	OJ990503_30.9A20.C13.o1.np	Method	AAT/NAP
Start	48	End	1059
GI	5091513	Score	1184
Exons	48..294, 349..1059		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	882	Seq. ID	OJ990503_30.9A20.C13
Gene No.	1823	Strand	-
Start	48	End	1409
Name	OJ990503_30.9A20.C13.o1.gs	Method	GENSCAN
Start	64	End	1409
GI	none	Score	.66
Exons	64..462, 519..1102, 1271..1409		

Seq. No.	883	Seq. ID	OJ990503_30.9A20.C14
Gene No.	1824	Strand	+
Start	1	End	742
Name	OJ990503_30.9A20.C14.o1.np	Method	AAT/NAP
Start	1	End	742
GI	5091513	Score	1117
Exons	1..742		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	883	Seq. ID	OJ990503_30.9A20.C14
Gene No.	1824	Strand	+
Start	1	End	742
Name	OJ990503_30.9A20.C14.o1.gs	Method	GENSCAN
Start	137	End	691
GI	none	Score	.95
Exons	137..691		

Seq. No.	884	Seq. ID	OJ990503_30.9A20.C15
Gene No.	1825	Strand	-
Start	1	End	703
Name	OJ990503_30.9A20.C15.o1.np	Method	AAT/NAP
Start	1	End	678
GI	5091513	Score	859
Exons	1..678		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	884	Seq. ID	OJ990503_30.9A20.C15
Gene No.	1825	Strand	-
Start	1	End	703
Name	OJ990503_30.9A20.C15.o1.gs	Method	GENSCAN
Start	30	End	703
GI	none	Score	.98
Exons	30..703		

Seq. No.	885	Seq. ID	OJ990503_30.9A20.C16
Gene No.	1826	Strand	-
Start	78	End	1009
Name	OJ990503_30.9A20.C16.o1.gp	Method	AAT/GAP
Start	78	End	1009
GI	342_1.R1084	Score	1702
Exons	78..1009		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	885	Seq. ID	OJ990503_30.9A20.C16
Gene No.	1826	Strand	-
Start	78	End	1009
Name	OJ990503_30.9A20.C16.o1.gs	Method	GENSCAN
Start	754	End	959
GI	none	Score	1
Exons	754..959		

Seq. No.	885	Seq. ID	OJ990503_30.9A20.C16
Gene No.	1826	Strand	-
Start	78	End	1009
Name	OJ990503_30.9A20.C16.o1.np	Method	AAT/NAP

Start	775	End	1009
GI	4680203	Score	174
Exons	775..1009		
GI Descrip.	(AF114171) TNP2-like protein [Sorghum bicolor]		

Seq. No.	886	Seq. ID	OJ990503_30.9A20.C17
Gene No.	1827	Strand	+
Start	1	End	1364
Name	OJ990503_30.9A20.C17.o1.np	Method	AAT/NAP
Start	1	End	1326
GI	2832636	Score	76
Exons	1..21, 1134..1326		
GI Descrip.	(AL021711) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	886	Seq. ID	OJ990503_30.9A20.C17
Gene No.	1827	Strand	+
Start	1	End	1364
Name	OJ990503_30.9A20.C17.o1.gs	Method	GENSCAN
Start	81	End	1280
GI	none	Score	.99
Exons	81..1280		

Seq. No.	886	Seq. ID	OJ990503_30.9A20.C17
Gene No.	1827	Strand	+
Start	1	End	1364
Name	OJ990503_30.9A20.C17.o1.gp	Method	AAT/GAP
Start	1016	End	1364
GI	3107800	Score	669
Exons	1016..1364		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1828	Strand	+
Start	292	End	5358
Name	OJ990503_30.9A20.C18.o1.gs	Method	GENSCAN
Start	292	End	5358
GI	none	Score	.76
Exons	292..318, 734..886, 2427..3350, 3524..3726, 3803..4158, 4236..4423, 4897..5358		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1828	Strand	+
Start	292	End	5358
Name	OJ990503_30.9A20.C18.o1.np	Method	AAT/NAP
Start	2466	End	5346
GI	6691716	Score	2443
Exons	2466..3360, 3552..3726, 3803..3938, 4014..4158, 4236..4423, 4498..4601, 4752..4864, 4927..5346		
GI Descrip.	(AP000492) hypothetical protein [Oryza sativa] gi|6691717|dbj|BAA89397.1| (AP000570) hypothetical protein [Oryza sativa]		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1829	Strand	+
Start	16972	End	17495
Name	OJ990503_30.9A20.C18.o1.gp	Method	AAT/GAP
Start	16972	End	17495
GI	2310235	Score	192

Exons	16972..17009, 17422..17495		
GI Descrip.	5852182/emb|CAB55420.1| 9.0e-13 (AL117265) zhb0012.1 [Oryza sativa]		
Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1830	Strand	+
Start	17422	End	17495
Name	OJ990503_30.9A20.C18.o4.np	Method	AAT/NAP
Start	17422	End	17495
GI	5852182	Score	76
Exons	17422..17495		
GI Descrip.	(AL117265) zhb0012.1 [Oryza sativa]		
Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o8.tw	Method	TBLASTX:Wheat
Start	2586	End	2876
GI	none	Score	212
Exons	2586..2876		
Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o2.gs	Method	GENSCAN
Start	5680	End	15549
GI	none	Score	.84
Exons	5680..6644, 6711..7482, 7681..8421, 8488..8761, 8858..10289, 11169..11365, 11973..12368, 12720..13185, 13417..13555, 15469..15549		
Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o5.tw	Method	TBLASTX:Wheat
Start	5692	End	6306
GI	none	Score	88
Exons	5692..5823, 5815..5973, 6028..6306, 6044..6151, 6197..6286		
Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o2.np	Method	AAT/NAP
Start	5716	End	13507
GI	5922631	Score	6625
Exons	5716..8243, 8850..9776, 9903..10053, 10096..10336, 12045..12376, 12422..12621, 12880..13124, 13383..13507		
GI Descrip.	(AP000492) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativa] gi|6016864|dbj|BAA85207.1| (AP000570) ESTs C26347(C12145),AU078074(C12145) correspond to a region of the predicted gene.; Similar to prpol; Zea mays retrotransposon Cinful-1. (AF049110) [Oryza sativ		
Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-

Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o4.tm	Method	TBLASTX:Maize
Start	5731	End	5973
GI	none	Score	96
Exons	5731..5832, 5732..5833, 5812..5973, 5813..5872		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o5.tm	Method	TBLASTX:Maize
Start	6076	End	6355
GI	none	Score	51
Exons	6076..6162, 6172..6255, 6185..6259, 6242..6355, 6250..6348		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o3.tw	Method	TBLASTX:Wheat
Start	6421	End	6808
GI	none	Score	109
Exons	6421..6606, 6421..6807, 6497..6808		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o1.tm	Method	TBLASTX:Maize
Start	6451	End	6813
GI	none	Score	242
Exons	6451..6498, 6490..6813, 6503..6793		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o10.tw	Method	TBLASTX:Wheat
Start	6811	End	7110
GI	none	Score	73
Exons	6811..6909, 6812..6922, 6976..7110, 6977..7078		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o6.tm	Method	TBLASTX:Maize
Start	7042	End	7368
GI	none	Score	190
Exons	7042..7368		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o6.tw	Method	TBLASTX:Wheat
Start	7126	End	7548
GI	none	Score	215
Exons	7126..7407, 7202..7543, 7438..7548		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200

Name	OJ990503_30.9A20.C18.o2.ts	Method	TBLASTX:Soybean
Start	7169	End	7557
GI	none	Score	101
Exons	7169..7417, 7171..7557, 7454..7549		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o4.tw	Method	TBLASTX:Wheat
Start	7585	End	8014
GI	none	Score	87
Exons	7585..8013, 7823..8014		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o3.tm	Method	TBLASTX:Maize
Start	7672	End	8113
GI	none	Score	157
Exons	7672..7698, 7696..7833, 7844..8101, 7861..8112, 7862..8113		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o1.ts	Method	TBLASTX:Soybean
Start	7810	End	8214
GI	none	Score	47
Exons	7810..8214, 7817..7987, 8057..8167		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o2.tw	Method	TBLASTX:Wheat
Start	8059	End	8478
GI	none	Score	228
Exons	8059..8478, 8060..8476		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o2.tm	Method	TBLASTX:Maize
Start	8347	End	8703
GI	none	Score	195
Exons	8347..8703, 8357..8662		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o3.ts	Method	TBLASTX:Soybean
Start	8428	End	8793
GI	none	Score	135
Exons	8428..8562, 8569..8793		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o7.tw	Method	TBLASTX:Wheat

Start	8478	End	8712
GI	none	Score	115
Exons	8478..8606, 8479..8691, 8479..8712, 8480..8692		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o1.tw	Method	TBLASTX:Wheat
Start	8713	End	9510
GI	none	Score	117
Exons	8713..9006, 8717..8941, 9053..9289, 9055..9285, 9322..9510		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o9.tw	Method	TBLASTX:Wheat
Start	9919	End	10338
GI	none	Score	205
Exons	9919..10338		

Seq. No.	887	Seq. ID	OJ990503_30.9A20.C18
Gene No.	1831	Strand	-
Start	5680	End	16200
Name	OJ990503_30.9A20.C18.o3.np	Method	AAT/NAP
Start	15442	End	16200
GI	5932428	Score	166
Exons	15442..15734, 16048..16200		
GI Descrip.	(AF187305) calmodulin [Myxine glutinosa]		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o1.gp	Method	AAT/GAP
Start	1	End	2446
GI	342_1.R1084	Score	4265
Exons	1..2446		
GI Descrip.	'4574406/gb|AAD24042.1| 0.0e+00 (AF121139) RIM2 protein [Oryza sativa]'		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o4.tw	Method	TBLASTX:Wheat
Start	3	End	296
GI	none	Score	47
Exons	3..47, 30..281, 31..255, 38..280, 39..296, 41..283, 49..291		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o1.ts	Method	TBLASTX:Soybean
Start	212	End	641
GI	none	Score	102
Exons	212..295, 213..287, 288..350, 345..641, 399..623		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+

Start	1	End	2446
Name	OJ990503_30.9A20.C19.o2.tc	Method	TBLASTX:Cress
Start	374	End	689
GI	none	Score	281
Exons	374..526, 381..689, 381..689		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o1.np	Method	AAT/NAP
Start	402	End	2358
GI	6742729	Score	3060
Exons	402..2358		
GI Descrip.	(AF121139) RIM2 protein [Oryza sativa]		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o2.tw	Method	TBLASTX:Wheat
Start	510	End	978
GI	none	Score	72
Exons	510..563, 518..562, 564..668, 575..664, 682..768, 683..769, 749..973, 769..978, 770..973, 772..978		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o1.tm	Method	TBLASTX:Maize
Start	555	End	1012
GI	none	Score	115
Exons	555..683, 567..689, 683..808, 689..808, 818..1012		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o2.ts	Method	TBLASTX:Soybean
Start	842	End	1084
GI	none	Score	216
Exons	842..1084		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o3.tw	Method	TBLASTX:Wheat
Start	1117	End	1527
GI	none	Score	80
Exons	1117..1167, 1118..1180, 1166..1408, 1186..1368, 1441..1527, 1442..1519		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o2.tm	Method	TBLASTX:Maize
Start	1442	End	1915
GI	none	Score	286
Exons	1442..1915, 1580..1657, 1711..1848		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o1.tw	Method	TBLASTX:Wheat
Start	1528	End	2443
GI	none	Score	730
Exons	1528..2073, 1529..2335, 2114..2335, 2338..2427, 2339..2443		

Seq. No.	888	Seq. ID	OJ990503_30.9A20.C19
Gene No.	1832	Strand	+
Start	1	End	2446
Name	OJ990503_30.9A20.C19.o1.tc	Method	TBLASTX:Cress
Start	1816	End	2263
GI	none	Score	137
Exons	1816..2253, 1816..2073, 1820..2263, 2114..2263		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1833	Strand	+
Start	1	End	3917
Name	OJ990503_30.9A20.C20.o1.np	Method	AAT/NAP
Start	1	End	3917
GI	5091513	Score	2428
Exons	1..52, 1111..2726, 3381..3917		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1833	Strand	+
Start	1	End	3917
Name	OJ990503_30.9A20.C20.o1.gp	Method	AAT/GAP
Start	311	End	416
GI	5816518	Score	159
Exons	311..416		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 3.0e-40 Oryza sativa DNA, similar sequence to Pib gene		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1833	Strand	+
Start	1	End	3917
Name	OJ990503_30.9A20.C20.o2.gp	Method	AAT/GAP
Start	424	End	654
GI	3761181	Score	337
Exons	424..654		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1834	Strand	-
Start	4103	End	10529
Name	OJ990503_30.9A20.C20.o2.gs	Method	GENSCAN
Start	4103	End	10508
GI	none	Score	.45
Exons	4103..4131, 5431..5512, 6053..6694, 6699..7003, 7009..7227, 7710..7788, 9188..9564, 9581..10508		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1834	Strand	-
Start	4103	End	10529

Name	OJ990503_30.9A20.C20.o3.np	Method	AAT/NAP
Start	4994	End	10529
GI	4680179	Score	612
Exons	4994..5059, 6502..6605, 9262..9396, 9566..10529		
GI Descrip.	(AF111709) polyprotein [Oryza sativa subsp. indica]		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1834	Strand	-
Start	4103	End	10529
Name	OJ990503_30.9A20.C20.o2.np	Method	AAT/NAP
Start	5411	End	7486
GI	6907087	Score	1261
Exons	5411..5512, 6053..6730, 7103..7486		
GI Descrip.	(AP001129) ESTs C72771(E2215),AU082313(E2215) correspond to a region of the predicted gene.; hypothetical protein [Oryza sativa]		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1834	Strand	-
Start	4103	End	10529
Name	OJ990503_30.9A20.C20.o1.tm	Method	TBLASTX:Maize
Start	9747	End	10046
GI	none	Score	73
Exons	9747..10046, 9943..10032		

Seq. No.	889	Seq. ID	OJ990503_30.9A20.C20
Gene No.	1834	Strand	-
Start	4103	End	10529
Name	OJ990503_30.9A20.C20.o1.tw	Method	TBLASTX:Wheat
Start	9927	End	10286
GI	none	Score	161
Exons	9927..10286, 9931..10284		

Seq. No.	890	Seq. ID	OJ990503_30.9A20.C21
Gene No.	1835	Strand	+
Start	1	End	2683
Name	OJ990503_30.9A20.C21.o1.np	Method	AAT/NAP
Start	1	End	2683
GI	5091513	Score	1129
Exons	1..940, 1015..1379, 1937..1997, 2032..2221, 2614..2683		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	890	Seq. ID	OJ990503_30.9A20.C21
Gene No.	1835	Strand	+
Start	1	End	2683
Name	OJ990503_30.9A20.C21.o1.gs	Method	GENSCAN
Start	59	End	1421
GI	none	Score	.78
Exons	59..835, 921..1067, 1110..1421		

Seq. No.	890	Seq. ID	OJ990503_30.9A20.C21
Gene No.	1836	Strand	-
Start	1864	End	2062
Name	OJ990503_30.9A20.C21.o2.gs	Method	GENSCAN
Start	1864	End	2062
GI	none	Score	.56
Exons	1864..1954, 2019..2062		

Seq. No.	891	Seq. ID	OJ990503_30.9A20.C22
Gene No.	1837	Strand	-
Start	1	End	134
Name	OJ990503_30.9A20.C22.o1.np	Method	AAT/NAP
Start	1	End	134
GI	6006381	Score	127
Exons	1..134		
GI Descrip.	(AP000559) hypothetical protein [Oryza sativa]		

Seq. No.	892	Seq. ID	OJ990503_30.9A20.C23
Gene No.	1838	Strand	-
Start	673	End	1236
Name	OJ990503_30.9A20.C23.o1.gs	Method	GENSCAN
Start	673	End	1236
GI	none	Score	.66
Exons	673..756, 991..1031, 1137..1236		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1839	Strand	+
Start	2625	End	2775
Name	OJ990503_30.9A20.C24.o1.gp	Method	AAT/GAP
Start	2625	End	2775
GI	21474_1.R1084	Score	211
Exons	2625..2775		
GI Descrip.	'3894159 2.0e-10 (AC005312) hypothetical protein [Arabidopsis thaliana]'		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1840	Strand	+
Start	2871	End	3080
Name	OJ990503_30.9A20.C24.o2.gp	Method	AAT/GAP
Start	2871	End	3080
GI	LIB3477-003-P1-K1-E9	Score	116
Exons	2871..2911, 3015..3080		
GI Descrip.	'2498586/sp|Q40638|MPO1_ORYSA 2.0e-24 MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]'		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1841	Strand	-
Start	3178	End	6926
Name	OJ990503_30.9A20.C24.o2.gs	Method	GENSCAN
Start	3178	End	6911
GI	none	Score	.65
Exons	3178..3363, 3443..3541, 3644..3716, 3804..3914, 4011..4184, 4296..4584, 4774..4981, 4983..5128, 5254..5395, 5491..5631, 5655..6911		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1841	Strand	-
Start	3178	End	6926
Name	OJ990503_30.9A20.C24.o1.np	Method	AAT/NAP
Start	3196	End	6926
GI	4680204	Score	1023
Exons	3196..3401, 3766..3914, 4011..4184, 4296..5395, 5491..6926		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1841	Strand	-
Start	3178	End	6926
Name	OJ990503_30.9A20.C24.o4.np	Method	AAT/NAP
Start	5201	End	6926
GI	4680204	Score	844
Exons	5201..5395, 5491..6926		
GI Descrip.	(AF114171) hypothetical protein [Sorghum bicolor]		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1842	Strand	-
Start	8012	End	8523
Name	OJ990503_30.9A20.C24.o3.gs	Method	GENSCAN
Start	8012	End	8523
GI	none	Score	.89
Exons	8012..8349, 8426..8523		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1843	Strand	-
Start	8554	End	8712
Name	OJ990503_30.9A20.C24.o2.tw	Method	TBLASTX:Wheat
Start	5183	End	5879
GI	none	Score	69
Exons	5183..5404, 5485..5559, 5799..5879		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1843	Strand	-
Start	8554	End	8712
Name	OJ990503_30.9A20.C24.o1.tw	Method	TBLASTX:Wheat
Start	5880	End	6285
GI	none	Score	36
Exons	5880..5975, 5880..6050, 6013..6285, 6045..6281		

Seq. No.	893	Seq. ID	OJ990503_30.9A20.C24
Gene No.	1843	Strand	-
Start	8554	End	8712
Name	OJ990503_30.9A20.C24.o3.gp	Method	AAT/GAP
Start	8554	End	8712
GI	3761181	Score	229
Exons	8554..8712		
GI Descrip.	4521193/dbj|AB013450.1|AB013450 1.0e-99 Oryza sativa DNA, similar sequence to Pib gene		

Seq. No.	894	Seq. ID	OJ990503_30.9A20.C25
Gene No.	1844	Strand	+
Start	174	End	257
Name	OJ990503_30.9A20.C25.o1.gs	Method	GENSCAN
Start	174	End	257
GI	none	Score	.71
Exons	174..257		

Seq. No.	894	Seq. ID	OJ990503_30.9A20.C25
Gene No.	1845	Strand	-
Start	1	End	2346
Name	OJ990503_30.9A20.C25.o1.np	Method	AAT/NAP
Start	1	End	2346

GI	5091513	Score	207
Exons	1..36, 1327..1458, 1510..1554, 1793..2098, 2141..2346		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	894	Seq. ID	OJ990503_30.9A20.C25
Gene No.	1845	Strand	-
Start	1	End	2346
Name	OJ990503_30.9A20.C25.o2.gs	Method	GENSCAN
Start	993	End	1533
GI	none	Score	.6
Exons	993..1016, 1333..1533		

Seq. No.	894	Seq. ID	OJ990503_30.9A20.C25
Gene No.	1845	Strand	-
Start	1	End	2346
Name	OJ990503_30.9A20.C25.o3.gs	Method	GENSCAN
Start	1741	End	2228
GI	none	Score	.9
Exons	1741..2036, 2126..2228		

Seq. No.	895	Seq. ID	OJ990503_30.9A20.C26
Gene No.	1846	Strand	-
Start	1	End	732
Name	OJ990503_30.9A20.C26.o1.np	Method	AAT/NAP
Start	1	End	732
GI	5091513	Score	739
Exons	1..732		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	895	Seq. ID	OJ990503_30.9A20.C26
Gene No.	1846	Strand	-
Start	1	End	732
Name	OJ990503_30.9A20.C26.o1.gs	Method	GENSCAN
Start	37	End	721
GI	none	Score	.85
Exons	37..388, 432..721		

Seq. No.	896	Seq. ID	OJ990503_30.9A20.C27
Gene No.	1847	Strand	-
Start	184	End	471
Name	OJ990503_30.9A20.C27.o1.gs	Method	GENSCAN
Start	184	End	471
GI	none	Score	.76
Exons	184..345, 427..471		

Seq. No.	897	Seq. ID	OJ990503_30.9A20.C28
Gene No.	1848	Strand	+
Start	1	End	718
Name	OJ990503_30.9A20.C28.o1.np	Method	AAT/NAP
Start	1	End	718
GI	5091513	Score	679
Exons	1..718		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	897	Seq. ID	OJ990503_30.9A20.C28
Gene No.	1848	Strand	+
Start	1	End	718

Name	OJ990503_30.9A20.C28.o1.gs	Method	GENSCAN
Start	145	End	572
GI	none	Score	.51
Exons	145..490, 514..572		

Seq. No.	898	Seq. ID	OJ990503_30.9A20.C29
Gene No.	1849	Strand	-
Start	1	End	726
Name	OJ990503_30.9A20.C29.o1.np	Method	AAT/NAP
Start	1	End	726
GI	4680183	Score	528
Exons	1..327, 353..726		
GI Descrip.	(AF111709) gag-pol protein [Oryza sativa subsp. indica]		

Seq. No.	898	Seq. ID	OJ990503_30.9A20.C29
Gene No.	1849	Strand	-
Start	1	End	726
Name	OJ990503_30.9A20.C29.o1.gs	Method	GENSCAN
Start	45	End	371
GI	none	Score	.81
Exons	45..371		

Seq. No.	899	Seq. ID	OJ990323_33.9A06.C1
Gene No.	1850	Strand	+
Start	5697	End	6582
Name	OJ990323_33.9A06.C1.o1.gp	Method	AAT/GAP
Start	5697	End	6582
GI	none	Score	754
Exons	5697..6046, 6544..6582		

Seq. No.	899	Seq. ID	OJ990323_33.9A06.C1
Gene No.	1851	Strand	+
Start	9176	End	9664
Name	OJ990323_33.9A06.C1.o2.gp	Method	AAT/GAP
Start	9176	End	9664
GI	702082	Score	860
Exons	9176..9664		

Seq. No.	899	Seq. ID	OJ990323_33.9A06.C1
Gene No.	1852	Strand	-
Start	126	End	513
Name	OJ990323_33.9A06.C1.o1.np	Method	AAT/NAP
Start	126	End	483
GI	3158374	Score	114
Exons	126..483		
GI Descrip.	(AF035384) endo-xyloglucan transferase [Arabidopsis thaliana]		

Seq. No.	899	Seq. ID	OJ990323_33.9A06.C1
Gene No.	1852	Strand	-
Start	126	End	513
Name	OJ990323_33.9A06.C1.o1.gs	Method	GENSCAN
Start	214	End	513
GI	none	Score	.53
Exons	214..513		

Seq. No.	899	Seq. ID	OJ990323_33.9A06.C1
Gene No.	1853	Strand	-

Start	10429	End	11234
Name	OJ990323_33.9A06.C1.o3.gp	Method	AAT/GAP
Start	9887	End	10787
GI	183,9.R1084	Score	1318
Exons	9887..10598, 10767..10787		
GI Descrip.	'5714761/gb|AF173881.1|AF173881 7.0e-17 Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds'		

Seq. No.	899	Seq. ID	OJ990323_33.9A06.C1
Gene No.	1853	Strand	-
Start	10429	End	11234
Name	OJ990323_33.9A06.C1.o3.gs	Method	GENSCAN
Start	10429	End	11234
GI	none	Score	.71
Exons	10429..10598, 10680..10766, 10933..11067, 11105..11234		

Seq. No.	900	Seq. ID	OJ990323_33.9A06.C2
Gene No.	1854	Strand	
Start	849	End	1088
Name	OJ990323_33.9A06.C2.o1.tm	Method	TBLASTX:Maize
Start	849	End	1088
GI	none	Score	206
Exons	849..1088, 854..901, 947..1006		

Seq. No.	901	Seq. ID	OJ990323_33.9A06.C3
Gene No.	1855	Strand	+
Start	545	End	626
Name	OJ990323_33.9A06.C3.o1.gs	Method	GENSCAN
Start	545	End	626
GI	none	Score	.73
Exons	545..626		

Seq. No.	902	Seq. ID	OJ990323_33.9A06.C4
Gene No.	1856	Strand	-
Start	108	End	163
Name	OJ990323_33.9A06.C4.o1.gs	Method	GENSCAN
Start	108	End	163
GI	none	Score	.58
Exons	108..163		

Seq. No.	903	Seq. ID	OJ990323_33.9A06.C6
Gene No.	1857	Strand	-
Start	808	End	863
Name	OJ990323_33.9A06.C6.o1.gp	Method	AAT/GAP
Start	808	End	863
GI	5055977	Score	89
Exons	808..863		
GI Descrip.	576937/emb|CAA58001| 2.0e-34 (X82683) Meri-5 [Arabidopsis thaliana]		

Seq. No.	904	Seq. ID	OJ990323_33.9A06.C7
Gene No.	1858	Strand	+
Start	315	End	1631
Name	OJ990323_33.9A06.C7.o1.np	Method	AAT/NAP
Start	315	End	1631
GI	6325052	Score	80

Exons	315..374, 1515..1631		
GI Descrip.	casein kinase I isoform; Hrr25p gi|123515|sp|P29295|HR25_YEAST CASEIN KINASE I HOMOLOG HRR25 gi|101506|pir||A40860 probable protein kinase HRR25 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) gi|234768|bbs|57421 HRR25=putative protein kinase [Saccharomyces cerevisiae, Peptide, 494 aa] gi|171706 (M68605) protein kinase [Saccharomyces cerevisiae] gi|1370424|emb|CA		

Seq. No.	904	Seq. ID	OJ990323_33.9A06.C7
Gene No.	1858	Strand	+
Start	315	End	1631
Name	OJ990323_33.9A06.C7.o1.gs	Method	GENSCAN
Start	543	End	1581
GI	none	Score	.62
Exons	543..635, 1489..1581		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1859	Strand	+
Start	14167	End	15418
Name	OJ990323_33.9A06.C8.o5.gp	Method	AAT/GAP
Start	14090	End	14576
GI	58722_1.R1084	Score	747
Exons	14090..14430, 14527..14576		
GI Descrip.	'2129771/pir||S71225 1.0e-15 xyloglucan endotransglycosylase-related protein XTR-6 - Arabidopsis thaliana >gi_1244758 (U43488) xyloglucan endotransglycosylase-related protein [Arabidopsis thaliana] >gi_4539299_emb_CAB39602.1_ (AL049480) xyloglucan endo-1, 4-beta-D-glucanase (XTR-6) [Arabidopsis thaliana]'		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1859	Strand	+
Start	14167	End	15418
Name	OJ990323_33.9A06.C8.o4.gs	Method	GENSCAN
Start	14167	End	15200
GI	none	Score	.93
Exons	14167..14430, 14527..14726, 14843..15200		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1859	Strand	+
Start	14167	End	15418
Name	OJ990323_33.9A06.C8.o3.np	Method	AAT/NAP
Start	14170	End	15194
GI	1890575	Score	713
Exons	14170..14437, 14540..14726, 14843..15194		
GI Descrip.	(X93174) xyloglucan endotransglycosylase (XET) [Hordeum vulgare]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1859	Strand	+
Start	14167	End	15418
Name	OJ990323_33.9A06.C8.o6.gp	Method	AAT/GAP
Start	14685	End	15418
GI	5055977	Score	1068
Exons	14685..14726, 14843..15418		
GI Descrip.	576937/emb|CAA58001| 2.0e-34 (X82683) Meri-5 [Arabidopsis thaliana]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1860	Strand	+
Start	17585	End	22602
Name	OJ990323_33.9A06.C8.o6.gs	Method	GENSCAN
Start	17585	End	22602
GI	none	Score	.75
Exons	17585..17676, 18131..18182, 18232..18370, 18384..18560, 19406..19476, 19552..19578, 21929..22078, 22495..22602		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1860	Strand	+
Start	17585	End	22602
Name	OJ990323_33.9A06.C8.o7.gp	Method	AAT/GAP
Start	19333	End	19731
GI	none	Score	593
Exons	19333..19731		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1861	Strand	+
Start	22720	End	23838
Name	OJ990323_33.9A06.C8.o4.np	Method	AAT/NAP
Start	22720	End	23838
GI	950299	Score	547
Exons	22720..23016, 23134..23318, 23439..23838		
GI Descrip.	(L46792) xyloglucan endotransglycosylase precursor [Actinidia deliciosa]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1861	Strand	+
Start	22720	End	23838
Name	OJ990323_33.9A06.C8.o7.gs	Method	GENSCAN
Start	22720	End	23832
GI	none	Score	.69
Exons	22720..23007, 23119..23318, 23439..23832		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1862	Strand	+
Start	24559	End	43092
Name	OJ990323_33.9A06.C8.o8.gs	Method	GENSCAN
Start	24559	End	43092
GI	none	Score	.46
Exons	24559..24668, 25481..25580, 25886..25954, 26371..26548, 26638..26770, 26929..27091, 27430..27580, 28186..28366, 28924..29098, 29330..29431, 29696..29833, 29930..30058, 31605..31740, 31907..31965, 32089..32154, 32642..32960, 33048..33208, 33794..33977, 33985..34208, 34732..34865, 35352..35361, 35753..35785, 36815..36906, 37738..37892, 38035..38110, 39540..39706, 40444..40511, 40626..40720, 41504..41775, 42031..42116, 42238..42548, 42890..42974, 43051..43092		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1862	Strand	+
Start	24559	End	43092
Name	OJ990323_33.9A06.C8.o5.np	Method	AAT/NAP
Start	24938	End	33405
GI	3093294	Score	2555

Exons	24938..24993, 25481..25580, 25886..25954, 26042..26284, 26371..26548, 26638..26770, 26929..27091, 27430..27580, 27671..27771, 28943..29098, 29363..29431, 29505..29573, 29696..29833, 29930..30058, 31226..31384, 31605..31745, 31840..31965, 32089..32154, 32642..33208, 33295..33405
GI Descrip.	(Y12782) putative villin [Arabidopsis thaliana] gi|5730126|emb|CAB52460.1| (AL109796) putative villin [Arabidopsis thaliana]

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1862	Strand	+
Start	24559	End	43092
Name	OJ990323_33.9A06.C8.o8.gp	Method	AAT/GAP
Start	32869	End	33357
GI	uC-osflcyp014a04b1	Score	541
Exons	32869..32960, 33048..33208, 33295..33357		
GI Descrip.	'3093294/emb|CAA73320| 3.0e-10 (Y12782) putative villin [Arabidopsis thaliana] >gi_5730126_emb_CAB52460.1_ (AL109796) putative villin [Arabidopsis thaliana]'		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1862	Strand	+
Start	24559	End	43092
Name	OJ990323_33.9A06.C8.o8.np	Method	AAT/NAP
Start	40634	End	42597
GI	1703447	Score	273
Exons	40634..40654, 42026..42207, 42238..42597		
GI Descrip.	L-ASPARAGINASE (L-ASPARAGINE AMIDOHYDROLASE) gi|496102 (L19141) L-asparaginase [Lupinus albus]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1863	Strand	+
Start	46356	End	47487
Name	OJ990323_33.9A06.C8.o10.gs	Method	GENSCAN
Start	46356	End	47487
GI	none	Score	.66
Exons	46356..46440, 47369..47487		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1864	Strand	-
Start	1502	End	2023
Name	OJ990323_33.9A06.C8.o1.gs	Method	GENSCAN
Start	1502	End	2023
GI	none	Score	1
Exons	1502..2023		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1865	Strand	-
Start	3188	End	11659
Name	OJ990323_33.9A06.C8.o1.gp	Method	AAT/GAP
Start	2910	End	3363
GI	LIB3431-045-P1-N1-A10	Score	848
Exons	2910..3363		
GI Descrip.	'5441876/dbj|AP000367.1|AP000367 0.0e+00 Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)'		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8

Gene No.	1865	Strand	-
Start	3188	End	11659
Name	OJ990323_33.9A06.C8.o2.gs	Method	GENSCAN
Start	3188	End	11659
GI	none	Score	.56
Exons	3188..3348, 3499..3701, 3706..3753, 3817..3948, 4049..4104, 4262..4444, 4537..4795, 4872..5170, 5263..5673, 5848..6094, 6200..6350, 6734..6931, 7247..8110, 9086..10456, 11530..11659		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1865	Strand	-
Start	3188	End	11659
Name	OJ990323_33.9A06.C8.o1.np	Method	AAT/NAP
Start	3467	End	9998
GI	5441880	Score	4756
Exons	3467..3701, 3817..3948, 4195..4292, 4537..4795, 4872..5170, 5758..6094, 6200..6350, 6854..7169, 7428..7459, 7904..8069, 9159..9998		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1865	Strand	-
Start	3188	End	11659
Name	OJ990323_33.9A06.C8.o2.gp	Method	AAT/GAP
Start	4545	End	5044
GI	LIB3475-007-P1-K1-G8	Score	801
Exons	4545..4795, 4872..5044		
GI Descrip.	'5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]'		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1865	Strand	-
Start	3188	End	11659
Name	OJ990323_33.9A06.C8.o3.gp	Method	AAT/GAP
Start	7874	End	9394
GI	5701669	Score	822
Exons	7874..8069, 9159..9394		
GI Descrip.	5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1865	Strand	-
Start	3188	End	11659
Name	OJ990323_33.9A06.C8.o2.np	Method	AAT/NAP
Start	10011	End	11067
GI	6721543	Score	179
Exons	10011..10127, 10940..11067		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1865	Strand	-
Start	3188	End	11659
Name	OJ990323_33.9A06.C8.o4.gp	Method	AAT/GAP

Start	10889	End	11053
GI	7406_1.R1084	Score	204
Exons	10889..11053		
GI Descrip.	'1122315/emb|CAA63901| 7.0e-10 (X94191) heat shock protein 17.0 [Pennisetum glaucum]'		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1866	Strand	-
Start	12880	End	13530
Name	OJ990323_33.9A06.C8.o3.gs	Method	GENSCAN
Start	12880	End	13530
GI	none	Score	.74
Exons	12880..13067, 13115..13137, 13472..13530		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1867	Strand	-
Start	16724	End	17173
Name	OJ990323_33.9A06.C8.o5.gs	Method	GENSCAN
Start	16724	End	17173
GI	none	Score	.61
Exons	16724..16808, 17034..17173		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1868	Strand	-
Start	34466	End	38742
Name	OJ990323_33.9A06.C8.o7.np	Method	AAT/NAP
Start	34466	End	38742
GI	6466937	Score	2235
Exons	34466..37898, 37947..38742		
GI Descrip.	(AC011621) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1868	Strand	-
Start	34466	End	38742
Name	OJ990323_33.9A06.C8.o6.np	Method	AAT/NAP
Start	34466	End	38742
GI	6466937	Score	2238
Exons	34466..37898, 37947..38742		
GI Descrip.	(AC011621) putative retroelement pol polyprotein [Arabidopsis thaliana]		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1869	Strand	-
Start	43728	End	45381
Name	OJ990323_33.9A06.C8.o9.gs	Method	GENSCAN
Start	43728	End	45381
GI	none	Score	.79
Exons	43728..44200, 44388..44506, 45311..45381		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o1.tw	Method	TBLASTX:Wheat
Start	7674	End	8054
GI	none	Score	79
Exons	7674..7850, 7704..7850, 7735..7854, 7848..8045, 7860..8054		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o1.tm	Method	TBLASTX:Maize
Start	14224	End	23574
GI	none	Score	289
Exons	14224..14430, 14239..14391, 14277..14435, 14509..14727, 14518..14655, 14529..14726, 14843..14977, 14844..14978, 22814..22843, 22873..23007, 22873..22998, 23121..23369, 23122..23319, 23440..23574, 23443..23574		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o1.ts	Method	TBLASTX:Soybean
Start	14230	End	23835
GI	none	Score	184
Exons	14230..14436, 14292..14420, 14554..14727, 14556..14699, 14840..15028, 14850..15029, 15074..15199, 15108..15194, 22879..23013, 22884..22997, 23143..23319, 23148..23309, 23190..23327, 23421..23609, 23446..23631, 23716..23835		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o1.tc	Method	TBLASTX:Cress
Start	14248	End	23820
GI	none	Score	197
Exons	14248..14433, 14292..14429, 14527..14727, 14541..14708, 14849..15013, 14850..15026, 15108..15191, 22864..23010, 22872..23000, 23128..23319, 23142..23306, 23149..23316, 23440..23634, 23445..23609, 23716..23820		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o2.tc	Method	TBLASTX:Cress
Start	24931	End	33441
GI	none	Score	71
Exons	24931..24990, 24934..24993, 24935..24991, 25479..25580, 25481..25579, 25485..25571, 25852..25959, 25892..25954, 26032..26226, 26039..26212, 26095..26214, 26225..26287, 26226..26285, 26359..26547, 26370..26546, 26586..26765, 26607..26705, 26636..26716, 26936..27091, 26977..27096, 27427..27558, 27459..27515, 27552..27578, 27553..27579, 27669..27785, 27670..27777, 28890..29024, 28924..29100, 28929..29102, 28937..29098, 29362..29430, 29502..29573, 29504..29572, 29695..29841, 29696..29842, 29929..30012, 29930..30058, 31217..31372, 31237..31362, 31589..31729, 31602..31745, 31602..31706, 31604..31753, 31839..31946, 31840..31944, 32038..32154, 32082..32153, 32648..32854, 32689..32874, 33139..33207, 33140..33208, 33288..33413, 33292..33408, 33415..33441		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-

Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o5.ts	Method	TBLASTX:Soybean
Start	26039	End	26283
GI	none	Score	251
Exons	26039..26224, 26040..26216, 26041..26226, 26090..26230, 26225..26281, 26236..26283		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o5.tm	Method	TBLASTX:Maize
Start	26051	End	26461
GI	none	Score	346
Exons	26051..26287, 26053..26286, 26239..26304, 26317..26424, 26347..26421, 26351..26461, 26370..26423		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o9.ts	Method	TBLASTX:Soybean
Start	26425	End	26686
GI	none	Score	182
Exons	26425..26547, 26433..26546, 26625..26684, 26636..26686		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o10.tm	Method	TBLASTX:Maize
Start	26462	End	26781
GI	none	Score	94
Exons	26462..26536, 26463..26540, 26463..26546, 26464..26547, 26501..26548, 26588..26716, 26634..26768, 26637..26765, 26638..26781		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o4.ts	Method	TBLASTX:Soybean
Start	26930	End	32154
GI	none	Score	73
Exons	26930..27091, 31316..31384, 31602..31745, 31602..31748, 31839..31961, 31840..31962, 32082..32153, 32083..32154		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o4.tm	Method	TBLASTX:Maize
Start	26933	End	32962
GI	none	Score	69
Exons	26933..27091, 29798..29842, 29803..29835, 29929..30012, 29930..30058, 29945..30058, 31217..31384, 31219..31389, 31583..31735, 31583..31753, 31602..31745, 31839..31961, 31839..31964, 31840..31968, 32082..32153, 32083..32154, 32639..32701, 32642..32704, 32702..32962, 32702..32842, 32704..32928		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8

Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o9.tm	Method	TBLASTX:Maize
Start	27422	End	27777
GI	none	Score	100
Exons	27422..27553, 27427..27555, 27427..27525, 27429..27554, 27661..27777, 27664..27774, 27669..27773		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o7.ts	Method	TBLASTX:Soybean
Start	28967	End	31315
GI	none	Score	191
Exons	28967..29098, 28969..29100, 29362..29430, 29502..29573, 29504..29572, 29666..29827, 29695..29835, 29696..29842, 29929..30012, 29930..30058, 31217..31315, 31219..31305		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o8.ts	Method	TBLASTX:Soybean
Start	32639	End	32929
GI	none	Score	50
Exons	32639..32662, 32642..32716, 32696..32929, 32713..32928		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o11.tm	Method	TBLASTX:Maize
Start	33096	End	33413
GI	none	Score	53
Exons	33096..33206, 33098..33208, 33105..33164, 33137..33208, 33275..33382, 33281..33406, 33292..33405, 33292..33411, 33297..33413		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o6.tw	Method	TBLASTX:Wheat
Start	33140	End	33408
GI	none	Score	79
Exons	33140..33208, 33142..33207, 33292..33408, 33300..33407, 33313..33408		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o7.tm	Method	TBLASTX:Maize
Start	34576	End	35109
GI	none	Score	256
Exons	34576..34695, 34810..35109		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o4.tw	Method	TBLASTX:Wheat

Start	34972	End	35508
GI	none	Score	59
Exons	34972..35112, 35185..35508, 35186..35395		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o2.tm	Method	TBLASTX:Maize
Start	35185	End	35815
GI	none	Score	178
Exons	35185..35541, 35186..35509, 35538..35720, 35540..35815		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o6.ts	Method	TBLASTX:Soybean
Start	35413	End	35785
GI	none	Score	64
Exons	35413..35541, 35423..35542, 35526..35681, 35540..35785, 35540..35779		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o5.tw	Method	TBLASTX:Wheat
Start	35648	End	36031
GI	none	Score	60
Exons	35648..35905, 35649..35909, 35954..36031		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o3.tm	Method	TBLASTX:Maize
Start	36206	End	36772
GI	none	Score	70
Exons	36206..36532, 36233..36439, 36351..36452, 36521..36772		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o10.ts	Method	TBLASTX:Soybean
Start	36245	End	36490
GI	none	Score	219
Exons	36245..36490		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o3.tw	Method	TBLASTX:Wheat
Start	36398	End	36793
GI	none	Score	38
Exons	36398..36532, 36432..36527, 36518..36793, 36566..36700, 36630..36758		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138

Name	OJ990323_33.9A06.C8.o3.ts	Method	TBLASTX:Soybean
Start	36515	End	36881
GI	none	Score	86
Exons	36515..36862, 36566..36847, 36630..36881		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o6.tm	Method	TBLASTX:Maize
Start	36791	End	37202
GI	none	Score	48
Exons	36791..36913, 36824..36892, 36903..37202, 36904..37191		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o2.tw	Method	TBLASTX:Wheat
Start	36903	End	37328
GI	none	Score	192
Exons	36903..37328, 36904..37212		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o11.ts	Method	TBLASTX:Soybean
Start	36978	End	37182
GI	none	Score	79
Exons	36978..37181, 36979..37182		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o2.ts	Method	TBLASTX:Soybean
Start	42026	End	42543
GI	none	Score	124
Exons	42026..42115, 42027..42116, 42028..42129, 42039..42116, 42228..42347, 42228..42353, 42229..42354, 42229..42354, 42248..42376, 42300..42431, 42349..42543, 42351..42542		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o3.tc	Method	TBLASTX:Cress
Start	42237	End	42543
GI	none	Score	125
Exons	42237..42353, 42238..42354, 42349..42543, 42351..42542		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-
Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o8.tm	Method	TBLASTX:Maize
Start	42363	End	42543
GI	none	Score	90
Exons	42363..42458, 42363..42542, 42364..42543		

Seq. No.	905	Seq. ID	OJ990323_33.9A06.C8
Gene No.	1870	Strand	-

Start	47934	End	48138
Name	OJ990323_33.9A06.C8.o11.gs	Method	GENSCAN
Start	47934	End	48138
GI	none	Score	.72
Exons	47934..48089, 48133..48138		

Seq. No.	906	Seq. ID	OJ990323_33.9A06.C9
Gene No.	1871	Strand	+
Start	1	End	396
Name	OJ990323_33.9A06.C9.o1.np	Method	AAT/NAP
Start	1	End	396
GI	6815072	Score	277
Exons	1..396		
GI Descrip.	(AP001080) Similar to Arabidopsis thaliana chromosome II BAC T13P21; hypothetical protein (AC006067) [Oryza sativa]		

Seq. No.	907	Seq. ID	OJ990503_27.9A20.C1
Gene No.	1872	Strand	-
Start	234	End	865
Name	OJ990503_27.9A20.C1.o1.gs	Method	GENSCAN
Start	234	End	747
GI	none	Score	.51
Exons	234..747		

Seq. No.	907	Seq. ID	OJ990503_27.9A20.C1
Gene No.	1872	Strand	-
Start	234	End	865
Name	OJ990503_27.9A20.C1.o1.tm	Method	TBLASTX:Maize
Start	505	End	865
GI	none	Score	120
Exons	505..612, 527..619, 614..865, 614..685, 616..864		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1873	Strand	+
Start	403	End	1596
Name	OJ990503_27.9A20.C2.o1.gs	Method	GENSCAN
Start	403	End	1596
GI	none	Score	.82
Exons	403..777, 1498..1596		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1874	Strand	+
Start	8764	End	9382
Name	OJ990503_27.9A20.C2.o1.gp	Method	AAT/GAP
Start	8764	End	9382
GI	67814_1.R1084	Score	1126
Exons	8764..9382		
GI Descrip.	'3641868/emb|CAA09458| 1.0e-09 (AJ011012) hypothetical protein [Cicer arietinum]'		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1875	Strand	+
Start	11563	End	13537
Name	OJ990503_27.9A20.C2.o5.gs	Method	GENSCAN
Start	11563	End	13537
GI	none	Score	.48
Exons	11563..11575, 12853..13092, 13263..13537		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1876	Strand	+
Start	16722	End	16860
Name	OJ990503_27.9A20.C2.o6.gs	Method	GENSCAN
Start	16722	End	16860
GI	none	Score	.89
Exons	16722..16860		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1877	Strand	-
Start	1766	End	7368
Name	OJ990503_27.9A20.C2.o2.gs	Method	GENSCAN
Start	1766	End	7368
GI	none	Score	.49
Exons	1766..2118, 2426..2531, 2775..3091, 4566..4741, 6434..6614, 7281..7368		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1878	Strand	-
Start	9050	End	10579
Name	OJ990503_27.9A20.C2.o4.gs	Method	GENSCAN
Start	9050	End	10564
GI	none	Score	1
Exons	9050..10564		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1878	Strand	-
Start	9050	End	10579
Name	OJ990503_27.9A20.C2.o1.np	Method	AAT/NAP
Start	9053	End	10576
GI	6850873	Score	915
Exons	9053..10151, 10177..10270, 10355..10576		
GI Descrip.	(AL132959) putative protein [Arabidopsis thaliana]		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1878	Strand	-
Start	9050	End	10579
Name	OJ990503_27.9A20.C2.o2.gp	Method	AAT/GAP
Start	10272	End	10579
GI	2442784	Score	596
Exons	10272..10579		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1879	Strand	-
Start	16674	End	16909
Name	OJ990503_27.9A20.C2.o1.tc	Method	TBLASTX:Cress
Start	9038	End	10103
GI	none	Score	219
Exons	9038..9325, 9051..9323, 9320..9502, 9354..9467, 9503..9616, 9581..9841, 9588..9650, 9729..9839, 9851..10069, 9858..10103		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1879	Strand	-
Start	16674	End	16909
Name	OJ990503_27.9A20.C2.o2.tm	Method	TBLASTX:Maize
Start	9048	End	9511

GI	none	Score	563
Exons	9048..9290, 9050..9442, 9051..9437, 9416..9481, 9419..9511		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1879	Strand	-
Start	16674	End	16909
Name	OJ990503_27.9A20.C2.o2.ts	Method	TBLASTX:Soybean
Start	9053	End	9235
GI	none	Score	123
Exons	9053..9235, 9060..9218		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1879	Strand	-
Start	16674	End	16909
Name	OJ990503_27.9A20.C2.o1.ts	Method	TBLASTX:Soybean
Start	9254	End	10103
GI	none	Score	143
Exons	9254..9559, 9255..9467, 9581..9754, 9729..9755, 9767..9847, 9810..9848, 9854..10069, 9861..10103		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1879	Strand	-
Start	16674	End	16909
Name	OJ990503_27.9A20.C2.o1.tm	Method	TBLASTX:Maize
Start	9512	End	10048
GI	none	Score	53
Exons	9512..9559, 9522..9578, 9555..9665, 9569..10048, 9671..9718, 9726..10046		

Seq. No.	908	Seq. ID	OJ990503_27.9A20.C2
Gene No.	1879	Strand	-
Start	16674	End	16909
Name	OJ990503_27.9A20.C2.o2.np	Method	AAT/NAP
Start	16674	End	16909
GI	6069646	Score	246
Exons	16674..16909		
GI Descrip.	(AP000616) similar to putative reverse transcriptase (AC005315) [Oryza sativa] gi|6907112|dbj|BAA90639.1| (AP001129) Similar to Arabidopsis thaliana chromosome II BAC F9O13 genomic sequence, putative non-LTR retroelement reverse transcriptase. (AC006248) [Oryza sativa]		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1880	Strand	+
Start	285	End	1885
Name	OJ990503_27.9A20.C3.o1.gs	Method	GENSCAN
Start	285	End	1885
GI	none	Score	.77
Exons	285..360, 1407..1885		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1881	Strand	+
Start	22778	End	24014
Name	OJ990503_27.9A20.C3.o2.np	Method	AAT/NAP
Start	22778	End	24014
GI	5257266	Score	215
Exons	22778..23200, 23271..23646, 23715..24014		

GI Descrip. (AP000364) EST C99024(E4337) corresponds to a region of the predicted gene.; Similar to Silk moth; silkworm final instar larvae posterior. (D83241) [Oryza sativa]

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1882	Strand	+
Start	26465	End	28895
Name	OJ990503_27.9A20.C3.o7.gs	Method	GENSCAN
Start	26465	End	28866
GI	none	Score	.94
Exons	26465..26520, 26622..27917, 28023..28866		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1882	Strand	+
Start	26465	End	28895
Name	OJ990503_27.9A20.C3.o2.gp	Method	AAT/GAP
Start	26691	End	27045
GI	none	Score	651
Exons	26691..27045		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1882	Strand	+
Start	26465	End	28895
Name	OJ990503_27.9A20.C3.o3.np	Method	AAT/NAP
Start	26920	End	28895
GI	4262226	Score	469
Exons	26920..27528, 27637..27703, 28165..28895		
GI Descrip.	(AC006200) unknown protein [Arabidopsis thaliana]		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1883	Strand	+
Start	30742	End	31726
Name	OJ990503_27.9A20.C3.o8.gs	Method	GENSCAN
Start	30742	End	31726
GI	none	Score	.84
Exons	30742..31052, 31588..31726		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1884	Strand	+
Start	35747	End	39020
Name	OJ990503_27.9A20.C3.o10.gs	Method	GENSCAN
Start	35747	End	38744
GI	none	Score	.77
Exons	35747..36535, 37154..37264, 37352..37568, 37716..38049, 38206..38267, 38377..38450, 38739..38744		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1884	Strand	+
Start	35747	End	39020
Name	OJ990503_27.9A20.C3.o5.np	Method	AAT/NAP
Start	36239	End	38333
GI	2632019	Score	291
Exons	36239..36523, 37148..37264, 37352..37568, 37716..38049, 38206..38333		
GI Descrip.	(AJ002571) YkfB [Bacillus subtilis] gi|2633652|emb|CAB13155| (Z99110) similar to chloromuconate cycloisomerase [Bacillus subtilis]		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1884	Strand	+
Start	35747	End	39020
Name	OJ990503_27.9A20.C3.o4.gp	Method	AAT/GAP
Start	37810	End	39020
GI	9414_1.R1084	Score	1204
Exons	37810..38049, 38206..38267, 38377..38450, 38739..39020		
GI Descrip.	'1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence'		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1885	Strand	+
Start	44592	End	49972
Name	OJ990503_27.9A20.C3.o12.gs	Method	GENSCAN
Start	44592	End	49972
GI	none	Score	.53
Exons	44592..44763, 45263..45403, 45559..45682, 45815..45912, 47864..47958, 48064..48130, 48282..48339, 48472..48533, 48763..48995, 49104..49137, 49791..49972		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1886	Strand	-
Start	5985	End	10969
Name	OJ990503_27.9A20.C3.o3.gs	Method	GENSCAN
Start	5985	End	10969
GI	none	Score	.73
Exons	5985..6862, 6885..6964, 7030..7117, 8498..8686, 8812..8887, 10627..10682, 10750..10969		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1887	Strand	-
Start	12302	End	15257
Name	OJ990503_27.9A20.C3.o1.np	Method	AAT/NAP
Start	12302	End	15257
GI	6957723	Score	859
Exons	12302..12335, 13527..13608, 13719..13778, 13865..14053, 14447..14540, 14650..14759, 14863..14950, 15042..15257		
GI Descrip.	(AC021640) putative phosphatidate phosphohydrolase [Arabidopsis thaliana]		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1888	Strand	-
Start	19542	End	19859
Name	OJ990503_27.9A20.C3.o5.gs	Method	GENSCAN
Start	19542	End	19859
GI	none	Score	.81
Exons	19542..19859		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1889	Strand	-
Start	24254	End	24594
Name	OJ990503_27.9A20.C3.o1.gp	Method	AAT/GAP
Start	24254	End	24594
GI	15591_1.R1084	Score	370
Exons	24254..24292, 24361..24594		
GI Descrip.	'5257255/dbj|AP000364.1|AP000364 2.0e-14 Oryza sativa genomic		

DNA, chromosome 8, clone:P0026F07'

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1890	Strand	-
Start	28685	End	29766
Name	OJ990503_27.9A20.C3.o3.gp	Method	AAT/GAP
Start	28685	End	29766
GI	5266_1.R1084	Score	2082
Exons	28685..29766		
GI Descrip.	'6015437/dbj|AB008112.1|AB008112 1.0e-09 Homo sapiens PEX1 mRNA, complete cds'		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1891	Strand	-
Start	32536	End	35018
Name	OJ990503_27.9A20.C3.o4.np	Method	AAT/NAP
Start	32526	End	35018
GI	5596468	Score	295
Exons	32526..32699, 32836..32905, 32986..33127, 33325..33505, 33643..33691, 34937..35018		
GI Descrip.	(AL096882) putative protein [Arabidopsis thaliana]		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1891	Strand	-
Start	32536	End	35018
Name	OJ990503_27.9A20.C3.o9.gs	Method	GENSCAN
Start	32536	End	33824
GI	none	Score	.68
Exons	32536..32699, 32836..32905, 32986..33031, 33325..33505, 33716..33824		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1892	Strand	-
Start	40371	End	41983
Name	OJ990503_27.9A20.C3.o11.gs	Method	GENSCAN
Start	40371	End	41869
GI	none	Score	.99
Exons	40371..41671, 41776..41869		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1892	Strand	-
Start	40371	End	41983
Name	OJ990503_27.9A20.C3.o6.np	Method	AAT/NAP
Start	40719	End	41869
GI	6899650	Score	942
Exons	40719..40856, 40884..41671, 41776..41869		
GI Descrip.	(AC012189) ESTs gb|T42473, gb|Z37710 come from this gene. [Arabidopsis thaliana]		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1892	Strand	-
Start	40371	End	41983
Name	OJ990503_27.9A20.C3.o5.gp	Method	AAT/GAP
Start	41609	End	41983
GI	2280541	Score	486
Exons	41609..41671, 41776..41983		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o12.tm	Method	TBLASTX:Maize
Start	4175	End	33694
GI	none	Score	75
Exons	4175..4303, 32557..32712, 32837..32902, 32983..33120, 33327..33500, 33327..33503, 33328..33504, 33644..33694		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o2.tw	Method	TBLASTX:Wheat
Start	6105	End	51120
GI	none	Score	90
Exons	6105..6185, 6264..6449, 6286..6453, 50937..51029, 51067..51120		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o6.tm	Method	TBLASTX:Maize
Start	6183	End	51041
GI	none	Score	100
Exons	6183..6455, 6307..6462, 50937..51041		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o11.tm	Method	TBLASTX:Maize
Start	6684	End	50711
GI	none	Score	118
Exons	6684..6782, 6795..6965, 6796..6966, 50462..50611, 50463..50609, 50616..50711		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o3.tc	Method	TBLASTX:Cress
Start	13532	End	14009
GI	none	Score	111
Exons	13532..13609, 13705..13779, 13851..14009, 13861..13998		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o4.tm	Method	TBLASTX:Maize
Start	13544	End	15251
GI	none	Score	39
Exons	13544..13600, 13572..13601, 13729..13785, 13738..13761, 13860..14051, 13861..14052, 13872..14054, 14430..14537, 14446..14526, 14653..14760, 14656..14760, 14861..14926, 14861..14950, 15039..15251, 15045..15194		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o1.tw	Method	TBLASTX:Wheat

Start	13712	End	14021
GI	none	Score	45
Exons	13712..13780, 13714..13779, 13848..14021, 13864..14019		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o5.ts	Method	TBLASTX:Soybean
Start	13742	End	14523
GI	none	Score	44
Exons	13742..13783, 13860..14066, 13864..14064, 14457..14522, 14458..14523		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o4.ts	Method	TBLASTX:Soybean
Start	14666	End	15267
GI	none	Score	70
Exons	14666..14764, 14668..14760, 14861..14950, 14862..14951, 15039..15218, 15039..15251, 15043..15267		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o5.tc	Method	TBLASTX:Cress
Start	14861	End	15269
GI	none	Score	91
Exons	14861..14950, 15037..15216, 15039..15242, 15039..15269		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o10.tm	Method	TBLASTX:Maize
Start	23716	End	23996
GI	none	Score	91
Exons	23716..23811, 23718..23774, 23726..23809, 23755..23811, 23803..23916, 23812..23898, 23886..23939, 23887..23913, 23933..23986, 23943..23996		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o2.ts	Method	TBLASTX:Soybean
Start	26803	End	27168
GI	none	Score	97
Exons	26803..26865, 26805..26864, 26907..26975, 26907..27131, 26908..27168		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o2.tc	Method	TBLASTX:Cress
Start	26907	End	27168
GI	none	Score	322
Exons	26907..27116, 26908..27168		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o9.tm	Method	TBLASTX:Maize
Start	26908	End	27168
GI	none	Score	141
Exons	26908..27051, 26913..27011, 27054..27131, 27055..27168		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o3.tm	Method	TBLASTX:Maize
Start	27301	End	27702
GI	none	Score	271
Exons	27301..27486, 27303..27551, 27513..27608, 27514..27702, 27563..27700		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o1.tm	Method	TBLASTX:Maize
Start	28020	End	29327
GI	none	Score	153
Exons	28020..28124, 28021..28113, 28177..28203, 28264..28341, 28275..28340, 28277..28360, 28385..28477, 28411..28506, 28412..28486, 28413..28505, 28476..28520, 28477..28737, 28510..28554, 28566..28634, 28632..28682, 28648..28686, 28678..28797, 28678..28797, 28679..28798, 28680..28799, 28765..28842, 28802..28840, 28812..28841, 28874..29008, 28888..29007, 29216..29245, 29218..29250, 29274..29327, 29275..29325		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o6.tc	Method	TBLASTX:Cress
Start	33295	End	33506
GI	none	Score	71
Exons	33295..33504, 33333..33506		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o4.tc	Method	TBLASTX:Cress
Start	36200	End	36415
GI	none	Score	236
Exons	36200..36415, 36202..36411		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o3.ts	Method	TBLASTX:Soybean
Start	36202	End	37810
GI	none	Score	258
Exons	36202..36414, 36203..36415, 36488..36541, 36496..36549, 37156..37263, 37157..37267, 37346..37558, 37351..37563, 37352..37573, 37697..37810, 37718..37786		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o2.tm	Method	TBLASTX:Maize
Start	37350	End	38444
GI	none	Score	176
Exons	37350..37523, 37351..37566, 37352..37567, 37352..37567, 37697..38056, 37714..37998, 37715..38056, 38193..38270, 38201..38284, 38202..38267, 38375..38440, 38378..38440, 38382..38444		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o6.ts	Method	TBLASTX:Soybean
Start	37813	End	38441
GI	none	Score	299
Exons	37813..38052, 37814..38056, 38201..38284, 38203..38265, 38207..38266, 38375..38440, 38376..38441, 38376..38441		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o1.ts	Method	TBLASTX:Soybean
Start	41193	End	41854
GI	none	Score	68
Exons	41193..41276, 41241..41486, 41326..41466, 41535..41678, 41572..41673, 41771..41854, 41772..41843		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o1.tc	Method	TBLASTX:Cress
Start	41235	End	41848
GI	none	Score	76
Exons	41235..41390, 41323..41382, 41370..41438, 41532..41678, 41572..41673, 41771..41848, 41772..41843		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o5.tm	Method	TBLASTX:Maize
Start	41382	End	41842
GI	none	Score	114
Exons	41382..41543, 41382..41543, 41532..41675, 41544..41669, 41569..41676, 41771..41842, 41772..41837		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o7.ts	Method	TBLASTX:Soybean
Start	47102	End	52696
GI	none	Score	96
Exons	47102..47176, 51943..52026, 52021..52110, 52232..52339, 52248..52397, 52447..52539, 52448..52495, 52631..52696		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o8.tm	Method	TBLASTX:Maize
Start	47105	End	52687
GI	none	Score	83
Exons	47105..47188, 52033..52134, 52259..52339, 52278..52340, 52447..52530, 52448..52531, 52628..52687		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o13.gs	Method	GENSCAN
Start	51901	End	54396
GI	none	Score	.85
Exons	51901..52340, 52651..52877, 53752..53969, 54274..54396		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o7.np	Method	AAT/NAP
Start	51922	End	54772
GI	6899649	Score	468
Exons	51922..52142, 52245..52340, 52451..52536, 52631..52916, 53785..53948, 54256..54343, 54639..54772		
GI Descrip.	(AC012189) T15D22.8 [Arabidopsis thaliana]		

Seq. No.	909	Seq. ID	OJ990503_27.9A20.C3
Gene No.	1893	Strand	-
Start	51901	End	54772
Name	OJ990503_27.9A20.C3.o7.tm	Method	TBLASTX:Maize
Start	53751	End	53981
GI	none	Score	130
Exons	53751..53930, 53751..53951, 53752..53943, 53786..53953, 53928..53981		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1894	Strand	+
Start	79	End	992
Name	OJ990503_27.9A20.C4.o1.gs	Method	GENSCAN
Start	79	End	992
GI	none	Score	.88
Exons	79..211, 462..626, 805..992		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1895	Strand	+
Start	12977	End	13687
Name	OJ990503_27.9A20.C4.o5.gs	Method	GENSCAN
Start	12977	End	13687
GI	none	Score	.66
Exons	12977..13084, 13604..13687		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1896	Strand	-
Start	918	End	16839
Name	OJ990503_27.9A20.C4.o1.np	Method	AAT/NAP
Start	918	End	16839

GI	5669663	Score	720
Exons	918..1038, 6685..7626, 10263..10392, 10565..10659, 11182..11246, 16165..16839		
GI Descrip.	(AF100765) receptor-like kinase [Oryza sativa]		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1896	Strand	-
Start	918	End	16839
Name	OJ990503_27.9A20.C4.o1.gp	Method	AAT/GAP
Start	1199	End	1842
GI	5002997	Score	919
Exons	1199..1431, 1544..1842		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1896	Strand	-
Start	918	End	16839
Name	OJ990503_27.9A20.C4.o2.gs	Method	GENSCAN
Start	1528	End	5213
GI	none	Score	.88
Exons	1528..2233, 2291..2765, 2964..2999, 4454..5213		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1896	Strand	-
Start	918	End	16839
Name	OJ990503_27.9A20.C4.o2.gp	Method	AAT/GAP
Start	4802	End	5206
GI	5002996	Score	785
Exons	4802..5206		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1896	Strand	-
Start	918	End	16839
Name	OJ990503_27.9A20.C4.o3.gs	Method	GENSCAN
Start	5693	End	10019
GI	none	Score	.66
Exons	5693..6035, 6679..6781, 6839..7588, 9251..10019		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1896	Strand	-
Start	918	End	16839
Name	OJ990503_27.9A20.C4.o4.gs	Method	GENSCAN
Start	10862	End	12375
GI	none	Score	.78
Exons	10862..11074, 11239..11553, 12373..12375		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o1.ts	Method	TBLASTX:Soybean
Start	1627	End	22035
GI	none	Score	211
Exons	1627..1746, 1876..2226, 1952..2203, 2293..2628, 2296..2421, 2306..2605, 6687..6845, 6699..6812, 6748..6855, 6790..7263, 6801..7268, 6863..7279, 7269..7646, 7311..7634, 21076..21234, 21089..21232, 21190..21657, 21328..21603, 21371..21652, 21658..22035, 21680..21871, 21687..21911, 21688..22023		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o3.tw	Method	TBLASTX:Wheat
Start	1627	End	21411
GI	none	Score	57
Exons	1627..1746, 1645..1737, 1825..1872, 1909..1974, 6687..6815, 6699..6860, 6748..6855, 6879..7022, 6939..6992, 6952..7014, 21076..21243, 21088..21249, 21268..21411, 21328..21381		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o2.tm	Method	TBLASTX:Maize
Start	1627	End	21408
GI	none	Score	80
Exons	1627..1722, 1627..1746, 1882..1974, 1897..1965, 6684..6836, 6687..6803, 6846..7019, 6892..7017, 21073..21225, 21253..21408		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o1.tc	Method	TBLASTX:Cress
Start	1633	End	21969
GI	none	Score	145
Exons	1633..1749, 1855..2220, 1909..2175, 1952..2221, 2299..2484, 2300..2485, 2488..2589, 2489..2569, 6702..6845, 6876..6920, 6933..7301, 6937..7263, 7293..7481, 7312..7482, 7468..7521, 7482..7580, 21091..21234, 21265..21309, 21322..21678, 21330..21572, 21340..21597, 21371..21652, 21682..21870, 21689..21871, 21871..21969		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o1.tm	Method	TBLASTX:Maize
Start	1978	End	22011
GI	none	Score	156
Exons	1978..2220, 1979..2221, 2290..2478, 2294..2479, 2492..2674, 2494..2628, 7020..7292, 7033..7272, 7287..7472, 7291..7524, 7312..7473, 7473..7622, 21409..21681, 21422..21661, 21676..21861, 21689..21862, 21862..22011		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o1.tw	Method	TBLASTX:Wheat
Start	1981	End	21808
GI	none	Score	90
Exons	1981..2229, 2060..2203, 2296..2424, 2306..2398, 7026..7418, 7102..7245, 7312..7419, 21415..21807, 21491..21634, 21689..21808		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o2.tw	Method	TBLASTX:Wheat
Start	2425	End	21991

GI	none	Score	219
Exons	2425..2607, 2426..2608, 2426..2608, 7422..7601, 7429..7485, 7549..7602, 21811..21990, 21818..21874, 21938..21991		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o3.np	Method	AAT/NAP
Start	19450	End	23254
GI	6721547	Score	85
Exons	19450..19487, 23163..23254		
GI Descrip.	(AP001073) Similar to Oryza sativa gene for Pib. (AB013448)		

Seq. No.	910	Seq. ID	OJ990503_27.9A20.C4
Gene No.	1897	Strand	-
Start	19450	End	23254
Name	OJ990503_27.9A20.C4.o2.np	Method	AAT/NAP
Start	21074	End	22015
GI	5669663	Score	699
Exons	21074..22015		
GI Descrip.	(AF100765) receptor-like kinase [Oryza sativa]		

Seq. No.	911	Seq. ID	OJ990503_27.9A20.C5
Gene No.	1898	Strand	-
Start	1195	End	2019
Name	OJ990503_27.9A20.C5.o1.gs	Method	GENSCAN
Start	1195	End	2019
GI	none	Score	.4
Exons	1195..1205, 1905..2019		

Seq. No.	911	Seq. ID	OJ990503_27.9A20.C5
Gene No.	1899	Strand	-
Start	4517	End	4686
Name	OJ990503_27.9A20.C5.o2.gs	Method	GENSCAN
Start	4517	End	4686
GI	none	Score	.97
Exons	4517..4686		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1900	Strand	+
Start	9437	End	10078
Name	OJ990503_27.9A20.C6.o2.gs	Method	GENSCAN
Start	9437	End	10078
GI	none	Score	.73
Exons	9437..9485, 9706..9790, 9832..9940, 10034..10078		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1901	Strand	-
Start	3483	End	8814
Name	OJ990503_27.9A20.C6.o1.gs	Method	GENSCAN
Start	3483	End	8814
GI	none	Score	.5
Exons	3483..3586, 3678..4391, 5626..5647, 5728..5784, 5848..5902, 5946..6064, 6430..7112, 7188..7254, 8743..8814		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1901	Strand	-

Start	3483	End	8814
Name	OJ990503_27.9A20.C6.o1.gp	Method	AAT/GAP
Start	4823	End	4884
GI	2312838	Score	72
Exons	4823..4884		
GI Descrip.	1420932/gb|U61383|ORU61383 7.0e-21 Oryza rufipogon 4-coumarate-CoA ligase gene, intron 1, partial sequence		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o2.tm	Method	TBLASTX:Maize
Start	10323	End	10681
GI	none	Score	74
Exons	10323..10457, 10444..10500, 10576..10680, 10577..10681		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o1.ts	Method	TBLASTX:Soybean
Start	10359	End	11397
GI	none	Score	80
Exons	10359..10448, 10360..10440, 10362..10448, 10447..10518, 10448..10516, 10567..10923, 10600..10890, 10604..10909, 10763..10927, 10951..11397, 10955..11245		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o1.tc	Method	TBLASTX:Cress
Start	10362	End	11247
GI	none	Score	249
Exons	10362..10475, 10447..10524, 10537..10596, 10576..10923, 10577..10933, 10607..10927, 10948..11103, 10957..11145, 10958..11146, 11146..11247, 11147..11242		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o3.gs	Method	GENSCAN
Start	10423	End	16061
GI	none	Score	.67
Exons	10423..11018, 11184..11384, 11692..11733, 12191..12322, 12809..13202, 13309..13601, 15830..16061		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o1.tm	Method	TBLASTX:Maize
Start	10684	End	11283
GI	none	Score	130
Exons	10684..10923, 10688..10927, 10760..10927, 10937..11137, 10951..11136, 11137..11283, 11138..11251		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619

Name	OJ990503_27.9A20.C6.o1.tw	Method	TBLASTX:Wheat
Start	10687	End	11083
GI	none	Score	78
Exons	10687..11082, 10757..10849, 10771..10905, 10880..11083		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o2.tw	Method	TBLASTX:Wheat
Start	11084	End	11265
GI	none	Score	145
Exons	11084..11251, 11086..11265, 11087..11260		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o2.gp	Method	AAT/GAP
Start	14126	End	14437
GI	72524_1.R1084	Score	435
Exons	14126..14437		
GI Descrip.	'5091496/dbj|AB023482.2|AB023482 3.0e-84 Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence'		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o1.np	Method	AAT/NAP
Start	15811	End	23619
GI	5091513	Score	2011
Exons	15811..16118, 16801..17169, 18005..19547, 23203..23619		
GI Descrip.	(AB023482) Hypothetical protein [Oryza sativa]		

Seq. No.	912	Seq. ID	OJ990503_27.9A20.C6
Gene No.	1902	Strand	-
Start	10423	End	23619
Name	OJ990503_27.9A20.C6.o3.gp	Method	AAT/GAP
Start	22030	End	22445
GI	3061177	Score	532
Exons	22030..22365, 22423..22445		
GI Descrip.	5679837/emb|AJ243961.1|OSA243961 2.0e-12 Oryza sativa chromosome 4 BAC 11332 genomic sequences		

Seq. No.	913	Seq. ID	OJ990503_27.9A20.C7
Gene No.	1903	Strand	-
Start	444	End	1731
Name	OJ990503_27.9A20.C7.o1.gs	Method	GENSCAN
Start	444	End	1716
GI	none	Score	.63
Exons	444..713, 1431..1494, 1583..1716		

Seq. No.	913	Seq. ID	OJ990503_27.9A20.C7
Gene No.	1903	Strand	-
Start	444	End	1731
Name	OJ990503_27.9A20.C7.o1.np	Method	AAT/NAP
Start	1528	End	1731
GI	5523856	Score	113
Exons	1528..1731		

GI Descrip. (AF085166) receptor-like kinase [Hordeum vulgare]

Seq. No.	914	Seq. ID	OJ990503_27.9A20.C8
Gene No.	1904	Strand	+
Start	108	End	167
Name	OJ990503_27.9A20.C8.o1.np	Method	AAT/NAP
Start	108	End	167
GI	2498930	Score	49
Exons	108..167		

GI Descrip. DORSAL-VENTRAL PATTERNING PROTEIN SOG (SHORT GASTRULATION PROTEIN) gi|1203794 (U18774) Sog [Drosophila melanogaster]

Seq. No.	914	Seq. ID	OJ990503_27.9A20.C8
Gene No.	1905	Strand	+
Start	108	End	167
Name	OJ990503_27.9A20.C8.o1.gs	Method	GENSCAN
Start	108	End	167
GI	none	Score	.99
Exons	108..167		

Seq. No.	915	Seq. ID	OJ990503_27.9A20.C9
Gene No.	1906	Strand	-
Start	16	End	380
Name	OJ990503_27.9A20.C9.o1.gs	Method	GENSCAN
Start	16	End	380
GI	none	Score	.99
Exons	16..193, 293..380		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1907	Strand	+
Start	8444	End	8872
Name	OJ990323_29.9A15.C1.o4.gp	Method	AAT/GAP
Start	8444	End	8872
GI	none	Score	745
Exons	8444..8872		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1908	Strand	+
Start	10585	End	14928
Name	OJ990323_29.9A15.C1.o2.np	Method	AAT/NAP
Start	10521	End	14928
GI	2961349	Score	1586
Exons	10521..10764, 10867..11131, 11737..12061, 12110..13054, 13379..14928		

GI Descrip. (AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1908	Strand	+
Start	10585	End	14928
Name	OJ990323_29.9A15.C1.o3.gs	Method	GENSCAN
Start	10585	End	14922
GI	none	Score	.73
Exons	10585..11707, 11810..12009, 12515..12810, 13104..13211, 13213..14237, 14324..14922		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1

Gene No.	1909	Strand	-
Start	1	End	3761
Name	OJ990323_29.9A15.C1.o1.np	Method	AAT/NAP
Start	1	End	3761
GI	6223639	Score	1422
Exons	1..133, 272..446, 550..677, 778..996, 1074..1203, 1648..1714, 1832..1926, 2020..2091, 2166..2221, 2314..2383, 2472..2574, 2653..2749, 3272..3560, 3651..3761		
GI Descrip.	(AC011698) putative casein kinase [Arabidopsis thaliana]		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1909	Strand	-
Start	1	End	3761
Name	OJ990323_29.9A15.C1.o1.gs	Method	GENSCAN
Start	272	End	3577
GI	none	Score	.81
Exons	272..446, 550..689, 778..910, 1648..1714, 2226..2383, 2472..2545, 2636..2749, 3272..3577		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1909	Strand	-
Start	1	End	3761
Name	OJ990323_29.9A15.C1.o1.gp	Method	AAT/GAP
Start	403	End	1116
GI	943_1.R1084	Score	731
Exons	403..446, 550..689, 778..996, 1074..1116		
GI Descrip.	'6006848/gb|AAF00624.1|AC009540_1 3.0e-50 (AC009540) unknown protein, 5'' partial [Arabidopsis thaliana]'		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1909	Strand	-
Start	1	End	3761
Name	OJ990323_29.9A15.C1.o2.gp	Method	AAT/GAP
Start	1070	End	2223
GI	736_1.R1084	Score	737
Exons	1070..1203, 1648..1714, 1832..1926, 2020..2091, 2166..2223		
GI Descrip.	'3643611 7.0e-71 (AC005395) putative casein kinase [Arabidopsis thaliana]'		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1909	Strand	-
Start	1	End	3761
Name	OJ990323_29.9A15.C1.o3.gp	Method	AAT/GAP
Start	2327	End	3373
GI	63395_1.R1084	Score	797
Exons	2327..2383, 2472..2749, 3272..3373		
GI Descrip.	'3643611 5.0e-26 (AC005395) putative casein kinase [Arabidopsis thaliana]'		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1910	Strand	-
Start	10043	End	10188
Name	OJ990323_29.9A15.C1.o5.gp	Method	AAT/GAP
Start	10043	End	10188
GI	none	Score	201
Exons	10043..10188		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1911	Strand	-
Start	14402	End	15070
Name	OJ990323_29.9A15.C1.o6.gp	Method	AAT/GAP
Start	14402	End	15070
GI	none	Score	205
Exons	14402..14428, 14936..15070		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o1.tm	Method	TBLASTX:Maize
Start	27	End	2531
GI	none	Score	95
Exons	27..134, 41..136, 44..136, 268..447, 270..422, 281..448, 285..449, 293..454, 540..653, 547..654, 621..677, 775..999, 776..997, 1074..1199, 1074..1208, 1081..1209, 1647..1715, 1648..1716, 1833..1934, 1837..1926, 2013..2090, 2014..2145, 2177..2221, 2180..2221, 2308..2394, 2309..2386, 2472..2531, 2474..2530		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o1.ts	Method	TBLASTX:Soybean
Start	27	End	2752
GI	none	Score	94
Exons	27..134, 41..133, 281..448, 288..449, 299..472, 540..656, 547..645, 775..999, 776..997, 1072..1206, 1074..1208, 1075..1206, 1647..1715, 1827..1925, 1834..1923, 1837..1929, 2013..2093, 2014..2169, 2164..2217, 2177..2221, 2308..2394, 2474..2545, 2478..2546, 2663..2752, 2670..2750		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o6.tc	Method	TBLASTX:Cress
Start	39	End	409
GI	none	Score	91
Exons	39..134, 41..136, 41..136, 270..404, 281..409, 291..404, 293..409		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o1.tc	Method	TBLASTX:Cress
Start	410	End	1691
GI	none	Score	44
Exons	410..448, 411..449, 540..647, 547..648, 618..692, 761..988, 775..999, 779..997, 1070..1183, 1072..1200, 1074..1202, 1074..1208, 1081..1206, 1647..1691		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o1.tw	Method	TBLASTX:Wheat
Start	778	End	1103

GI	none	Score	268
Exons	778..999, 779..997, 780..998, 1074..1103		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o2.tc	Method	TBLASTX:Cress
Start	1827	End	2501
GI	none	Score	101
Exons	1827..1925, 1834..1923, 1837..1926, 2013..2090, 2014..2127, 2177..2221, 2181..2240, 2308..2394, 2309..2389, 2474..2500, 2478..2501		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o5.tm	Method	TBLASTX:Maize
Start	8706	End	15188
GI	none	Score	83
Exons	8706..8807, 8706..8810, 8707..8808, 8708..8812, 8991..9038, 8993..9058, 8997..9038, 9126..9230, 9126..9230, 9128..9232, 9309..9356, 9312..9356, 9313..9357, 9313..9363, 9503..9580, 9503..9589, 9516..9590, 9679..9777, 9681..9779, 9870..9917, 9871..9918, 9875..9940, 15123..15188, 15125..15187		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o2.tw	Method	TBLASTX:Wheat
Start	11718	End	12090
GI	none	Score	114
Exons	11718..11855, 11737..11865, 11836..12078, 11872..12090, 11879..12079		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o7.tm	Method	TBLASTX:Maize
Start	11987	End	12327
GI	none	Score	126
Exons	11987..12082, 11989..12081, 12147..12248, 12154..12249, 12247..12327		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o5.tc	Method	TBLASTX:Cress
Start	12154	End	12432
GI	none	Score	47
Exons	12154..12174, 12250..12432, 12313..12432		

Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o5.tw	Method	TBLASTX:Wheat
Start	12325	End	12757
GI	none	Score	95

Exons	12325..12501, 12494..12757		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o3.tm	Method	TBLASTX:Maize
Start	12361	End	13000
GI	none	Score	90
Exons	12361..12435, 12494..12748, 12776..13000		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o4.ts	Method	TBLASTX:Soybean
Start	12539	End	13000
GI	none	Score	291
Exons	12539..13000		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o3.tc	Method	TBLASTX:Cress
Start	12563	End	12997
GI	none	Score	287
Exons	12563..12997, 12706..12984		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o4.tw	Method	TBLASTX:Wheat
Start	12784	End	13081
GI	none	Score	317
Exons	12784..13023, 12785..13081		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o3.ts	Method	TBLASTX:Soybean
Start	13397	End	13903
GI	5509260	Score	332
Exons	13397..13813, 13820..13903		
GI Descrip.	-		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o4.tc	Method	TBLASTX:Cress
Start	13532	End	13792
GI	none	Score	286
Exons	13532..13792, 13537..13758, 13544..13792		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o3.tw	Method	TBLASTX:Wheat
Start	13574	End	14101
GI	none	Score	215

Exons	13574..13816, 13591..13701, 13820..13912, 13970..14101		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o4.tm	Method	TBLASTX:Maize
Start	13574	End	14017
GI	none	Score	199
Exons	13574..13801, 13820..14017		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o6.tw	Method	TBLASTX:Wheat
Start	14105	End	14505
GI	none	Score	71
Exons	14105..14239, 14252..14320, 14320..14505		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o2.tm	Method	TBLASTX:Maize
Start	14243	End	15027
GI	none	Score	67
Exons	14243..14317, 14317..14676, 14526..14663, 14685..14855, 14686..14913, 14974..15027		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o2.ts	Method	TBLASTX:Soybean
Start	14273	End	14913
GI	none	Score	64
Exons	14273..14320, 14320..14913, 14448..14768		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o4.gs	Method	GENSCAN
Start	15675	End	15974
GI	none	Score	.83
Exons	15675..15698, 15731..15829, 15912..15974		
Seq. No.	916	Seq. ID	OJ990323_29.9A15.C1
Gene No.	1912	Strand	-
Start	15675	End	16019
Name	OJ990323_29.9A15.C1.o6.tm	Method	TBLASTX:Maize
Start	15725	End	16019
GI	none	Score	108
Exons	15725..15829, 15728..15838, 15733..15843, 15775..15843, 15896..15979, 15909..15980, 15911..15985, 15912..16019		
Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1913	Strand	+
Start	10436	End	13977
Name	OJ990323_29.9A15.C2.o3.gs	Method	GENSCAN
Start	10436	End	13977

GI	none	Score	.93
Exons	10436..11252, 11350..12470, 12564..12752, 12781..13364, 13815..13977		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1914	Strand	-
Start	1	End	3677
Name	OJ990323_29.9A15.C2.o1.np	Method	AAT/NAP
Start	1	End	3677
GI	6598515	Score	436
Exons	1..62, 289..467, 554..628, 1737..1940, 2071..2148, 2239..2301, 2400..3009, 3086..3170, 3250..3330, 3650..3677		
GI Descrip.	(AC006081) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1914	Strand	-
Start	1	End	3677
Name	OJ990323_29.9A15.C2.o1.gs	Method	GENSCAN
Start	396	End	3677
GI	none	Score	.88
Exons	396..467, 554..628, 719..775, 2071..2148, 2400..3038, 3230..3330, 3650..3677		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1915	Strand	-
Start	7621	End	8083
Name	OJ990323_29.9A15.C2.o2.tm	Method	TBLASTX:Maize
Start	396	End	1862
GI	none	Score	88
Exons	396..467, 396..467, 397..468, 536..631, 554..628, 716..778, 717..776, 719..778, 1735..1848, 1782..1862, 1782..1862		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1915	Strand	-
Start	7621	End	8083
Name	OJ990323_29.9A15.C2.o1.ts	Method	TBLASTX:Soybean
Start	438	End	2149
GI	none	Score	115
Exons	438..467, 554..589, 584..628, 719..778, 1750..1860, 1785..1949, 1795..1941, 1809..1943, 1844..1951, 2064..2147, 2071..2148, 2096..2149		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1915	Strand	-
Start	7621	End	8083
Name	OJ990323_29.9A15.C2.o1.tm	Method	TBLASTX:Maize
Start	1865	End	2610
GI	none	Score	88
Exons	1865..1942, 1866..1943, 1867..1941, 2041..2148, 2059..2148, 2076..2150, 2231..2296, 2254..2304, 2399..2584, 2400..2585, 2400..2585, 2401..2610		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1915	Strand	-
Start	7621	End	8083
Name	OJ990323_29.9A15.C2.o3.np	Method	AAT/NAP
Start	7621	End	8083

GI	3643605	Score	224
Exons	7621..8083		
GI Descrip.	(AC005395) hypothetical protein [Arabidopsis thaliana]		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1915	Strand	-
Start	7621	End	8083
Name	OJ990323_29.9A15.C2.o1.tc	Method	TBLASTX:Cress
Start	7765	End	7962
GI	none	Score	111
Exons	7765..7962, 7769..7960		

Seq. No.	917	Seq. ID	OJ990323_29.9A15.C2
Gene No.	1915	Strand	-
Start	7621	End	8083
Name	OJ990323_29.9A15.C2.o3.tm	Method	TBLASTX:Maize
Start	7786	End	7965
GI	none	Score	121
Exons	7786..7965, 7799..7954		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o1.gs	Method	GENSCAN
Start	1109	End	3238
GI	none	Score	.88
Exons	1109..3238		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o1.np	Method	AAT/NAP
Start	1112	End	3270
GI	4378066	Score	1724
Exons	1112..3270		
GI Descrip.	(AF098806) polyprotein [Sorghum bicolor] gi|4680208|gb|AAD27571.1|AF114171_12 (AF114171) polyprotein [Sorghum bicolor]		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o4.tw	Method	TBLASTX:Wheat
Start	1127	End	1717
GI	none	Score	72
Exons	1127..1246, 1442..1573, 1449..1574, 1584..1670, 1593..1682, 1601..1711, 1613..1717		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o3.tm	Method	TBLASTX:Maize
Start	1439	End	1675
GI	none	Score	143
Exons	1439..1675, 1467..1658		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3

Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o1.ts	Method	TBLASTX:Soybean
Start	1691	End	2066
GI	none	Score	66
Exons	1691..1915, 1916..2038, 1923..2066		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o2.tm	Method	TBLASTX:Maize
Start	1707	End	1876
GI	none	Score	145
Exons	1707..1871, 1709..1876, 1731..1874		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o1.tw	Method	TBLASTX:Wheat
Start	1838	End	2227
GI	none	Score	68
Exons	1838..2227, 1917..2030, 2064..2186		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o1.tm	Method	TBLASTX:Maize
Start	1877	End	2335
GI	none	Score	184
Exons	1877..2335, 1878..2231		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o2.tw	Method	TBLASTX:Wheat
Start	2529	End	2944
GI	none	Score	69
Exons	2529..2747, 2531..2941, 2829..2936, 2843..2944		

Seq. No.	918	Seq. ID	OJ990323_29.9A15.C3
Gene No.	1916	Strand	-
Start	1109	End	3270
Name	OJ990323_29.9A15.C3.o3.tw	Method	TBLASTX:Wheat
Start	2945	End	3266
GI	none	Score	54
Exons	2945..3133, 2946..3128, 3140..3259, 3141..3266		

Seq. No.	919	Seq. ID	OJ990323_29.9A15.C4
Gene No.	1917	Strand	-
Start	1	End	1064
Name	OJ990323_29.9A15.C4.o1.np	Method	AAT/NAP
Start	1	End	433
GI	4378066	Score	248
Exons	1..433		
GI Descrip.	(AF098806) polyprotein [Sorghum bicolor] gi|4680208|gb|AAD27571.1|AF114171_12 (AF114171) polyprotein [Sorghum bicolor]		

Seq. No.	919	Seq. ID	OJ990323_29.9A15.C4
Gene No.	1917	Strand	-
Start	1	End	1064
Name	OJ990323_29.9A15.C4.o1.gs	Method	GENSCAN
Start	39	End	1064
GI	none	Score	.77
Exons	39..1064		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1918	Strand	+
Start	466	End	13245
Name	OJ990323_29.9A15.C5.o1.gs	Method	GENSCAN
Start	466	End	8673
GI	none	Score	.78
Exons	466..683, 1892..2090, 2345..2635, 3706..4511, 4618..5203, 5304..5434, 5443..5609, 6216..6448, 6525..6571, 7079..7309, 7314..7627, 7776..7845, 7994..8228, 8234..8268, 8557..8673		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1918	Strand	+
Start	466	End	13245
Name	OJ990323_29.9A15.C5.o1.gp	Method	AAT/GAP
Start	5080	End	5775
GI	48729_1.R1084	Score	1148
Exons	5080..5203, 5304..5775		
GI Descrip.	'4519615/dbj|BAA75667.1| 5.0e-09 (AB017594) RPE65 [Gallus gallus]'		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1918	Strand	+
Start	466	End	13245
Name	OJ990323_29.9A15.C5.o1.np	Method	AAT/NAP
Start	6935	End	13242
GI	6498441	Score	3146
Exons	6935..6963, 9954..10162, 10346..10480, 10653..11297, 11484..12867, 12961..13242		
GI Descrip.	(AP000815) EST C72786(E2258) corresponds to a region of the predicted gene.; Similar to Sorghum bicolor Gypsy-Ty3 type retrotransposon RetroSor1. (AF098806) [Oryza sativa]		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1918	Strand	+
Start	466	End	13245
Name	OJ990323_29.9A15.C5.o2.gs	Method	GENSCAN
Start	9204	End	13245
GI	none	Score	.45
Exons	9204..9272, 10023..10491, 10777..10911, 11237..11512, 11756..12155, 12410..12455, 12475..13245		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1919	Strand	-
Start	13459	End	17644
Name	OJ990323_29.9A15.C5.o3.gs	Method	GENSCAN
Start	13459	End	17644
GI	none	Score	.42
Exons	13459..13686, 13970..14320, 14329..14460, 14485..14844,		

14962..15537, 15730..15881, 16103..17470, 17566..17644

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1919	Strand	-
Start	13459	End	17644
Name	OJ990323_29.9A15.C5.o2.np	Method	AAT/NAP
Start	13961	End	17411
GI	6907089	Score	1900
Exons	13961..14604, 14674..14877, 14992..15596, 15666..16022, 16058..16393, 16424..17411		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o5.tm	Method	TBLASTX:Maize
Start	3957	End	4169
GI	none	Score	65
Exons	3957..4007, 3959..4027, 4008..4169, 4010..4168		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o2.tm	Method	TBLASTX:Maize
Start	10002	End	10283
GI	none	Score	339
Exons	10002..10283, 10004..10273, 10050..10283		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o7.tw	Method	TBLASTX:Wheat
Start	10002	End	10151
GI	none	Score	231
Exons	10002..10151, 10013..10150		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o1.tw	Method	TBLASTX:Wheat
Start	10152	End	10571
GI	none	Score	451
Exons	10152..10571, 10154..10558		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o3.tm	Method	TBLASTX:Maize
Start	10310	End	10692
GI	none	Score	255
Exons	10310..10585, 10311..10586, 10585..10692		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o2.ts	Method	TBLASTX:Soybean
Start	10362	End	10580

GI	none	Score	188
Exons	10362..10580, 10463..10579		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o8.tw	Method	TBLASTX:Wheat
Start	10584	End	10895
GI	none	Score	140
Exons	10584..10673, 10585..10737, 10761..10895		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o5.tw	Method	TBLASTX:Wheat
Start	11164	End	11613
GI	none	Score	222
Exons	11164..11388, 11235..11390, 11257..11394, 11466..11612, 11473..11613		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o9.tw	Method	TBLASTX:Wheat
Start	11668	End	11955
GI	none	Score	190
Exons	11668..11955		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o1.tm	Method	TBLASTX:Maize
Start	12087	End	12435
GI	none	Score	346
Exons	12087..12422, 12112..12435		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o4.tw	Method	TBLASTX:Wheat
Start	12249	End	12617
GI	none	Score	338
Exons	12249..12494, 12250..12603, 12418..12591, 12525..12617		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o3.tw	Method	TBLASTX:Wheat
Start	12625	End	13233
GI	none	Score	370
Exons	12625..13077, 12774..12923, 13108..13233		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o7.tm	Method	TBLASTX:Maize
Start	12847	End	13110

GI	none	Score	220
Exons	12847..13110		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o4.gs	Method	GENSCAN
Start	19984	End	22876
GI	none	Score	.78
Exons	19984..20181, 20311..20367, 20508..20595, 20754..20869, 20918..21064, 21243..21299, 21734..21890, 22853..22876		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o2.tw	Method	TBLASTX:Wheat
Start	20059	End	21003
GI	none	Score	160
Exons	20059..20199, 20060..20200, 20060..20200, 20308..20385, 20309..20371, 20500..20598, 20505..20600, 20508..20600, 20675..20749, 20676..20801, 20918..21001, 20919..20996, 20920..20997, 20923..21003		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o3.np	Method	AAT/NAP
Start	20435	End	22936
GI	3688172	Score	749
Exons	20435..20595, 20678..20748, 20918..21064, 21352..21477, 21734..21900, 22086..22224, 22676..22936		
GI Descrip.	(AL031804) putative protein [Arabidopsis thaliana]		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o4.gp	Method	AAT/GAP
Start	20545	End	21301
GI	426919	Score	569
Exons	20545..20595, 20678..20748, 20918..21064, 21243..21301		
GI Descrip.	3688172/emb|CAA21200| 3.0e-24 (AL031804) putative protein [Arabidopsis thaliana]		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o6.tw	Method	TBLASTX:Wheat
Start	21393	End	21995
GI	none	Score	98
Exons	21393..21476, 21393..21476, 21395..21478, 21731..21889, 21734..21892, 21975..21995		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o6.tm	Method	TBLASTX:Maize
Start	21731	End	21995

GI	none	Score	118
Exons	21731..21883, 21732..21887, 21733..21891, 21734..21892, 21968..21994, 21969..21995		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o4.tm	Method	TBLASTX:Maize
Start	22160	End	22891
GI	none	Score	94
Exons	22160..22225, 22168..22224, 22674..22805, 22676..22804, 22676..22807, 22802..22891, 22802..22885, 22803..22886		

Seq. No.	920	Seq. ID	OJ990323_29.9A15.C5
Gene No.	1920	Strand	-
Start	19984	End	22936
Name	OJ990323_29.9A15.C5.o1.ts	Method	TBLASTX:Soybean
Start	22665	End	22897
GI	none	Score	121
Exons	22665..22895, 22673..22897, 22674..22877, 22676..22885		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1921	Strand	+
Start	5411	End	9055
Name	OJ990323_29.9A15.C6.o2.gs	Method	GENSCAN
Start	5411	End	8119
GI	none	Score	.78
Exons	5411..5498, 7794..8119		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1921	Strand	+
Start	5411	End	9055
Name	OJ990323_29.9A15.C6.o3.np	Method	AAT/NAP
Start	6710	End	9055
GI	464900	Score	155
Exons	6710..6736, 8858..9055		
GI Descrip.	PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR gi|539008|pir||S39476 kinase-like transmembrane protein TMKL1 precursor - Arabidopsis thaliana gi|313190|emb|CAA51385| (X72863) TMKL1 [Arabidopsis thaliana]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1922	Strand	+
Start	21445	End	26667
Name	OJ990323_29.9A15.C6.o6.gs	Method	GENSCAN
Start	21445	End	26667
GI	none	Score	.65
Exons	21445..21714, 22239..22309, 22684..22738, 23539..23721, 24976..25284, 25795..26667		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1922	Strand	+
Start	21445	End	26667
Name	OJ990323_29.9A15.C6.o6.np	Method	AAT/NAP
Start	24480	End	26664
GI	3688170	Score	414
Exons	24480..24521, 25786..26142, 26248..26505, 26563..26664		

GI Descrip. (AL031804) putative protein [Arabidopsis thaliana]

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1922	Strand	+
Start	21445	End	26667
Name	OJ990323_29.9A15.C6.o5.gp	Method	AAT/GAP
Start	24736	End	25227
GI	none	Score	949
Exons	24736..25227		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1923	Strand	+
Start	32048	End	34501
Name	OJ990323_29.9A15.C6.o7.np	Method	AAT/NAP
Start	30745	End	32199
GI	6907088	Score	950
Exons	30745..30882, 31058..31295, 31793..32199		
GI Descrip.	(AP001129) hypothetical protein [Oryza sativa]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1923	Strand	+
Start	32048	End	34501
Name	OJ990323_29.9A15.C6.o7.gp	Method	AAT/GAP
Start	31555	End	31747
GI	5667165	Score	349
Exons	31555..31747		
GI Descrip.	5670155/gb|AF161269.1|AF161269 4.0e-86 Oryza sativa subsp. japonica BAC clone 34K24, complete sequence		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1923	Strand	+
Start	32048	End	34501
Name	OJ990323_29.9A15.C6.o8.gs	Method	GENSCAN
Start	32048	End	32470
GI	none	Score	.86
Exons	32048..32470		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1923	Strand	+
Start	32048	End	34501
Name	OJ990323_29.9A15.C6.o8.np	Method	AAT/NAP
Start	32184	End	34501
GI	5734635	Score	173
Exons	32184..32312, 32364..32744, 34460..34501		
GI Descrip.	(AP000391) hypothetical protein [Oryza sativa]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1924	Strand	+
Start	36130	End	37045
Name	OJ990323_29.9A15.C6.o9.gs	Method	GENSCAN
Start	36130	End	37045
GI	none	Score	.82
Exons	36130..36132, 36354..36536, 36881..37045		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1925	Strand	-
Start	301	End	3605

Name	OJ990323_29.9A15.C6.o1.gs	Method	GENSCAN
Start	301	End	3605
GI	none	Score	.47
Exons	301..357, 733..816, 1139..1241, 3178..3605		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1925	Strand	-
Start	301	End	3605
Name	OJ990323_29.9A15.C6.o1.np	Method	AAT/NAP
Start	301	End	3599
GI	3688172	Score	355
Exons	301..357, 393..515, 918..1238, 3178..3599		
GI Descrip.	(AL031804) putative protein [Arabidopsis thaliana]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1926	Strand	-
Start	8254	End	12130
Name	OJ990323_29.9A15.C6.o2.np	Method	AAT/NAP
Start	8254	End	12130
GI	5734703	Score	499
Exons	8254..8771, 12092..12130		
GI Descrip.	(AC008075) Similar to gb|X90982 phosphoenolpyruvate carboxylase (ppc1) from Solanum tuberosum. [Arabidopsis thaliana]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o1.gp	Method	AAT/GAP
Start	12030	End	13845
GI	LIB3431-045-P1-N1-A10	Score	817
Exons	12030..12139, 13502..13845		
GI Descrip.	'5441876/dbj|AP000367.1|AP000367 0.0e+00 Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)'		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o4.gs	Method	GENSCAN
Start	12346	End	13443
GI	none	Score	.76
Exons	12346..12504, 12956..13033, 13100..13258, 13441..13443		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o5.gs	Method	GENSCAN
Start	13670	End	19898
GI	none	Score	.49
Exons	13670..13830, 13981..14183, 14188..14235, 14299..14430, 14677..14774, 14801..14926, 15019..15277, 15354..15652, 15744..16154, 16239..16575, 16681..16831, 17270..19053, 19126..19898		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o4.np	Method	AAT/NAP

Start	13949	End	19445
GI	5441880	Score	4700
Exons	13949..14183, 14299..14430, 14677..14774, 15019..15277, 15354..15652, 16239..16575, 16681..16831, 17390..17705, 17964..17995, 18440..19445		
GI Descrip.	(AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o2.gp	Method	AAT/GAP
Start	15027	End	15526
GI	LIB3475-007-P1-K1-G8	Score	797
Exons	15027..15277, 15354..15526		
GI Descrip.	'5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]'		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o3.gp	Method	AAT/GAP
Start	18410	End	18841
GI	5701669	Score	845
Exons	18410..18841		
GI Descrip.	5441880/dbj|BAA82378.1| 5.0e-75 (AP000367) EST C28952(C62945) corresponds to a region of the predicted gene.; Similar to maize transposon MuDR mudrA protein. (AC003981) [Oryza sativa]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o5.np	Method	AAT/NAP
Start	19458	End	20515
GI	6721543	Score	168
Exons	19458..19574, 20387..20515		
GI Descrip.	(AP001073) hypothetical protein [Oryza sativa]		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1927	Strand	-
Start	12346	End	20515
Name	OJ990323_29.9A15.C6.o4.gp	Method	AAT/GAP
Start	20351	End	20501
GI	7406_1.R1084	Score	230
Exons	20351..20501		
GI Descrip.	'1122315/emb|CAA63901| 7.0e-10 (X94191) heat shock protein 17.0 [Pennisetum glaucum]'		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1928	Strand	-
Start	25936	End	26273
Name	OJ990323_29.9A15.C6.o6.gp	Method	AAT/GAP
Start	25936	End	26273
GI	uC-osflcyp168g07a1	Score	616
Exons	25936..26273		

GI Descrip. '5670155/gb|AF161269.1|AF161269 4.0e-86 Oryza sativa subsp. japonica BAC clone 34K24, complete sequence'

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1929	Strand	-
Start	28293	End	29231
Name	OJ990323_29.9A15.C6.o7.gs	Method	GENSCAN
Start	28293	End	29231
GI	none	Score	.63
Exons	28293..28483, 28498..28653, 28964..29231		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1930	Strand	-
Start	29854	End	32783
Name	OJ990323_29.9A15.C6.o1.tm	Method	TBLASTX:Maize
Start	3210	End	3649
GI	none	Score	86
Exons	3210..3296, 3210..3281, 3338..3418, 3339..3377, 3369..3419, 3405..3644, 3421..3573, 3629..3649		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1930	Strand	-
Start	29854	End	32783
Name	OJ990323_29.9A15.C6.o2.ts	Method	TBLASTX:Soybean
Start	8242	End	8504
GI	none	Score	53
Exons	8242..8334, 8243..8296, 8332..8418, 8348..8407, 8412..8504		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1930	Strand	-
Start	29854	End	32783
Name	OJ990323_29.9A15.C6.o2.tc	Method	TBLASTX:Cress
Start	8858	End	9052
GI	none	Score	65
Exons	8858..8914, 8918..9052		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1930	Strand	-
Start	29854	End	32783
Name	OJ990323_29.9A15.C6.o4.tm	Method	TBLASTX:Maize
Start	8873	End	9052
GI	none	Score	257
Exons	8873..9052, 8874..9041, 8968..9048		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1930	Strand	-
Start	29854	End	32783
Name	OJ990323_29.9A15.C6.o1.tw	Method	TBLASTX:Wheat
Start	18192	End	18590
GI	none	Score	79
Exons	18192..18386, 18240..18386, 18271..18390, 18384..18581, 18396..18590		

Seq. No.	921	Seq. ID	OJ990323_29.9A15.C6
Gene No.	1930	Strand	-
Start	29854	End	32783
Name	OJ990323_29.9A15.C6.o2.tm	Method	TBLASTX:Maize